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Qy      481 ACCTGTGTCTGTATGAGAGAGAGTGAAGAGCCCTCATCATCATCAGCTCTCATCG 540
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Qy      661 GCATGTACTTTCGATGAGAGATGAGGTGTCCGGGGCTCCAGGCTTACGATCGGGGC 720
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RESULT 2
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DEFINITION Sequence 18 from patent US 6274140.
ACCESSION  ARI64500
VERSION     ARI64500.1 GI:16237548
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 1277)
AUTHORS     Jones S. and Tang J.
TITLE       Calcium independent cytosolic phospholipase A2/B enzymes
JOURNAL     Patent: US 6274140-A 18 14-AUG-2001;
            Location/Qualifiers
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Query Match      100.0%; Score 1277; DB 6; Length 1277;
Best Local Similarity 100.0%; Pred. No. 6e-252;
Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      181 TCCACCTCCAGCCCATTTCTCTCTGTGGGCTGTGAGCTTCTCTGGGACAGAGTC 240
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Qy      421 GGGGCCCCGAGACAGAGCTTATCTGTGGGCTCCATGAGGAGCGAGAGCCGACCCAGACC 480
Db      421 GGGGCCCCGAGACAGAGCTTATCTGTGGGCTCCATGAGGAGCGAGAGCCGACCCAGACC 480
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Db      481 ACCTGTGTCTGTATGAGAGAGTGAAGAGCCCTCATCATCATCAGCTCTCATCG 540
Qy      541 CCATCGAAGAGGCTCTGGGCTGTGGCCACCAAGACCTGTTTGACTGGGTGGCGGACCA 600
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Qy      601 GCACTGAGGAGCATCTGGGCTGTGGCCATCTGACAGTATGCTCATGAGCCTATAGTGGCG 660
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Qy      661 GCATGTACTTTCGATGAGAGATGAGGTGTCCGGGGCTCCAGGCTTACGATCGGGGC 720
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Qy      721 CCTGTGAGAGATTCTGTAGCGGAGTTTGGGAGCACCAGAGATGACGAGCTCAGAG 780
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DB 841 TCCGGAAGTACGATGCTCCAGAACTGTCCGGGAGCTCGTTCAACGAAAGTTAAC 900
QY 901 TCAAGCCTCAGCTCAGCCCTCAGACCAAGCTGTGTGGCGGGCGGCCGAAAGCGGG 960
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QY 961 CAGCTCTACTTACTTCTCCGACCCCAATGGGGCTTCTGAGACGCTGTGGCTTGGCCACA 1020
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DEFINITION Sequence 18 from patent US 6645736.
ACCESSION AR429678
VERSION AR429678.1 GI:40189996
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1277)
AUTHORS Jones, S. and Tang, J.
TITLES Calcium independent cytosolic phospholipase A2/B enzymes
JOURNAL Patent: US 6645736-A 18 11-NOV-2003;
FEATURES
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Query Match 100.0%; Score 1277; DB 6; Length 1277;
Best Local Similarity 100.0%; Pred. No. 6e-252;
Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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[illegible]

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| Query March | 69.4% | Score 885.8; | DB 6; | Length 2112; |
| Best Local | 99.8% | Pred. No. 1.2e-171; | | |
| Matches 887; | Conservative 2; | Indels 0; | Gaps 0; | |
| | | Mismatches | | |

Dy 389 CACAGACTACAGGATCTCATGCACATTCACGGGCCCGAAGCAGGCTTCACTCGGG 448
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Dδ 1224 CAGACAATTACAGGATCTCATGCACATTCACGGGCCCGAAGCAGGCTTCACTCGGG 1283

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| DY | 449 | CCTCATGAGGGACGAGAAAGCCGATCCACGCATCACC156115621563A1564A1565GAAGAGAGT | 508 |
| Db | 1284 | CTCCATGAGGGA CGAGAGCGGACCCAGACCACTCTGTGCCCTTGATGGAAGGAGAT | 1343 |

| QY | 509 | GAAGAGCCTCATCATCAGCTCTCTCATGCGCATCGAAGAGCCTCGGGGTGTGGCCAC | 568 |
|------|---|---|-----|
| 1344 | GAAGAGCCTCATCATCAGCTCTCTCATGCGCATCGAAGAGCCTCGGGGTGTGGCCAC | 1403 | |

QY 569 CAAAGACCTGTTTGA CTGGGTGGCGG CACAGCACTGAGG CATTCTTGCCCTTGCCCAT 628
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QY 629 TCTGCACAGTAAGTCCATG6CCTACATGCGCGGATGTACTTTCGCATGAAGGATGAGGT 688
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QY 689 GTTCCGGGCTCCAGAGCCCTACGAGTCGGGGCCCTCGAGAGATTCTGAAACGGAGTT 748
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Oy GTCGACCGGAGCGCGGTGAACTCCACTCTCTCCGAATACGATGCTCCAGAACTGT 868
 809
 1664 GTTTGACCTGGGACGCTGGGCTGAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1703

| | | |
|------|--|------|
| OY | CGGGAGCCTCGTTTCAACGAGAACGTAACTCAGGCGCTCCAGCTCAGCCCTCAGACCA | 928 |
| 869 | | |
| 1704 | CGGGAGCCTCGTTTCAACGAGAACGTAACTCAGGCGCTCCAGCTCAGCCCTCAGACCA | 1753 |

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| Db | 1884 | CAATGAGTAACATATAGGAACCTGATCCGCAAGGGTCAGGCCAA | CAAGGTGAAGAACTCTC | 1943 |
| QY | 1109 | CATCGTGTCTCCCTGGGGACAGGGAAGTCCCA | CAAGTGCCTGTGA | 1168 |
| Db | 1944 | CATCGTGTCTCCCTGGGGACAGGGAAGTCCCA | CAAGTGCCTGTGA | 2003 |
| QY | 1169 | CTTCCGTCACAGCAACCCCTGGGAGCTGGCC | CAAGACTGTTTTTGGGGCCAAAGAACTGGG | 1228 |
| Db | 2004 | CTTCCGTCACAGCAACCCCTGGGAGCTGGCC | CAAGACTGTTTTTGGGGCCAAAGAACTGGG | 2063 |
| QY | 1229 | CAAAATGATGTGATCTGTTGCAACGATCC | CAAGACGGGCGGCCGGAATTC | 1277 |
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| | | | PAT 17-OCT-2001 |

KEYWORDS

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| ORGANISM | Unknown. |
| | Unclassified. |
| REFERENCE | 1 (pages 1 to 2112) |

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| TITLE | Calcium independent cytosolic phospholipase A2/B enzymes |
| JOURNAL | Patent: US 6274140-A 22 14-AUG-2001; |
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| Best Local Similarity | 99.8% | Pred. No. 1,2e-11; | | |
| Matches 887; Conservative | 0; | Mismatches 2; | Indels 0; | Gaps 0; |

Qy 389 CACGAACTACAGGATCTCATGCACATCTCACGGGCCCCGGAAGCCAGCGTTTCATCTCTGGG 448

Db 1,234 CACACAACTACAGGATCTCATGCACATCTCACGGGCCCCGGAAGCCAGCGTTTCATCTCTGGG 1,283

QY 449 CTCCTATGAGGAGCAGAAAGCGGCCACGACCACTCTGTCTGTGATGAGAGAGAGT 508

Db 1284 CTCCTATGAGGAGCAGAAAGCGGCCACGACCACTCTGTCTGTGATGAGAGAGAGT 1343

QY 509 GAAAGGCTCATCATCCAGCTCCTCATCGGCATCGAAGGCTTGGGTGTGGCCAC 568

Db 1344 GAAAGGCTCATCATCCAGCTCCTCATCGGCATCGAAGGCTTGGGTGTGGCCAC 1403

QY 569 CAAGAGCCTGTTGACTGCGTGGCGGGCACCAGACCTGGAGGCATCCTGGCCCTGGCCAT 628

Dh 1464 CAGGAGCCTGTTTGCATCTGGATGGCGGGGACCCAGGACCTGGAGGCATCCTGGCCCTGGCCAT 1463

629 TCTGCACAGTAAGTCCATGGCCATCGCGGCATGTACTTTCGCATGAGATGAGGT 688
1464 TCTGCACAGTAAGTCCATGGCCATCGCGGCATGTACTTTCGCATGAGATGAGGT 1523

| | | | |
|----|------|--|------|
| QY | 689 | GTTCCGGGAGCTCCAGGCGCTACGAGTCGGGGCCCTGAGAGAGTTCCTGAACGGGAGTT | 748 |
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1374 CATCGAAGAGGCTTGGGCTGCTGACCAAGAGACTGTTGATGCTGGTGGCGGACCG 1433
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1914 TCAGGCAACAAGATGAGAACTCTCATGATGATGATGATGATGATGATGATGATGATGAT 1973
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1974 ACAAGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2033
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RESULT 8
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LOCUS ARA64501 2109 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 20 from patent US 6274140.
ACCESSION ARA64501
VERSION ARA64501.1 GI:16237549
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2109)
AUTHORS Jones, S. and Tang, J.
TITLE Calcium independent cytosolic phospholipase A2/B enzymes
JOURNAL Patent: US 6274140-A 20 14-AUG-2001.
FEATURES
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ORIGIN

Query Match 69.4%; Score 885.6; DB 6; Length 2109;
Best Local Similarity 97.9%; Pred. No. 1.3e-171;
Matches 897; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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1194 GACTCTACATCTCTGACCTCCAAATCGGCAAACTACAGAGATCTCATGACATCTCAGC 1253
422 GCGCCGGAAGCCAGGCTTCACTCTGGGCTTCATGAGGAGCAGAGAGCGGACCAAGCA 481
1254 GCGCCGGAAGCCAGGCTTCACTCTGGGCTTCATGAGGAGCAGAGAGCGGACCAAGCA 1313
482 CCTGCTGTGCTGATGAGAGAGATGAGTGAAGGCTTCATCATCATCAGCTCTCATCGC 541
1314 CCTGCTGTGCTGATGAGAGAGATGAGTGAAGGCTTCATCATCATCAGCTCTCATCGC 1373
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602 CATGAGAGGCTCTGGGCTGTGGCCACCAAGACTGTTGACTGGGCTGGCGGACCAAG 661
1434 CATGAGAGGCTCTGGGCTGTGGCCACCAAGACTGTTGACTGGGCTGGCGGACCAAG 1493
662 CATGATCTTGGATGAGAGATGAGTGTTCGGGGCTTCCAGGCTTCAAGTGGGGCC 721
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722 CCTGAGAGGATCTTGAAGCGGAGTGTGGGAGCACCAAGATGACGGAAGCTTCAGGA 781
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2034 GACTGTTTTGGGGCCCAAGAACTGGGCAAGATGATGATGATGATGATGATGATGATGATGAT 2093
1262 CGGGCGGCGGGAATTC 1277
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| LOCUS | AR429679 | | | | |
| DEFINITION | Sequence 20 from patent US 6645736. | | | | |
| ACCESSION | AR429679 | | | | |
| VERSION | AR429679.1 | GI:40189997 | | | |
| KEYWORDS | | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unknown. | | | | |
| REFERENCE | 1 (bases 1 to 2109) | | | | |
| AUTHORS | Jones, S. and Tang, J. | | | | |
| TITLE | Calcium independent cytosolic phospholipase A2/B enzymes | | | | |
| JOURNAL | Patent: US 6645736-A 20 11-NOV-2003; | | | | |
| FEATURES | Location/Qualifiers | | | | |
| source | 1..2109 | | | | |
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| Query Match | 69.4%; Score 885.6; DB 6; Length 2109; | | | | |
| Best Local Similarity | 97.9%; Pred. No. 1.3e-171; | | | | |
| Matches 897; Conservative | 0; Mismatches 19; Indels 0; Gaps 0; | | | | |
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| Db | 1194 GACTCTTACATTTCTTACGCTCCCAAAATGCGCAAACTACAGATCTCAGCAATCTCACG | 1253 | | | |
| QY | 422 GGCCCGAAGCCAGCGCTTCATCTGGCTCCATGAGGACGAGAACGCCAGCA | 481 | | | |
| Db | 1254 GGCCCGAAGCCAGCGCTTCATCTGGCTCCATGAGGACGAGAACGCCAGCA | 1313 | | | |
| QY | 482 CCTGCTGTGCTGATGAGGAGAGGAAAGCCTCATCATCATGCTCTTCATGCG | 541 | | | |
| Db | 1314 CCTGCTGTGCTGATGAGGAGAGGAAAGCCTCATCATCATGCTCTTCATGCG | 1373 | | | |
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| Db | 1374 CATGAGAAAGCCTTGGGTGTGGCCACCAAGACTGTTTGACTGTGGGGGACAG | 1433 | | | |
| QY | 602 CACTGAGAGCATCTGGGCTTGGCCATTTGCAACGTAAAGTCCATAGGCTACATCGCGG | 661 | | | |
| Db | 1434 CACTGAGAGCATCTGGGCTTGGCCATTTGCAACGTAAAGTCCATAGGCTACATCGCGG | 1493 | | | |
| QY | 662 CATGACTTTGCGATGAAGATGAGGTGTTCCGGGCTCCAGGCCCTACAGTCCGGGCT | 721 | | | |
| Db | 1494 CATGACTTTGCGATGAAGATGAGGTGTTCCGGGCTCCAGGCCCTACAGTCCGGGCT | 1553 | | | |
| QY | 722 CCTGAGAGAGTTCCTGAAGCCGGAGTTGGGGACACACCAAGATGACGAGCTTACGAA | 781 | | | |
| Db | 1554 CCTGAGAGAGTTCCTGAAGCCGGAGTTGGGGACACACCAAGATGACGAGCTTACGAA | 1613 | | | |
| QY | 782 ACCCAAGGTGATGCTGACAGGGACACTGCTGACCGGAGCGCGGTAACTCCACTCTT | 841 | | | |
| Db | 1614 ACCCAAGGTGATGCTGACAGGGACACTGCTGACCGGAGCGCGGTAACTCCACTCTT | 1673 | | | |
| QY | 842 CCGGAATCAAGATGCTCCAGAACTGTCCGGAGCGCTGTTTCAACACGAAAGTTAACT | 901 | | | |
| Db | 1674 CCGGAATCAAGATGCTCCAGAACTGTCCGGAGCGCTGTTTCAACACGAAAGTTAACT | 1733 | | | |
| QY | 902 CAGGCTTCAAGCTACGCCCTTCAGACCAAGCTGTGGCGGGCGGCCGAGAGCGGGGCT | 961 | | | |
| Db | 1734 CAGGCTTCAAGCTACGCCCTTCAGACCAAGCTGTGGCGGGCGGCCGAGAGCGGGGCT | 1793 | | | |
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| Db | 1794 AGCTCTTACCTTACCTTCGACCCCAATGAGCGCTTCTCGACCGGTGGGCTGTGGCCACAA | 1855 | | | |
| QY | 1022 CCCCAAGCTGATGCTGACGAGCCGAGATCCATAGTACATCAGACCTGATCCGCAAGG | 1081 | | | |
| Db | 1854 CCCCAAGCTGATGCTGACGAGCCGAGATCCATAGTACATCAGACCTGATCCGCAAGG | 1913 | | | |
| QY | 1082 TCAGGCAACAAGATGAAAGAACTCTTCATGCTGTCTTCCCTGGGACAGGAGGTCCC | 1141 | | | |

Db 1914 TCAGGCCAACAGGTGAAGAAACTCTCATGTTGTCTCCCTGGGGACAGGGAATCCCC 1973

QY 1142 ACAAGTCCCTGTGACCTGTGTGATGTCCTTCCGTCACAGCAACCCCTGGAGCTGGCCAA 1201

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Db 2034 GACTGTTTTTGGGGCCAAAGAACTGGGCAAGATGGTGTGACTGTTGCCAGATCCAGA 2093

QY 1262 CGGCGGCGCGAATTC 1277

Db 2094 CGGCGGCGCGAATTC 2109

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| LOCUS | CR456543 |
| DEFINITION | Homo sapiens PLA2G6 full length open reading frame (ORF) cDNA clone (cDNA clone C22ORF:PGEM.PLA2G6.V4). |
| ACCESSION | CR456543 |
| VERSION | CR456543.1 |
| KEYWORDS | CDNA; chromosome 22; ORF. |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |
| AUTHORS | Collins,D.B., Wright,C.L., Edwards,C.A., Davis,M.P., Grixham,J.A., Huckle,C.G., Goward,M.B., Aguado,B., Mallya,M., Mokrab,Y., Huckle,E.J., Beare,D.M. and Dunham,I. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (UK-May-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript Sanger Institute name : PGEM.PLA2G6.V4 |
| COMMENT | Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see http://www.sanger.ac.uk/Hgp/Chr22/ . |
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| | /chromosome="22" |
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| | KDLDMVAGTSGIILATILHRSKMAVNGMFRMKDQVYFSGRPFTESGILEFPLKQEFEGHTMTVRKPKVMTGLSDRQPAELHFNVDYAPETVSRFNQNNVLEPPAQPSDQVMTWRARSSGAATYFRPNGRFPLDGLLANPPLDAMTEIHEYNODLIRGQANAKVGLSLVLSIGTGRSPQVPTCVDVPRSPNPELATIVEGAKSLGMVVDCCDPDQGRVAVRARACMCMVGIOYFRINPQLGDTIMLDEVSDTVLNAALMETSIVYIEHRECFQNLQGLLSP" |

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| Query March | 68.6% | Score 876.2 | DB 9.2 | Length 2600 | |
| Best Local Similarity | 99.7% | Pred. No. 1.1e-169 | | | |
| Matches 878 | Conservative 0 | Mismatches 3 | Indels 0 | Gaps 0 | |
| QY | 392 | AGAACTACAGGATCTCATGCAATCTCAACGGGCGCGGAGGCGAGCTTCATCTGGGCTC | 451 | | |
| Db | 1411 | AGAACTACAGGATCTCATGCAATCTCAACGGGCGCGGAGGCGAGCTTCATCTGGGCTC | 1470 | | |
| QY | 452 | CATAGAGGACGAGAAAGCGGACCCCAAGACCACTCTGTGCTCGATGGAGAGAGACTGA | 511 | | |
| Db | 1471 | CATAGAGGACGAGAAAGCGGACCCCAAGACCACTCTGTGCTCGATGGAGAGAGACTGA | 1530 | | |
| QY | 512 | AGGCTCATCATCATCCAGCTCTCATGCGCATGGAGAGAAAGGCTCGGGTGTGGCCACCA | 571 | | |
| Db | 1531 | AGGCTCATCATCATCCAGCTCTCATGCGCATGGAGAGAAAGGCTCGGGTGTGGCCACCA | 1590 | | |
| QY | 572 | GGACCTGTTTGACTGGGTGTGGGCGACGAGCACTGGAGCAATCTGGCCCTGGCCATTCT | 631 | | |
| Db | 1591 | GGACCTGTTTGACTGGGTGTGGGCGACGAGCACTGGAGCAATCTGGCCCTGGCCATTCT | 1656 | | |
| QY | 632 | GCACAGTAAGTCCATGCGCTCAATGCGCGCAATGTACTTTGGCATGAAGATGAGCTTT | 691 | | |
| Db | 1651 | GCACAGTAAGTCCATGCGCGCTCAATGCGCGCAATGTACTTTGGCATGAAGATGAGCTTT | 1710 | | |
| QY | 692 | CCGGGGGCTCCAGGGGCTCTACGATGGGGGCGCTGGAGAGTTCCGAAAGCGGAGTTGG | 751 | | |
| Db | 1711 | CCGGGGGCTCCAGGGGCTCTACGATGGGGGCGCTGGAGAGTTCCGAAAGCGGAGTTGG | 1770 | | |
| QY | 752 | GGAGCACAACCAAGATGACGGAAGTACAGGAAACCAAGGTGATGCTGACAGGAGCACTGTC | 811 | | |
| Db | 1771 | GGAGCACAACCAAGATGACGGAAGTACAGGAAACCAAGGTGATGCTGACAGGAGCACTGTC | 1830 | | |
| QY | 812 | TGACCGGCAAGCGGCTGAATCTCACCTTTCCGGAATGAGATGCTCCAGAACTGTCCG | 871 | | |
| Db | 1831 | TGACCGGCAAGCGGCTGAATCTCACCTTTCCGGAATGAGATGCTCCAGAACTGTCCG | 1890 | | |
| QY | 872 | GGAGCCCTCGTTTCAACCAAGAGTTTAACCTGAGGCTCCAGCTCAGGCCCTCAGACCACT | 931 | | |
| Db | 1891 | GGAGCCCTCGTTTCAACCAAGAGTTTAACCTGAGGCTCCAGCTCAGGCCCTCAGACCACT | 1956 | | |
| QY | 932 | GGTGTGGCGGGCGGCGCCGAGCAGCGGGGAGCTCTTAATCTTCCGACCCTGAGGCGG | 991 | | |
| Db | 1951 | GGTGTGGCGGGCGGCGCCGAGCAGCGGGGAGCTCTTAATCTTCCGACCCTGAGGCGG | 2010 | | |
| QY | 992 | CTTCTCTGAGCGGTGGGCTGTGGCCCAACACCCACGCTGATGTCATGACCGAGATCCA | 1051 | | |
| Db | 2011 | CTTCTCTGAGCGGTGGGCTGTGGCCCAACACCCACGCTGATGTCATGACCGAGATCCA | 2070 | | |
| QY | 1052 | TGAGTATCAATCAGGACCTGATCCCAAGAGGTCAAGGCAACAAAGGTGAAGAACTCTCAT | 1111 | | |
| Db | 2071 | TGAGTATCAATCAGGACCTGATCCCAAGAGGTCAAGGCAACAAAGGTGAAGAACTCTCAT | 2130 | | |
| QY | 1112 | CGTTGTCTCCCTGGGGACAGGAGAGTCCCAACAATGCTGTGACTGTGTGATGTCTT | 1171 | | |
| Db | 2131 | CGTTGTCTCCCTGGGGACAGGAGAGTCCCAACAATGCTGTGACTGTGTGATGTCTT | 2190 | | |
| QY | 1172 | CCGTCCAGCAACCCCTGGGAGCTGGCCAGAACTGTTTTGGGGCCAAAGAACTGGGCAA | 1231 | | |
| Db | 2191 | CCGTCCAGCAACCCCTGGGAGCTGGCCAAAGAACTGTTTTGGGGCCAAAGAACTGGGCAA | 2250 | | |
| QY | 1232 | GATGTGTGTGATCTGTTGACAGGATCCAGAGCGGCGCGCGG | 1272 | | |
| Db | 2251 | GATGTGTGTGATCTGTTGACAGGATCCAGAGCGGCGCGCGG | 2291 | | |

| RESULT 11 | | | | | |
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| VERSION | AX834211.1 | GI:39920346 | | | |
| KEYWORDS | | | | | |
| SOURCE | Homo sapiens (human) | | | | |

| | |
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| ORGANISM | Homo sapiens |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |
| TITLE | 1 Ibogaï,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,... Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Maubuo,Y. Full-length cDNA sequences |
| JOURNAL | Patent: EP 1347046-A 1335 24-SEP-2003; |
| FEATURES | Research Association for Biotechnology (JP) |
| source | Location/Qualifiers 1..2755 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" |
| ORIGIN | |
| Query Match | 68.6%; Score 876.2; DB 6; Length 2755; |
| Best Local Similarity | 99.7%; Pred. No. 1.1e-169 |
| Matches | 878; Conservative 3; Indels 0; Gaps 0; |
| QY | 392 AGAAGCTACAGAGTCTCATGCAATCTCAACGGGCGCGAAGGACAGCTTCATCTGGGGCTC 451 |
| DB | 1016 AGAAGCTACAGAGTCTCATGCAATCTCAACGGGCGCGAAGGACAGCTTCATCTGGGGCTC 1075 |
| QY | 452 CATGAGGGAGCAGAGAGGCGGACCCACGACCACTGTCTGTCTGTAGTGGAGGAGAGTGA 511 |
| DB | 1076 CATGAGGGAGCAGAGAGGCGGACCCACGACCACTGTCTGTCTGTAGTGGAGGAGTGA 1135 |
| QY | 512 AGGCTCTCATCATCATCCAGCTCTCATCTGCGCATGAGAGAGGCTCTGGGTGGACACCA 571 |
| DB | 1136 AGGCTCTCATCATCATCCAGCTCTCATCTGCGCATGAGAGAGGCTCTGGGTGGACACCA 1195 |
| QY | 572 GGAAGCTGTTGACATGGGTGGGCGGACACAGACATGAGAGCATCTGTGGCCCTGGCCATCT 631 |
| DB | 1196 GGAAGCTGTTGACATGGGTGGGCGGACACAGACATGAGAGCATCTGTGGCCCTGGCCATCT 1255 |
| QY | 632 GCACAGTAAAGTCCATGCGCTTACATGCGGGGCAATGTAATTTGCAATGAAGATGAGTGT 691 |
| DB | 1256 GCACAGTAAAGTCCATGCGCTTACATGCGGGGCAATGTAATTTGCAATGAAGATGAGTGT 1315 |
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| DB | 1316 CCGGGGGCTCCAGAGGCTTACGAGTGGGGGCGCTGAGAGAGTTCGTAAGCGGAGTTGG 1375 |
| QY | 752 GGAACACACCAAGATGACGAGCGTCAGAGAAACCAAGGTGATGTGACAGGAGACACTGT 811 |
| DB | 1376 GGAACACACCAAGATGACGAGCGTCAGAGAAACCAAGGTGATGTGACAGGAGACACTGT 1435 |
| QY | 812 TGACCGGACAGCGGCTGAATCTTCACTCTTCGGGAATGACATGCTCCAGAACTGTGCG 871 |
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| DB | 1736 CGTTGTCTCTCTGGGGACAAGGAGTCCCAACAAGTCTGTGACCTGTGTGAGATGCTT 1795 |

REFERENCE
AUTHORS
TITLE

1
Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.

JOURNAL Patent: WO 02068579-A 16461 06-SEP-2002;
PE Corporation (NY) (US)

| FEATURES | Location/Qualifiers |
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| source | 1. .3223 |

ORIGIN

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| Query Match% | 68.6% | Score 876.2 | DB 6 | Length 3223 |
| Best Local Similarity | 99.7% | Pred. No. 1e-169 | | |
| Matches 878 | Conservative 0 | Mismatches 3 | Indels 0 | Gaps 0 |

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| QY | 392 | AGAACTACAGGATCTCAGGACATCTCAAGGACCAGGAAGCCAGGGTTCATCTTGAGCTC | 451 |
| Db | 1483 | AGAACTACAGGATCTCATTGCAATCTCAAGGACCAGGAAGCCAGGGTTCATCTTGAGCTC | 1544 |
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| Db | 1543 | CATGAGGACGAGAGCGGACCACAGACCACTGTGTGCTCGATGAGAGAGTGA | 1602 |
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| Db | 1663 | GGACCTGTTTACCTGGGTGGCGGGACACAGCACTGGAAGCATCTGTGACCCTTGACCATCT | 1722 |
| QY | 632 | GCAACGTAAGTCCATGAGCTTACATGCGGGCACATGTACTTTCGCATGAAGATGAGTGT | 691 |
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| Db | 1843 | GGAACACACACAAAGATGACGAGCTCAGAGAAACCAGGATGATGTGACAGGGACACTGTG | 1902 |
| QY | 812 | TGACCGGACGCGGCTGAACTTCACCTCTTCGGAACTACGATGCTCCAGAAACTGTGCG | 871 |
| Db | 1903 | TGACCGGACGCGGCTGAACTTCACCTCTTCGGAACTACGATGCTCCAGAAACTGTGCG | 1962 |
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ORIGIN /gene="DKFZp434A102"

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Best Local Similarity 99.7%; Pred. No. 1e-169;
Matches 878; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 392 AGAAGTCAAGGATCATGACATCTCAAGGAGCCCGAAGCCAGCCGTTCACTCTGGGCTC 451
DB 1483 AGAAGTCAAGGATCATGACATCTCAAGGAGCCCGAAGCCAGCCGTTCACTCTGGGCTC 1542
QY 452 CATGAGGAGCAGAGAGCGAGCCACGACCACTGCTGTGCTGATGAGAGAGTGA 511
DB 1543 CATGAGGAGCAGAGAGCGAGCCACGACCACTGCTGTGCTGATGAGAGAGTGA 1602
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DB 1603 AGGCTCATCATCATCCAGCTCTCATGCGCATGAGAGGCTCGGGTGTGCCACCA 1662
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QY 1172 CCGTCCAGCAACCCCTGGAGCTGGCCAAAGACTGTTTTTGGGGCCAAAGAACTGGGCA 1231
DB 2263 CCGTCCAGCAACCCCTGGAGCTGGCCAAAGACTGTTTTTGGGGCCAAAGAACTGGGCA 2322
QY 1232 GATGTGTGTGACTGTTTGCAGGATCCAGACGAGCGGCGG 1272
DB 2323 GATGTGTGTGACTGTTTGCAGGATCCAGACGAGCGGCGGCTG 2363
```

Search completed: December 16, 2004, 13:54:14
Job time : 5528 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 08:16:24 ; Search time 678 Seconds
(without alignments)
9887.184 Million cell updates/sec

Title: US-10-612-668-18

Perfect score: 1277
Sequence: 1 GAATCTTAGCCCGCCGATTC 1277

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001s:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 1277 | 100.0 | 1277 | 2 | AAT68824 |
| 2 | 1277 | 100.0 | 1277 | 6 | ABV73009 |
| 3 | 885.8 | 69.4 | 2112 | 2 | AAT68826 |
| 4 | 885.8 | 69.4 | 2112 | 6 | ABV73011 |
| 5 | 885.6 | 69.4 | 2109 | 2 | AAT68825 |
| 6 | 885.6 | 69.4 | 2109 | 2 | AAT68825 |
| 7 | 876.2 | 68.6 | 2755 | 11 | ADM02650 |
| 8 | 876.2 | 68.6 | 3240 | 6 | AAD42941 |
| 9 | 876.2 | 68.6 | 3240 | 12 | ADO19775 |
| 10 | 876 | 68.6 | 3215 | 10 | ADD93466 |
| 11 | 809.8 | 63.4 | 2392 | 4 | AAH41129 |
| 12 | 708 | 55.4 | 2935 | 2 | AAT05842 |
| 13 | 708 | 55.4 | 2935 | 2 | AAT44578 |
| 14 | 708 | 55.4 | 2935 | 2 | AAT59199 |
| 15 | 708 | 55.4 | 2935 | 2 | AAT68827 |
| 16 | 708 | 55.4 | 2935 | 2 | AAV64840 |
| 17 | 708 | 55.4 | 2935 | 6 | ABV73007 |
| 18 | 698.6 | 54.7 | 3273 | 10 | ADB53536 |
| 19 | 698.6 | 54.7 | 3273 | 12 | ADP72870 |
| 20 | 472.2 | 37.0 | 70000 | 6 | AAD42934 |
| 21 | 268 | 21.0 | 411 | 9 | ACH47835 |

| | | | | | | |
|----|-------|------|--------|----|-------------|---------------------------------|
| 22 | 223 | 17.5 | 2634 | 4 | ABU11615 | ABU11615 Drosophila |
| 23 | 157.8 | 12.4 | 5498 | 4 | ABU11614 | ABU11614 Drosophila |
| 24 | 131.6 | 10.3 | 348 | 4 | AAH98967 | AAH98967 Human EST |
| 25 | 60 | 4.7 | 60 | 6 | ABN36726 | ABN36726 Human sp1 |
| 26 | 60 | 4.7 | 60 | 6 | ABN59116 | ABN59116 Human sp1 |
| 27 | 53.6 | 4.2 | 2000 | 8 | ADA71938 | ADA71938 Rice gene |
| 28 | 50 | 3.9 | 3798 | 6 | ABZ13238 | ABZ13238 Arabidopsis |
| 29 | 48.4 | 3.8 | 2000 | 8 | ADA71938 | ADA71938 Rice gene |
| 30 | 45 | 3.5 | 36955 | 6 | ABV73608 | ABV73608 S. albula |
| 31 | 43.2 | 3.4 | 2237 | 6 | ABU70109 | ABU70109 Pancreas |
| 32 | 43.2 | 3.4 | 3126 | 3 | AAH36740 | AAH36740 Humanised |
| 33 | 43.2 | 3.4 | 3126 | 3 | AAH36743 | AAH36743 Humanised |
| 34 | 42.6 | 3.3 | 2718 | 10 | ADG93416 | ADG93416 Maize 11p |
| 35 | 42.6 | 3.3 | 3074 | 10 | ADG93414 | ADG93414 Maize 11p |
| 36 | 42.4 | 3.3 | 9369 | 10 | ADG75175 | ADG75175 Human her |
| 37 | 42.4 | 3.3 | 9369 | 10 | ADG75118 | ADG75118 Human her |
| 38 | 42.4 | 3.3 | 21034 | 2 | AAV62154 | AAV62154 HSV-2 str |
| 39 | 42.4 | 3.3 | 26338 | 2 | AAV62134 | AAV62134 HSV-2 str |
| 40 | 42.4 | 3.3 | 117213 | 2 | AAV62176 | AAV62176 HSV-2 str |
| 41 | 42.4 | 3.3 | 154746 | 6 | AAD25519 | AAD25519 Human her |
| 42 | 42 | 3.3 | 110000 | 11 | ADM27081_11 | ADM27081_11 Contamination (12 o |
| 43 | 41.8 | 3.3 | 670 | 4 | AAH15649 | AAH15649 Human RXR |
| 44 | 41.8 | 3.3 | 672 | 4 | AAH15650 | AAH15650 Human RXR |
| 45 | 41.8 | 3.3 | 850 | 4 | AAH15648 | AAH15648 Human RXR |

ALIGNMENTS

| | | |
|----------|---|--------------------------|
| RESULT 1 | | |
| ID | AAT68824 | standard; cDNA; 1277 BP. |
| AC | AAT68824; | |
| DT | 07-AUG-1997 | (first entry) |
| DE | Cytosolic phospholipase A2/B clone 19b. | |
| KW | Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade; | |
| XX | inflammation; inhibitor; antiinflammatory; ds. | |
| OS | Homo sapiens. | |
| FT | Key | Location/Qualifiers |
| FT | CDS | 396..1271 |
| FT | | /*tag= a |
| PN | W09717448-A2. | |
| XX | | |
| PD | 15-MAY-1997. | |
| XX | | |
| PF | 07-NOV-1996; | 96WO-US017794. |
| XX | | |
| PR | 08-NOV-1995; | 95US-00555568. |
| XX | | |
| PA | (GEMY) GENETICS INST INC. | |
| PI | Jones S, Tang J; | |
| XX | | |
| DR | WPI: 1997-281037/25. | |
| DR | P-PSDB; AAW17846. | |
| XX | | |
| FT | Calcium independent phospholipase A2/B - used to reduce inflammation in a | |
| XX | mammalian subject. | |
| XX | | |
| PS | Claim 6; Page 46-47; 74pp; English. | |
| XX | | |
| CC | A cDNA clone (AAT68824), designated 19b and deposited as ATCC 69949, | |
| CC | codes for a novel human cytosolic phospholipase A2/B (sPLA2/B) (AAW17845) | |
| CC | involved in the arachidonic cascade. Clones 19b and 19a (see also | |
| CC | AAT68823) were isolated from a Raji cell DNA library derived from | |
| CC | Burkitt's lymphoma (ATCC CCL86) using a probe derived from a CHO-derived | |

CC clone (see also AAT6827). Clones 19a and 19b are both partial clones of
 CC the full-length enzyme. Spline variants (see also AAT6825-26) of 19a and
 CC 19b have also been identified. The isolated polynucleotides can be used
 CC to identify full-length clones and to produce recombinant sPLA2/B
 CC polypeptides in transfected host cells. sPLA2/B polypeptides can be used
 CC to identify PLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit
 CC the arachidonic acid cascade

XX Sequence 1277 BP; 262 A; 362 C; 411 G; 242 T; 0 U; 0 Other;

Query Match 100.0%; Score 1277; DB 2; Length 1277;
 Best Local Similarity 100.0%; Pred. No. 2.8e-295;
 Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCTTAGAGCCCGAGTGTATTGACATCGGCTCCGATGCAAGAAAGCACTTT 60
 DB 1 GAATCTTAGAGCCCGAGTGTATTGACATCGGCTCCGATGCAAGAAAGCACTTT 60
 QY 61 GTCTGAAGAGACACGCAAGGATATTGATGCTTTGGGTTTCAAGAAAGATTGAG 120
 DB 61 GTCTGAAGAGACACGCAAGGATATTGATGCTTTGGGTTTCAAGAAAGATTGAG 120
 QY 121 GGAACCTGGAGAGCTGCTGGGCAAGGCTGGGAGACCTTCCAGAGAGTGGCCCTT 180
 DB 121 GGAACCTGGAGAGCTGCTGGGCAAGGCTGGGAGACCTTCCAGAGAGTGGCCCTT 180
 QY 121 GGAACCTGGAGAGCTGCTGGGCAAGGCTGGGAGACCTTCCAGAGAGTGGCCCTT 180
 DB 121 GGAACCTGGAGAGCTGCTGGGCAAGGCTGGGAGACCTTCCAGAGAGTGGCCCTT 180
 QY 181 TCCACTCCAGACCATTTCTCTCTGATGAGCTGAGCTTCTCTCTGAGACAGATC 240
 DB 181 TCCACTCCAGACCATTTCTCTCTGATGAGCTGAGCTTCTCTCTGAGACAGATC 240
 QY 181 TCCACTCCAGACCATTTCTCTCTGATGAGCTGAGCTTCTCTCTGAGACAGATC 240
 DB 181 TCCACTCCAGACCATTTCTCTCTGATGAGCTGAGCTTCTCTCTGAGACAGATC 240
 QY 241 CTTCCTGTGGGAGAGGAGACAGATGACAGGGGAGTGGGGGATGAGGGCTGGCCCTG 300
 DB 241 CTTCCTGTGGGAGAGGAGACAGATGACAGGGGAGTGGGGGATGAGGGCTGGCCCTG 300
 QY 241 CTTCCTGTGGGAGAGGAGACAGATGACAGGGGAGTGGGGGATGAGGGCTGGCCCTG 300
 DB 241 CTTCCTGTGGGAGAGGAGACAGATGACAGGGGAGTGGGGGATGAGGGCTGGCCCTG 300
 QY 301 CGAGGACAGCCCGAGTTTGAATCTAGGAGCTCTGGGTTGCAAGGCTTGGGAGCCACC 360
 DB 301 CGAGGACAGCCCGAGTTTGAATCTAGGAGCTCTGGGTTGCAAGGCTTGGGAGCCACC 360
 QY 301 CGAGGACAGCCCGAGTTTGAATCTAGGAGCTCTGGGTTGCAAGGCTTGGGAGCCACC 360
 DB 301 CGAGGACAGCCCGAGTTTGAATCTAGGAGCTCTGGGTTGCAAGGCTTGGGAGCCACC 360
 QY 361 TGACCAAGAGATCCCTGCTCTGCTGCTTCAAGAACTACAGATCTCATCTCAC 420
 DB 361 TGACCAAGAGATCCCTGCTCTGCTGCTTCAAGAACTACAGATCTCATCTCAC 420
 QY 361 TGACCAAGAGATCCCTGCTCTGCTGCTTCAAGAACTACAGATCTCATCTCAC 420
 DB 361 TGACCAAGAGATCCCTGCTCTGCTGCTTCAAGAACTACAGATCTCATCTCAC 420
 QY 421 GGGCCCGGAGAGCAGCGTTTATCTTGGGCTTCAATGAGAGAGAGAGCCACAGACC 480
 DB 421 GGGCCCGGAGAGCAGCGTTTATCTTGGGCTTCAATGAGAGAGAGAGCCACAGACC 480
 QY 421 GGGCCCGGAGAGCAGCGTTTATCTTGGGCTTCAATGAGAGAGAGAGCCACAGACC 480
 DB 421 GGGCCCGGAGAGCAGCGTTTATCTTGGGCTTCAATGAGAGAGAGAGCCACAGACC 480
 QY 481 ACCTGCTGCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 481 ACCTGCTGCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 481 ACCTGCTGCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 481 ACCTGCTGCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 QY 541 CCATCGAAG 600
 DB 541 CCATCGAAG 600
 QY 541 CCATCGAAG 600
 DB 541 CCATCGAAG 600
 QY 601 GCACTGAG 660
 DB 601 GCACTGAG 660
 QY 601 GCACTGAG 660
 DB 601 GCACTGAG 660
 QY 661 GCACTGAG 720
 DB 661 GCACTGAG 720
 QY 661 GCACTGAG 720
 DB 661 GCACTGAG 720
 QY 721 CCCTGAG 780
 DB 721 CCCTGAG 780
 QY 721 CCCTGAG 780
 DB 721 CCCTGAG 780
 QY 781 AACCCAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 781 AACCCAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 781 AACCCAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 DB 781 AACCCAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 QY 841 TCCGGAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
 DB 841 TCCGGAAGTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900

QY 901 TCAGGCTCCAGCTCAGCCCTCAGACCACTGCTGCTGGGCGGCGCCGAGAGAGAGAGAG 960
 DB 901 TCAGGCTCCAGCTCAGCCCTCAGACCACTGCTGCTGGGCGGCGCCGAGAGAGAGAGAG 960
 QY 961 CAGCTCTTACTTACTTCCGAGCCCAATGAGGCGCTTCTGAGAGGCTGTTGGCCACA 1020
 DB 961 CAGCTCTTACTTACTTCCGAGCCCAATGAGGCGCTTCTGAGAGGCTGTTGGCCACA 1020
 QY 1021 ACCCCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 DB 1021 ACCCCAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 QY 1081 GTCAGGCAACAAGTGAAGAACTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 DB 1081 GTCAGGCAACAAGTGAAGAACTCTGATGATGATGATGATGATGATGATGATGATGATGAT 1140
 QY 1141 CACAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 DB 1141 CACAGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 QY 1201 AGACTGTTTTGGGCGCAAGAACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 DB 1201 AGACTGTTTTGGGCGCAAGAACTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 QY 1261 ACGGCGCGCGGAGATTC 1277
 DB 1261 ACGGCGCGCGGAGATTC 1277

RESULT 2

ABV73009
 ABV73009 standard; cDNA; 1277 BP.

XX
 AC ABV73009;

DT 08-JAN-2003 (first entry)

DE
 XX

XX Calcium independent phospholipase A2/B (sPLA2/B) cDNA (clone 19b).

KW Calcium independent phospholipase A2/B; sPLA2/B; phospholipase; gene;

KW antiinflammatory; antidiarrhetic; antipsoriatic; antineumatic; cytosolic;

KW antilesthetic; human; ss.

XX
 OS

XX Homo sapiens.

XX
 FT

FT Key

FT CDS

XX
 PD

XX US2002106364-A1.

XX 08-AUG-2002.

XX 09-AUG-2001, 2001US-00927180.

XX 27-JUL-1994, 94US-00281193.

XX 14-APR-1995, 95US-00422106.

XX 14-APR-1995, 95US-00422106.

XX 26-JUN-1995, 95WO-00422420.

XX 08-NOV-1995, 95US-00555568.

XX 09-SEP-1998, 98US-00149988.

XX 06-MAR-2000, 2000US-00519223.

(GEMV) GENETICS INST INC.

Jones S, Tang J;

WPI, 2002-739923/80.

P-PDB; ABB82230.

XX Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
PT phospholipase activity, is active in the absence of calcium.

XX Claim 6; Page 21-22; 41pp; English.

XX The invention relates to a purified mammalian calcium independent
CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
CC characterized by activity in the absence of calcium and has a molecular
CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying an
CC inhibitor of phospholipase activity which involves combining (I),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC by increased levels of prostaglandins, leukotriene or platelet activating
CC factor. A composition comprising an antibody which binds to (I) is useful
CC as research and diagnostic tool, and is also useful in the study of
CC phospholipase A2 activity and inflammatory conditions. The present
CC sequence represents a human cPLA2/B enzyme encoding cDNA (clone 19b)

XX Sequence 1277 BP; 262 A; 362 C; 411 G; 242 T; 0 U; 0 Other;

Query Match 100.0%; Score 1277; DB 6; Length 1277;
Best Local Similarity 100.0%; Pred. No. 2,8e-295;
Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCCTAGAGCCCGAGGAGGATGACATCGGCTCCGAGCAAGAAAGCACTT 60
DB 1 GAATTCCTAGAGCCCGAGGAGGATGACATCGGCTCCGAGCAAGAAAGCACTT 60
QY 61 GTCTGAAGAGACACGACGAGGATTCATGCTGGGTTTCAAGAGAAAGATTGAG 120
DB 61 GTCTGAAGAGACACGACGAGGATTCATGCTGGGTTTCAAGAGAAAGATTGAG 120
QY 121 GGAACCTGGAGCTGCTGGGCAAGGCTGGGAGGCTTCCCAAGACAGTGGCCCCCTT 180
DB 121 GGAACCTGGAGCTGCTGGGCAAGGCTGGGAGGCTTCCCAAGACAGTGGCCCCCTT 180
QY 181 TCAACCTCAGCCATTTCTCTCTGAGGCTGAGGCTCAGCTTCTCTGAGCAAGGTC 240
DB 181 TCAACCTCAGCCATTTCTCTCTGAGGCTGAGGCTCAGCTTCTCTGAGCAAGGTC 240
QY 241 CTTCTGTGGGGAAGGACAGATGACAGGGGAGTGGGGGATGAGGGCGTGGCG 300
DB 241 CTTCTGTGGGGAAGGACAGATGACAGGGGAGTGGGGGATGAGGGCGTGGCG 300
QY 301 CGAGGACAGCCAGGATTGATCTAGGACCTCTGGGATGACAGGGCTTGGGACCCACC 360
DB 301 CGAGGACAGCCAGGATTGATCTAGGACCTCTGGGATGACAGGGCTTGGGACCCACC 360
QY 361 TGACCAAGATGCGCTGCTGCTGCTCAAGAACTACAGGATCTATGACATCTCAC 420
DB 361 TGACCAAGATGCGCTGCTGCTGCTCAAGAACTACAGGATCTATGACATCTCAC 420
QY 421 GGGCCCGGAGACGAGCTTATCTCTGGGCTCAATGAGGAGAGAGACCCACGACC 480
DB 421 GGGCCCGGAGACGAGCTTATCTCTGGGCTCAATGAGGAGAGAGACCCACGACC 480
QY 481 ACCTGCTGTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 ACCTGCTGTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 CCAATCGAAGAGGCTGAGGAGTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 CCAATCGAAGAGGCTGAGGAGTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 GCACTGAGGAGCATCTGCGCTGAGCATCTGCAAGTAAGTCCATGAGCTACATGCGCG 660
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DB 601 GCACTGAGGAGCATCTGCGCTGAGCATCTGCAAGTAAGTCCATGAGCTACATGCGCG 660
QY 661 GCATGATCTTGGCAAGAGATGAGTGTTCGGGGCTCCAGGCCCTACGATCGGGGC 720
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DB 721 CCTGGAGAGTCTCGAAGCGGAGTTTGGGAGACACCAAGATGACGAGCTGAGCA 780
QY 781 AACCAAGTATGATGACAGGAGACATGCTGACCGGACCGGCTGAACTCCACTCT 840
DB 781 AACCAAGTATGATGACAGGAGACATGCTGACCGGACCGGCTGAACTCCACTCT 840
QY 841 TCCGGAATCAATGCTCCAGAACTGTCCGGAGGCTGTTCAACCAAGATTAACC 900
DB 841 TCCGGAATCAATGCTCCAGAACTGTCCGGAGGCTGTTCAACCAAGATTAACC 900
QY 901 TCAGGCTCCAGCTCAGCCCTCAGACAGCTGTGGCGGGCCCGAAGCAGCGGG 960
DB 901 TCAGGCTCCAGCTCAGCCCTCAGACAGCTGTGGCGGGCCCGAAGCAGCGGG 960
QY 961 CAGCTCTACTTACTTCCGACCCCAATGGGGCTTCTGAGCGGTGTGGCCAA 1020
DB 961 CAGCTCTACTTACTTCCGACCCCAATGGGGCTTCTGAGCGGTGTGGCCAA 1020
QY 1021 ACCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
DB 1021 ACCCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1080
QY 1081 GTGAGGCAAGAGTGAAGAACTCTCATGCTGTCTCCCTGGGAGACAGGAGTCCC 1140
DB 1081 GTGAGGCAAGAGTGAAGAACTCTCATGCTGTCTCCCTGGGAGACAGGAGTCCC 1140
QY 1141 CACAAGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
DB 1141 CACAAGTCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
QY 1201 AGACTGTTTGGGGCCAGAGAACTGGGCAAGTGTGTGTGTGTGTGTGTGTGTGT 1260
DB 1201 AGACTGTTTGGGGCCAGAGAACTGGGCAAGTGTGTGTGTGTGTGTGTGTGTGT 1260
QY 1261 ACCGGCGGCCGGAATTC 1277
DB 1261 ACCGGCGGCCGGAATTC 1277

RESULT 3
AAT68826
ID AAT68826 standard; cDNA; 2112 BP.
AC AAT68826;
DT 07-AUG-1997 (first entry)
XX
DE Cytosolic phospholipase A2/B clone 19b splice variant.
KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
KW Inflammation; inhibitor; antiinflammatory; ds.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 43..2106
FT /*tag= a
FT /*tag= b
FT /*note= "alternative splice site"
XX
XX MO9717448-A2.
XX 15-MAY-1997.

PF 07-NOV-1996; 96MO-US017794.
 XX
 PR 08-NOV-1995; 95US-00555568.
 XX
 PA (GENY) GENETICS INST INC.
 XX
 PI Jones S, Tang J;
 XX
 DR WPI; 1997-281037/25.
 P-PSDB; AAM17848.
 XX
 PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
 PS mammalian subject.
 XX
 PS Claim 6; Page 54-56; 74pp; English.
 CC
 CC A cDNA clone (AAT68826) codes for a novel human cytosolic phospholipase
 CC A2/B (sPLA2/B) (AAM17848) that is involved in the arachidonic acid
 CC cascade. It is a splice variant of clone 19b (see also AAT68824), the
 CC splice occurring after nucleotide 1228. Isolated sPLA2/B polynucleotides
 CC can be used to produce recombinant sPLA2/B polypeptides in transformed
 CC host cells. The sPLA2/B polypeptides can be used to identify PLA2/B
 CC inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic
 CC acid cascade
 CC
 SQ Sequence 2112 BP; 451 A; 645 C; 630 G; 386 T; 0 U; 0 Other;

Query Match 69.4%; Score 885.8; DB 2; Length 2112;

Best Local Similarity 99.8%; Pred. NO. 1.1e-201; Matches 88; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 389 CACAGACTACAGAGATCTCATGCAATCTCACGGGCCCGAAGCCAGCTTCCTGGG 448
 DB 1224 CAGACACTACAGAGATCTCATGCAATCTCACGGGCCCGAAGCCAGCTTCCTGGG 1283
 QY 449 CTCCTAGAGGAG 508
 DB 1284 CTCCTAGAGGAG 1343
 QY 509 GAAAGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 568
 DB 1344 GAAAGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1403
 QY 569 CAAAGACTTGTGATGAGTGGGCGGCAACAGCACTGAGGCACTCTCTGGCCCTGGCCAT 628
 DB 1404 CAAAGACTTGTGATGAGTGGGCGGCAACAGCACTGAGGCACTCTCTGGCCCTGGCCAT 1463
 QY 629 TCTGCACAGTAAGTCCATGCGCTTATGCGCGGATATCTTTGGCATGAAAGATGAGGT 688
 DB 1464 TCTGCACAGTAAGTCCATGCGCTTATGCGCGGATATCTTTGGCATGAAAGATGAGGT 1523
 QY 689 GTTCCGGGGCTCCAGAGGCTTACAGAGTGGGGCCCTGAGGAGAGTTCCTGAAGCGGAGTT 748
 DB 1524 GTTCCGGGGCTCCAGAGGCTTACAGAGTGGGGCCCTGAGGAGAGTTCCTGAAGCGGAGTT 1583
 QY 749 TGGGAGACACCAAGATGACGACGTCAAGAAACCAAGATGATGCTGACAGGACACT 808
 DB 1584 TGGGAGACACCAAGATGACGACGTCAAGAAACCAAGATGATGCTGACAGGACACT 1643
 QY 809 GTCTGACCGGACAGCGGCTGAACTCCACCTCTTCCGAACTAGCATGCTCCAGAACTGT 868
 DB 1644 GTCTGACCGGACAGCGGCTGAACTCCACCTCTTCCGAACTAGCATGCTCCAGAACTGT 1703
 QY 869 CCGGAGACCTGTTTCAACGAGAACGTTAATCTCAGGCTCCAGCTCAGGCTCCAGACCA 928
 DB 1704 CCGGAGACCTGTTTCAACGAGAACGTTAATCTCAGGCTCCAGCTCAGGCTCCAGACCA 1763
 QY 929 GCTGCTGTGGCGGCGCGCGCGAGACAGCGGCGGAGCTCTACTACTTCCAGCCCATGG 988
 DB 1764 GCTGCTGTGGCGGCGCGCGCGAGACAGCGGCGGAGCTCTACTACTTCCAGCCCATGG 1823
 QY 989 GCGCTTCTTGGAGGCTGCTGTTGGCCAAACCAACCCACGCTGATGCCATGACCGAGAT 1048

DB 1824 GCGCTTCTTGGAGGCTGCTGTTGGCCAAACCCACGCTGATGCCATGACCGAGAT 1883
 QY 1049 CCATGAGTACATCAGGACCTGATCCGCAAGGCTCAGGCCCAAGATGAAAGAACTCTC 1108
 DB 1884 CCATGAGTACATCAGGACCTGATCCGCAAGGCTCAGGCCCAAGATGAAAGAACTCTC 1943
 QY 1109 CATGTTGTCTCCCTGGGAGCAGGAGGTCCCAAGATGCTGTGATGATGT 1168
 DB 1944 CATGTTGTCTCCCTGGGAGCAGGAGGTCCCAAGATGCTGTGATGATGT 2003
 QY 1169 CTTCGGTCCCGAGAACCCCTGGGAGCTGGCCAGACCTGTTTGGGGCCAGGAACTGGG 1228
 DB 2004 CTTCGGTCCCGAGAACCCCTGGGAGCTGGCCAGACCTGTTTGGGGCCAGGAACTGGG 2063
 QY 1229 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1277
 DB 2064 CAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2112

RESULT 4
 ID AAV73011 standard; cDNA; 2112 BP.
 XX AAV73011;
 AC
 XX 08-JAN-2003 (first entry)
 XX
 DE Human cPLA2/B splice variant cDNA (clone 19b).
 KM Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; gene;
 KM antiinflammatory; antithrombotic; antiprostaglandin; antipneumatic; cytosolic;
 KM antithrombotic; human; ss.
 XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 43..2106
 FT /tag= a
 FT /product= "cPLA2/B"
 FT /partial
 FT /note= "splice variant"
 XX
 PN US2002106364-A1.
 PD 08-AUG-2002.
 XX
 PF 09-AUG-2001; 2001US-00927180.
 XX
 PR 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-00422420.
 PR 26-JUN-1995; 95MO-US008069.
 PR 08-NOV-1995; 95US-00555568.
 PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX
 PA (GENY) GENETICS INST INC.
 XX
 PI Jones S, Tang J;
 XX
 DR WPI; 2002-739923/80.
 DR P-PSDB; ABB82232.
 XX
 PT Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 XX
 PS Claim 6; Page 28-30; 41pp; English.
 CC The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (i) comprising a purified

CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (1),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (1) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant encoding
 CC cDNA (clone 19b)
 XX
 SQ Sequence 2112 BP; 451 A; 645 C; 630 G; 386 T; 0 U; 0 Other;

Query Match 69.4%; Score 885.8; DB 6; Length 2112;
 Best Local Similarity 99.8%; Pred. No. 1.1e-201;
 Matches 887; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 389 CACAGAACTACAGAGTCTCATGACATCTCAGCGGCCCGGAGCCGTTCACTCTGGG 448
 DB 1224 CAGACAACTACAGAGTCTCATGACATCTCAGCGGCCCGGAGCCGTTCACTCTGGG 1283
 QY 449 CTCCTAGAGGAGGAGAGAGGAGGAGCCACGACACCTGCTGCTGGATGAGAGAGAGT 508
 DB 1284 CTCCTAGAGGAGGAGAGAGGAGGAGCCACGACACCTGCTGCTGGATGAGAGAGAGT 1343
 QY 509 GAAAGGCTCATCATCATCTCAGCTCTCATGCGCATGAGAGAGGCTCGGGGTGAGCCAC 568
 DB 1344 GAAAGGCTCATCATCATCTCAGCTCTCATGCGCATGAGAGAGGCTCGGGGTGAGCCAC 1403
 QY 569 CAAAGACTGTGTTGACTGGGTGGCGGACAGACATGAGAGCATCTGAGCCCTGGCCAT 628
 DB 1404 CAAAGACTGTGTTGACTGGGTGGCGGACAGACATGAGAGCATCTGAGCCCTGGCCAT 1463
 QY 629 TCTGCACTAGTAATCCATGAGCCCTTACATGCGCGGATATCTTTGCGATGAAGATAGGT 688
 DB 1464 TCTGCACTAGTAATCCATGAGCCCTTACATGCGCGGATATCTTTGCGATGAAGATAGGT 1523
 QY 689 GTTCCGGGGGCTCCAGGCGCTTACAGAGTGGGGGCCCTTGAAGAGTCTCTGAAGCGGAGTT 748
 DB 1524 GTTCCGGGGGCTCCAGGCGCTTACAGAGTGGGGGCCCTTGAAGAGTCTCTGAAGCGGAGTT 1583
 QY 749 TGGGAGACACCAAGATGACGAGCTGAGAGAAACCAAGGTGATGCTGACAGGACACT 808
 DB 1584 TGGGAGACACCAAGATGACGAGCTGAGAGAAACCAAGGTGATGCTGACAGGACACT 1643
 QY 809 GTCTGACCGGACCGGCTGAACTCCACTCTTCCGGAATAGAGTCTCCAGAAACTGT 868
 DB 1644 GTCTGACCGGACCGGCTGAACTCCACTCTTCCGGAATAGAGTCTCCAGAAACTGT 1703
 QY 869 CCGGAGACCTCGTTTCAACAGAGAGCTTAACTCAGGCTCCAGCTCAGGCTCAGACCA 928
 DB 1704 CCGGAGACCTCGTTTCAACAGAGAGCTTAACTCAGGCTCCAGCTCAGGCTCAGACCA 1763
 QY 929 GCTGTGTGGCGGGCGGCGGAGACGCGGGGAGCTCTTAATTACTTCCGACCCAAATGG 988
 DB 1764 GCTGTGTGGCGGGCGGCGGAGACGCGGGGAGCTCTTAATTACTTCCGACCCAAATGG 1823
 QY 989 GCGCTTCTTGAAGAGGTGGGCTGTGGCCAAACCCCAAGCTGATGCCATGACCGAGAT 1048
 DB 1824 GCGCTTCTTGAAGAGGTGGGCTGTGGCCAAACCCCAAGCTGATGCCATGACCGAGAT 1083
 QY 1049 CCATGAGTAAATCAGGACCTGATCCGCAAGGGTCAAGGCCAAACAAGGTGAAGAACTCTC 1108
 DB 1884 CCATGAGTAAATCAGGACCTGATCCGCAAGGGTCAAGGCCAAACAAGGTGAAGAACTCTC 1143
 QY 1109 CATGTGTCTCTCTGGGGAAGGAGAGTCCCAAAAGTCCCTGTGACCTGTGTGATGT 1168
 DB 1944 CATGTGTCTCTCTGGGGAAGGAGAGTCCCAAAAGTCCCTGTGACCTGTGTGATGT 2003

QY 1169 CTTCGCTCCAGACACCCGCGGAGCTGGCCAGAGCTGTTTGGGCGCAAGAGACTGGG 1228
 DB 2004 CTTCGCTCCAGACACCCGCGGAGCTGGCCAGAGCTGTTTGGGCGCAAGAGACTGGG 2063

QY 1229 CAAAGATGTGTGAGTGTGACGTTGACAGGATCCAGACGCGCGCGGAATTC 1277
 DB 2064 CAAAGATGTGTGAGTGTGACGTTGACAGGATCCAGACGCGCGCGGAATTC 2112

RESULT 5
 ID AAT68825 standard; cDNA; 2109 BP.
 AC AAT68825;
 XX
 DT 07-AUG-1997 (first entry)
 XX
 DE Cytosolic phospholipase A2/B clone 19a splice variant.
 XX
 KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
 KW inflammation; inhibitor; antiinflammatory; de.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 43..2103
 FT misc_RNA /tag= a
 FT /*tag= b
 FT /*note= "alternative splice site"
 XX
 XX W09717448-A2.
 XX
 PD 15-MAY-1997.
 XX
 PF 07-NOV-1996; 96MO-US017794.
 XX
 PR 08-NOV-1995; 95US-00555568.
 XX
 PA (GENY) GENETICS INST INC.
 XX
 PI Jones S, Tang J;
 XX
 XX WPI; 1997-281037/25.
 DR P-PDB; AAM17847.
 PT
 PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
 XX mammalian subject.
 PS Claim 6; Page 49-51; 74pp; English.
 XX
 XX A cDNA clone (AAT68825) codes for a novel human cytosolic phospholipase
 CC A2/B (sPLA2/B) (AAM17847) that is involved in the arachidonic acid
 CC cascade. It is a splice variant of clone 19a (see also AAT68823), the
 CC splice occurring after nucleotide 1225. Isolated sPLA2/B polynucleotides
 CC can be used to produce recombinant sPLA2/B polypeptides in transformed
 CC host cells. The sPLA2/B polypeptides can be used to identify PLA2/B
 CC inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic
 CC acid cascade
 XX
 SQ Sequence 2109 BP; 450 A; 644 C; 629 G; 386 T; 0 U; 0 Other;

Query Match 69.4%; Score 885.6; DB 2; Length 2109;
 Best Local Similarity 97.9%; Pred. No. 1.2e-201;
 Matches 897; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 362 GACACAGATGCGCTGCTGTGCTTCAAGAACTACAGATCTCATGACATCTCAGC 421
 DB 1194 GACTCTACATCTCTAGCTTCCCAAAATCGCAACTACAGATCTCATGACATCTCAGC 1253
 QY 422 GGCCTCGGAAAGCCAGCTTATCTGTGGCTTCAATGAGGAGAGAGAGCCAGCA 481
 DB 1254 GGCCTCGGAAAGCCAGCTTATCTGTGGCTTCAATGAGGAGAGAGAGCCAGCA 1313

QY 482 CTTGCTGTGCTGGATGAGAGAGTGAAGGCTTCATCATCTCAGCTCCTCATGCG 541
 DB 1314 CTTGCTGTGCTGGATGAGAGAGTGAAGGCTTCATCATCTCAGCTCCTCATGCG 1373
 QY 542 CATCGAAGAGGCTCGGGGTGCGCACCAAGACCTTTGACTGGGTGGCGGACACAG 601
 DB 1374 CATCGAAGAGGCTCGGGGTGCGCACCAAGACCTTTGACTGGGTGGCGGACACAG 1433
 QY 602 CATCGAAGAGGCTCGGGGTGCGCACCAAGACCTTTGACTGGGTGGCGGACACAG 661
 DB 1434 CATCGAAGAGGCTCGGGGTGCGCACCAAGACCTTTGACTGGGTGGCGGACACAG 1493
 QY 662 CATGTACTTTGCGATGAAGATGAGTGTTCGGGGGCTCCAGGCTCCAGAGTCGGGGCC 721
 DB 1494 CATGTACTTTGCGATGAAGATGAGTGTTCGGGGGCTCCAGGCTCCAGAGTCGGGGCC 1553
 QY 722 CTTGGAAGAGTTCCTGAAGCGGAGATTGGGGAGCACCAAGATGACGAGCTCAGGAA 781
 DB 1554 CTTGGAAGAGTTCCTGAAGCGGAGATTGGGGAGCACCAAGATGACGAGCTCAGGAA 1613
 QY 782 ACCCAAGGTATGCTGACAGAGGACACTGTCTGACCGGACGCGGCTGAACTCCACCTCTT 841
 DB 1614 ACCCAAGGTATGCTGACAGAGGACACTGTCTGACCGGACGCGGCTGAACTCCACCTCTT 1673
 QY 842 CCGGAACCTACGATGCTCAGAGAACTGTCCGGAGGCTCGTTTCAACCAAGACCTTAACT 901
 DB 1674 CCGGAACCTACGATGCTCAGAGAACTGTCCGGAGGCTCGTTTCAACCAAGACCTTAACT 1733
 QY 902 CAGGCTCCAGCTCAGAGCTCAGAGCCAGAGCTGTGTGTGGCGGGCGGCGGAGACAGGGGCG 961
 DB 1734 CAGGCTCCAGCTCAGAGCTCAGAGCCAGAGCTGTGTGTGGCGGGCGGCGGAGACAGGGGCG 1793
 QY 962 AGCTCTACTTACTTCCGACCCCAATGAGGCGCTTCTTGAAGGTGGCTGTGGCCAAACA 1021
 DB 1794 AGCTCTACTTACTTCCGACCCCAATGAGGCGCTTCTTGAAGGTGGCTGTGGCCAAACA 1053
 QY 1022 CCCCACGCTGGATGCCATGACCGAGATCATGAGTACATCAGAGCTGATCCGCAAGGG 1081
 DB 1854 CCCCACGCTGGATGCCATGACCGAGATCATGAGTACATCAGAGCTGATCCGCAAGGG 1913
 QY 1082 TCAGGCCAACAAAGTGAAGAAACTCTCCATCCGTGTCTCCCTGGGGGACAGGAGGTCCCC 1141
 DB 1914 TCAGGCCAACAAAGTGAAGAAACTCTCCATCCGTGTCTCCCTGGGGGACAGGAGGTCCCC 1973
 QY 1142 ACAAGTGCCTGTGACCTGTGTGATGCTTCCGTCACAGAACCCCTGGAGCTGGCCAA 1201
 DB 1974 ACAAGTGCCTGTGACCTGTGTGATGCTTCCGTCACAGAACCCCTGGAGCTGGCCAA 2033
 QY 1202 GACTGTTTTTGGGGCCAAAGAACTGGGCAAGATGTGTGACTGTTGACGAGTCCAGA 1261
 DB 2034 GACTGTTTTTGGGGCCAAAGAACTGGGCAAGATGTGTGACTGTTGACGAGTCCAGA 2093
 QY 1262 CGGGCGCGCGGAAATTC 1277
 DB 2094 CGGGCGCGCGGAAATTC 2109
 RESULT 6
 ABV73010
 ID ABV73010 standard; cDNA; 2109 BP.
 XX
 AC ABV73010;
 XX
 DT 08-JAN-2003 (first entry)
 DE Human cPLA2/B splice variant cDNA (clone 19a).
 XX
 XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; gene;
 KW antiinflammatory; antidiarrhetic; antipruritic; antirheumatic; cytosolic;
 KM antilesthetic; human; ss.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH CDS 43..2103
 FT /tag= a
 FT /product= "cPLA2/B"
 FT /partial
 FT /note= "splice variant"
 PN US2002106364-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 09-AUG-2001; 2001US-00927180.
 XX
 PR 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00423106.
 PR 14-APR-1995; 95US-00423420.
 PR 26-JUN-1995; 95MO-US008069.
 PR 08-NOV-1995; 95US-00555568.
 PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX
 PA (GENY) GENETICS INST INC.
 XX
 PI Jones S, Tang J;
 XX
 DR WPI; 2002-739923/80.
 DR P-PSDB; ABB82231.
 XX
 PT Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 PS Claim 6; Page 23-25; 41pp; English.
 XX
 CC The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (I),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant encoding
 CC cDNA (clone 19a)
 CC
 SQ Sequence 2109 BP; 450 A; 644 C; 629 G; 386 T; 0 U; 0 Other;
 Query Match 69.4%; Score 885.6; DB 6; Length 2109;
 Best Local Similarity 97.9%; Pred. No. 1.2e-201;
 Matches 897; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
 QY 362 GACCACAGCATGCCCTGCTCTGTGCTCAGAGAACTACAGGATCTATGACATCTCAGG 421
 DB 1194 GACTCTTACTATCTTGTAGCTCCAAATTCGCAAACTACAGGATCTATGACATCTCAGG 1253
 QY 422 GGGCCGGAAGCCAGGTTTCATCTGGGCTCCATGAGAGGAGAGAGCGAGCCAGCACGACCA 481
 DB 1254 GGGCCGGAAGCCAGGTTTCATCTGGGCTCCATGAGAGGAGAGAGCGAGCCAGCACGACCA 1313
 QY 482 CTTGCTGTGCTGGATGAGAGAGTGAAGGCTTCATCATCTCAGCTCCTCATGCG 541
 DB 1314 CTTGCTGTGCTGGATGAGAGAGTGAAGGCTTCATCATCTCAGCTCCTCATGCG 1373
 QY 542 CATCGAAGAGGCTCGGGGTGCGCACCAAGACCTTTGACTGGGTGGCGGACACAG 601

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Db 1374 CATCGAGAGGCTCGGGTGTGGCCACCAAGACCTGTTGATCGGTGGCGGGACACAG 1433
QY 602 CACTGAGAGGATCTGGCCCTGGCCATTTCTGACAGTAAGTCCATGCTTACATGCGCGG 661
Db 1434 CACTGAGAGGATCTGGCCCTGGCCATTTCTGACAGTAAGTCCATGCTTACATGCGCGG 1493
QY 662 CATTGATCTTCCGATGAAGATAGAGGTGTCCGGGGCTCCAGGCCCTTACAGATCGGGGGC 721
Db 1494 CATGATCTTCCGATGAAGATAGAGGTGTCCGGGGCTCCAGGCCCTTACAGATCGGGGGC 1553
QY 722 CCTGAGAGATTTCTTAAGCGGAGTTTGGGAGACACACCAAGATGACGAGCTCAGAA 781
Db 1554 CCTGAGAGATTTCTTAAGCGGAGTTTGGGAGACACACCAAGATGACGAGCTCAGAA 1613
QY 782 ACCCAAGGTGATGCTGACAGAGACACTGTCTGACCGGACCGGCTGAACTCCACTCTT 841
Db 1614 ACCCAAGGTGATGCTGACAGAGACACTGTCTGACCGGACCGGCTGAACTCCACTCTT 1673
QY 842 CCGGAATCTAGATGCTCCAGAACTGTCCGGGAGCTTCCTTTCACCAAGACCTTAACCT 901
Db 1674 CCGGAATCTAGATGCTCCAGAACTGTCCGGGAGCTTCCTTTCACCAAGACCTTAACCT 1733
QY 902 CAGGCTCTCAGCTCAGCCCTCAGACCAAGCTGTGTGGCGGGCGGCCGGAAGACGGGGC 961
Db 1734 CAGGCTCTCAGCTCAGCCCTCAGACCAAGCTGTGTGGCGGGCGGCCGGAAGACGGGGC 1793
QY 962 AGCTCTACTTACTTCTCGACCCCAATGAGCGCTTCTTGACGATGGCTGTGGCCAA 1021
Db 1794 AGCTCTACTTACTTCTCGACCCCAATGAGCGCTTCTTGACGATGGCTGTGGCCAA 1853
QY 1022 CCCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1081
Db 1854 CCCCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1913
QY 1082 TCAGGCAACAAAGTGAAGAACTCTCATGTTGCTCCCTGGGAGCAGGAGTCCCTC 1141
Db 1914 TCAGGCAACAAAGTGAAGAACTCTCATGTTGCTCCCTGGGAGCAGGAGTCCCTC 1973
QY 1142 ACAAGTGTCTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1201
Db 1974 ACAAGTGTCTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2033
QY 1202 GACTGTTTTTGGGCGCAAGAACTGTGGCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGT 1261
Db 2034 GACTGTTTTTGGGCGCAAGAACTGTGGCAAGATGTGTGTGTGTGTGTGTGTGTGTGTGT 2093
QY 1262 CGGGCGGCGGGAATTC 1277
Db 2094 CGGGCGGCGGGAATTC 2109

```

RESULT 7
ADM02650
ID ADM02650 standard; cDNA; 2755 BP.
AC ADM02650;

20-MAY-2004 (first entry)
Human cDNA of the invention SEQ ID NO:1335.
XX 88; gene; human; gene therapy; diagnostic marker; pharmaceutical.
XX Homo sapiens.
XX BP1347046-AL.
XX
XX
XX 24-SEP-2003.
XX
XX 12-APR-2002; 2002BP-00008400.
XX
XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX PA
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
XX Yamamoto J, Isono Y, Hito Y, Otsuka K, Nagai K, Irie R, Tamechika I,
XX Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuno Y;
XX WPI: 2003-723558/59.
XX P-PSDB; ADM05093.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
XX developing a diagnostic marker or medicines for regulating their
XX expression and activity, or as a target of gene therapy.
XX
XX Claim 1; SEQ ID NO 1335; 305bp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
XX polypeptide. A polynucleotide of the invention may have a use in gene
XX therapy. An oligonucleotide of the invention ADM05202-ADM06773 is useful
XX as a primer for synthesizing the polynucleotide or as a probe for
XX detecting the polynucleotide. The polynucleotides ADM03316-ADM03758 are
XX useful in gene therapy, for developing a diagnostic marker or medicines
XX for regulating their expression and activity, or as a target of gene
XX therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
XX are useful as pharmaceutical agents. The present sequence represents a
XX cDNA sequence of the invention.

XX Sequence 2755 BP; 578 A; 887 C; 787 G; 503 T; 0 U; 0 Other;

XX Query Match 68.6%; Score 876.2; DB 11; Length 2755;
XX Best Local Similarity 99.7%; Pred. No. 2.3e-199;
XX Matches 878; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 392 AGAATCAAGATCTCATGATCTCATGATCTCATGATCTCATGATCTCATGATCTCATGATCT 451
Db 1016 AGAATCAAGATCTCATGATCTCATGATCTCATGATCTCATGATCTCATGATCTCATGATCT 1075
QY 452 CATGAGGAGCGAAGACCGGACCGACGACGACGACGACGACGACGACGACGACGACGACGAC 511
Db 1076 CATGAGGAGCGAAGACCGGACCGACGACGACGACGACGACGACGACGACGACGACGACGAC 1135
QY 512 AGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 571
Db 1136 AGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1195
QY 572 GGAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 631
Db 1196 GGAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1255
QY 632 GCAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 691
Db 1256 GCAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1315
QY 692 CCGGGGCTCAAGGCTTACAGATCGGGGCGGCTGAGAGATTCCTGAACGGGAGTTTGG 751
Db 1316 CCGGGGCTCAAGGCTTACAGATCGGGGCGGCTGAGAGATTCCTGAACGGGAGTTTGG 1375
QY 752 GGAACACCAAGATGACGAGCGTGAAGAACTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 811
Db 1376 GGAACACCAAGATGACGAGCGTGAAGAACTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1435
QY 812 TGAACGGGAGCGGGCTGAACTCACTCTTCCGGGAGCTTCAAGTGTGTGTGTGTGTGTGTGTGT 871
Db 1436 TGAACGGGAGCGGGCTGAACTCACTCTTCCGGGAGCTTCAAGTGTGTGTGTGTGTGTGTGTGT 1495
QY 872 GGAAGCTCTTCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 931
Db 1496 GGAAGCTCTTCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1555
QY 932 GGTGTGGCGGGCGGCGGCGGAGGAGCGGGGAGCTCTTCACTTCACTTCACTTCACTTCACTT 991
Db 1556 GGTGTGGCGGGCGGCGGCGGAGGAGCGGGGAGCTCTTCACTTCACTTCACTTCACTTCACTT 1615

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QY 992 CTTCTGAGAGGCTGTTGGCAACACCCAGCTGGATGCCATGACCGAGATCCA 1051
 DB 1616 CTTCTGAGAGGCTGTTGGCAACACCCAGCTGGATGCCATGACCGAGATCCA 1675
 QY 1052 TGAAGTCAATCAGGACCTGATCCGCAAGGCTGAGGCAACAAGTGAAGAACTTCCAT 1111
 DB 1676 TGAAGTCAATCAGGACCTGATCCGCAAGGCTGAGGCAACAAGTGAAGAACTTCCAT 1735
 QY 1112 CGTTGTCTCCCTGGGACAGAGGAGTCCCAAGTGCCTGTGACCTGTGTGATGCTT 1171
 DB 1736 CGTTGTCTCCCTGGGACAGAGGAGTCCCAAGTGCCTGTGACCTGTGTGATGCTT 1795
 QY 1172 CGGTCCAGCAACCCCTGGGAGCTGGCCAAAGACTGTTTGGGCGCAAGAACTGGGCAA 1231
 DB 1796 CGGTCCAGCAACCCCTGGGAGCTGGCCAAAGACTGTTTGGGCGCAAGAACTGGGCAA 1855
 QY 1232 GATGTGTGTGACTGTTCGACGGATCCAGACGGGCGGCGG 1272
 DB 1856 GATGTGTGTGACTGTTCGACGGATCCAGACGGGCGGCGG 1896
 RESULT 8
 AAD42941
 ID AAD42941 standard; DNA; 3240 BP.
 AC AAD42941;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human PLA2 group VI (Ca2+-independent) DNA #1.
 XX
 KW Human; antisense; phospholipase A2; infection; inflammation; tumour;
 XX antisense therapy; PLA2; ds.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 137..2557
 FT /*tag= a
 FT /product= "Human phospholipase 2 protein"
 XX
 PN US6410325-B1.
 XX
 PD 25-JUN-2002.
 XX
 PF 09-MAY-2001; 2001US-00851896.
 XX
 PR 09-MAY-2001; 2001US-00851896.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Pfeifer SM, Watt AT;
 XX
 DR MPI; 2002-616513/66.
 DR P-PSDB; AAE25968.
 XX
 PT Novel antisense compounds useful for inhibiting gene expression of human
 PT phospholipase A2, group VI and for treating diseases associated with
 PT expression of phospholipase A2, group VI.
 XX
 PS Example 15; Col 109-116; 72pp; English.
 XX
 CC The present invention relates to novel antisense compounds which inhibit
 CC the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
 CC The invention is useful for inhibiting the expression of PLA2, group VI
 CC (Ca2+-independent) in human cells or tissues and for treating an animal,
 CC particularly a human suspected of having or being prone to a disease or
 CC condition associated with expression of human PLA2, group VI (Ca2+-
 CC independent). It is useful for diagnostics, therapeutics and as research
 CC reagent, e.g. prophylactically to prevent or delay infection, tumour
 CC formation or inflammation. The present sequence is human PLA2 group VI
 CC (Ca2+-independent) DNA
 CC
 XX

SQ Sequence 3240 BP; 681 A; 1048 C; 912 G; 598 T; 0 U; 1 Other;
 Query Match 68.6%; Score 876.2; DB 6; Length 3240;
 Best Local Similarity 99.7%; Pred. No. 2,4e-199;
 Matches 878; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 392 AGAATCAAGATCTCATCATCTTCAAGGCGCGGAAGCCAGCTTATCTGGGCTC 451
 DB 1483 AGAATCAAGATCTCATCATCTTCAAGGCGCGGAAGCCAGCTTATCTGGGCTC 1542
 QY 452 CATGAGGAGAGAAACCGAGACCAAGACCACTGCTGTGCTGATGAGGAGAGTGA 511
 DB 1543 CATGAGGAGAGAAACCGAGACCAAGACCACTGCTGTGCTGATGAGGAGAGTGA 1602
 QY 512 AGGCTCATCATCATCTTCAAGGCGCGGAAGCCAGCTTATCTGGGCTC 571
 DB 1603 AGGCTCATCATCATCTTCAAGGCGCGGAAGCCAGCTTATCTGGGCTC 1662
 QY 572 GGAAGCTGTTGACTGAGTGGCGGAGCAAGCACTGAGAGGATCTGGCCATTCT 631
 DB 1663 GGAAGCTGTTGACTGAGTGGCGGAGCAAGCACTGAGAGGATCTGGCCATTCT 1722
 QY 632 GCAAGTAACTGATGAGTGGCTTACATGCGGCGGCAATGTAATTCGATGAGAGTGT 691
 DB 1723 GCAAGTAACTGATGAGTGGCTTACATGCGGCGGCAATGTAATTCGATGAGAGTGT 1782
 QY 692 CGGAGGCTCCAGGCGCTTACAGATCGGAGGCGCTTGAAGAGTTCCTGAAACGGGAGTTTG 751
 DB 1783 CGGAGGCTCCAGGCGCTTACAGATCGGAGGCGCTTGAAGAGTTCCTGAAACGGGAGTTTG 1842
 QY 752 GGAGCACACCAAGATGACGAGAGTCAAGAAACCAAGGATGATGCTGACAGGACACTGTC 811
 DB 1843 GGAGCACACCAAGATGACGAGAGTCAAGAAACCAAGGATGATGCTGACAGGACACTGTC 1902
 QY 812 TGACCGGAGCGGCGGCTGAACTCACTCTTCCGGAATGATGCTCAAGAACTGTCCG 871
 DB 1903 TGACCGGAGCGGCGGCTGAACTCACTCTTCCGGAATGATGCTCAAGAACTGTCCG 1962
 QY 872 GGAGCTCGTTTCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 931
 DB 1963 GGAGCTCGTTTCAACCAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2022
 QY 932 GGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 991
 DB 2023 GGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2082
 QY 992 CTTCTGAGAGGCTGTTGGCAACACCCAGCTGGATGCCATGACCGAGATCCA 1051
 DB 2083 CTTCTGAGAGGCTGTTGGCAACACCCAGCTGGATGCCATGACCGAGATCCA 2142
 QY 1052 TGAAGTCAATCAGGACCTGATCCGCAAGGCTGAGGCAACAAGTGAAGAACTTCCAT 1111
 DB 2143 TGAAGTCAATCAGGACCTGATCCGCAAGGCTGAGGCAACAAGTGAAGAACTTCCAT 2202
 QY 1112 CGTTGTCTCCCTGGGACAGAGGAGTCCCAAGTGCCTGTGACCTGTGTGATGCTT 1171
 DB 2203 CGTTGTCTCCCTGGGACAGAGGAGTCCCAAGTGCCTGTGACCTGTGTGATGCTT 2262
 QY 1172 CGGTCCAGCAACCCCTGGGAGCTGGCCAAAGACTGTTTGGGCGCAAGAACTGGGCAA 1231
 DB 2263 CGGTCCAGCAACCCCTGGGAGCTGGCCAAAGACTGTTTGGGCGCAAGAACTGGGCAA 2322
 QY 1232 GATGTGTGTGACTGTTCGACGGATCCAGACGGGCGGCGG 1272
 DB 2323 GATGTGTGTGACTGTTCGACGGATCCAGACGGGCGGCGG 2363
 RESULT 9
 ADO19775
 ID ADO19775 standard; cDNA; 3240 BP.
 AC ADO19775;
 XX
 XX

DT 12-AUG-2004 (first entry)
 XX Human PRO polynucleotide #350.
 DE
 XX Human; PRO; gene; ss; immune related disorder;
 KM systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
 KM juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
 KM vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
 KM autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
 KM renal disease; demyelinating disease; central nervous system;
 KM peripheral nervous system; demyelinating polyneuropathy;
 KM Guillain-Barre syndrome;
 KM chronic inflammatory demyelinating polyneuropathy.
 XX Homo sapiens.
 OS
 PN .MO2004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003MO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM,
 PI Wood WI, Wu TD;
 XX
 DR WPI; 2004-42067/39.
 XX P-PSDB; AD019776.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS Claim 1; SEQ ID NO 724; 1731bp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polynucleotide of
 CC the invention.
 CC
 SQ Sequence 3240 BP; 681 A; 1048 C; 912 G; 598 T; 0 U; 1 Other;
 XX
 Query Match 68.6%; Score 876.2; DB 12; Length 3240;
 Best Local Similarity 99.7%; Pred. No. 2.4e-199;
 Matches 878; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 392 AGAAGTACAGAGATCTCATGACATCTTCAACGGGCCCGGAGCCAGCTTCACTCTGGGCTC 451
 DB 1483 AGAAGTACAGAGATCTCATGACATCTTCAACGGGCCCGGAGCCAGCTTCACTCTGGGCTC 1542
 QY 452 CATGAGGAGCAGAGAGCGGAGCCAGCAACGACCTGTGCTGCTGAGTGAAGAGAGTAA 511
 DB 1543 CATGAGGAGCAGAGAGCGGAGCCAGCAACGACCTGTGCTGCTGAGTGAAGAGAGTAA 1602
 QY 512 AGGCTCATCATCATCATCATGCTCTCATGCGCATGCGAAGGCTCCGGCTGTGGCAACAA 571
 DB 1603 AGGCTCATCATCATCATCATGCTCTCATGCGCATGCGAAGGCTCCGGCTGTGGCAACAA 1662
 QY 572 GGAAGCTGTTGATGAGTGGGCGGGGACACAGACATGAGAGGATCTGGCCCTGACATTC 631
 DB 1663 GGAAGCTGTTGATGAGTGGGCGGGGACACAGACATGAGAGGATCTGGCCCTGACATTC 1722

QY 632 GCACAGTAAGTCCATGAGGCTTACATGCGCGGCAATGTAATTTCGANTGAAGATAGTGT 691
 DB 1723 GCACAGTAAGTCCATGAGGCTTACATGCGCGGCAATGTAATTTCGANTGAAGATAGTGT 1782
 QY 692 CCGGGGCTCAGAGCCCTTACAGAGTGGGGCCCTGAGAGATTCTTGAACGGGAGTTTG 751
 DB 1783 CCGGGGCTCAGAGCCCTTACAGAGTGGGGCCCTGAGAGATTCTTGAACGGGAGTTTG 1842
 QY 752 GGAGCACACCAAGATGACGAGAGCTCAGAGAAACCAAGTGTGCTGACAGGACACTGTC 811
 DB 1843 GGAGCACACCAAGATGACGAGAGCTCAGAGAAACCAAGTGTGCTGACAGGACACTGTC 1902
 QY 812 TGACCGGCGAGCGGCTGAACTCCACTCTCCGGAATGAGTCCGAGAAATGTCGG 871
 DB 1903 TGACCGGCGAGCGGCTGAACTCCACTCTCCGGAATGAGTCCGAGAAATGTCGG 1962
 QY 872 GGAGCTCGTTTCAACCAAGAGTTAACTTACAGGCTCCAGCTCAGCCCTCAGAGCAGCT 931
 DB 1963 GGAGCTCGTTTCAACCAAGAGTTAACTTACAGGCTCCAGCTCAGCCCTCAGAGCAGCT 2022
 QY 932 GGTGTGGCGGGCGGCGCCGAGAGCGGGCAAGCTCTTACTTACTTCCAGACCAATGGCG 991
 DB 2023 GGTGTGGCGGGCGGCGCCGAGAGCGGGCAAGCTCTTACTTACTTCCAGACCAATGGCG 2082
 QY 992 CTTCCTGAGACGCTGGGCTGTGGCCCAACACCCCAAGCTGTGATGATGATGATGATGAT 1051
 DB 2083 CTTCCTGAGACGCTGGGCTGTGGCCCAACACCCCAAGCTGTGATGATGATGATGATGAT 2142
 QY 1052 TGAGTCAATCAAGAGCTGATCCGCAAGGATGAGGCCAACAAGTGAAGAACTCTCCAT 1111
 DB 2143 TGAGTCAATCAAGAGCTGATCCGCAAGGATGAGGCCAACAAGTGAAGAACTCTCCAT 2202
 QY 1112 CGTTGTCTCCCTGGGAGACAGGAGTCCCAAGTGTGCTGTGATGATGATGATGATGAT 1171
 DB 2203 CGTTGTCTCCCTGGGAGACAGGAGTCCCAAGTGTGCTGTGATGATGATGATGATGAT 2262
 QY 1172 CCGTCCCAAGCAACCTCGGAGAGTGGCCCAAGACTGTTTGGGGCCCAAGAACTGGGCA 1231
 DB 2263 CCGTCCCAAGCAACCTCGGAGAGTGGCCCAAGACTGTTTGGGGCCCAAGAACTGGGCA 2322
 QY 1232 GATGTGTGTGAGACTGTTGACAGGATCCAGACGGGCGGCGG 1272
 DB 2323 GATGTGTGTGAGACTGTTGACAGGATCCAGACGGGCGGCGG 2363

RESULT 10
 ADD93426
 ID ADD93426 strand; cDNA; 3215 BP.
 XX
 AC ADD93426;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human lipid-associated molecule LIPM-14 polynucleotide.
 XX
 KM Human; lipid-associated molecule; LIPM-14; neuroprotective; relaxant;
 KM antihypertensive; antidiabetic; cytoskeletal; dermatological; immunosuppressive;
 KM antiinflammatory; chylomicron; antiallergic; cerebroprotective;
 KM gastrointestinal; hepatotropic; nephrotropic; anticonvulsant;
 KM antiparasitism; antibacterial; antiparasitic; fungicide; protozoacide;
 KM virucide; uterotropic; antineumatic; cardiant; cardiovascular; anti-HIV;
 KM noctropic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 192..2546
 FT CDS /tag= a
 FT /product= "Human LIPM-14"
 XX
 XX MO2003083081-A2.

PD 09-OCT-2003.
 XX 27-MAR-2003; 2003MO-US009755.
 PF
 XX 29-MAR-2002; 2002US-0168722P.
 PR 03-MAY-2002; 2002US-0377576P.
 PR 05-JUL-2002; 2002US-039394P.
 PR 27-SEP-2002; 2002US-0414269P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Emerling BM, Margulis JP, Chawla NK, Lee SY, Duggan BM, Warren BM,
 PI Baugman MK, Lee EA, Griffin JA, Kable AE, Elliott VS, Chang H;
 PI Lee S, Ramkumar J, Bulloch SA, Hafalia AJA, Khare R, Jiang X;
 PI Jackson AA;
 XX
 DR MPI: 2003-788347/74.
 DR P-PSDB; ADD93407.
 XX
 PT New LIPM polypeptides, useful for diagnosing, preventing, and treating
 PT disorders associated with abnormal expression or activity of LIPM, e.g.
 PT neuromuscular, immunological, cardiovascular disorders, cancer and/or
 PT infections.
 XX
 PS Claim 88, Page 232-233; 238pp; English.
 XX
 CC The present sequence is the nucleotide sequence of human lipid-associated
 CC molecule LIPM-14 (incyte polynucleotide 7512662CB1), which encodes a
 CC protein that shows homology to human Ca2+-independent phospholipase A2
 CC short isoform. This is one of 19 LIPM polynucleotides of the invention.
 CC The invention relates to novel LIPMs and the nucleic acids encoding
 CC them, and to the use of nucleic acids and proteins in the diagnosis,
 CC treatment and prevention of disorders associated with abnormal expression
 CC or activity of LIPM such as neurodegenerative disorders (e.g.
 CC Parkinson's disease, Alzheimer's disease), muscular disorders (e.g.
 CC myotonic dystrophy, cataract), endocrine disorders (e.g. diabetes,
 CC Grave's disease), cancers (e.g. leukemia, cervical or breast cancer),
 CC immunological disorders (e.g. scleroderma, systemic lupus erythematosus,
 CC allergies), gastrointestinal disorders (e.g. Crohn's disease), renal
 CC disorders (e.g. Goodpasture's syndrome), infections (e.g. viral,
 CC bacterial, fungal, parasitic, protozoal, helminthic), cardiovascular
 CC disorders (e.g. atherosclerosis), or hepatic diseases (e.g. cirrhosis).
 CC The invention also relates to the assessment of the effects of exogenous
 CC compounds on the expression of nucleic acids and LIPMs. The invention
 CC provides expression vectors, host cells, antibodies, agonists and
 CC antagonists, transgenic organisms, and arrays and microarrays of the
 CC polynucleotides.
 CC
 XX
 SQ Sequence 3215 BP; 666 A; 1021 C; 923 G; 605 T; 0 U; 0 Other;
 Query Match 68.6%; Score 876; DB 10; Length 3215;
 Best Local Similarity 99.4%; Pred. No. 2.6e-199;
 Matches 879; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 389 CACAGAACTACAGGATCTTATGACATCTTACAGGGCCCGAAGCCGCTTCTCTGGG 448
 DB 1469 CAGACAACTACAGGATCTTATGACATCTTACAGGGCCCGAAGCCGCTTCTCTGGG 1528
 QY 449 CTCCTATGAGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 508
 DB 1529 CTCCTATGAGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1588
 QY 509 GAAAGGCTTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 568
 DB 1589 GAAAGGCTTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1648
 QY 569 CAAGAGCTTGTGATCTGGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 628
 DB 1649 CAAGAGCTTGTGATCTGGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1708
 QY 629 TCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 688
 DB 1709 TCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1768

QY 689 GTTCCGGGGCTCCAGGCGCTTACAGATCGGGGCCCTGAGAGATTCTGAGCGGAGATT 748
 DB 1769 GTTCCGGGGCTCCAGGCGCTTACAGATCGGGGCCCTGAGAGATTCTGAGAGCGGAGATT 1828
 QY 749 TGGGAGACACCAACCAATGACGAGCTCAGAGAAACCCAGGTATGCTGACAGGACACT 808
 DB 1829 TGGGAGACACCAACCAATGACGAGCTCAGAGAAACCCAGGTATGCTGACAGGACACT 1888
 QY 809 GTCTGACCGGACCGGCTGAACTCCACCTCTCCGGAATACAGATGCTCCAGAACTGT 868
 DB 1889 GTCTGACCGGACCGGCTGAACTCCACCTCTCCGGAATACAGATGCTCCAGAACTGT 1948
 QY 869 CCGGAGCGCTCGTTTCAACCAAGACGTTAACTCAGCGCTCCAGCTCAGCCCTCAGACCA 928
 DB 1949 CCGGAGCGCTCGTTTCAACCAAGACGTTAACTCAGCGCTCCAGCTCAGCCCTCAGACCA 2008
 QY 929 GCTGTGTGTGGCGGGCGGGCCGGAAGACGCGGGGAGCTCTTACTTACTTCCAGCCCAATGG 988
 DB 2009 GCTGTGTGTGGCGGGCGGGCCGGAAGACGCGGGGAGCTCTTACTTACTTCCAGCCCAATGG 2068
 QY 989 GCGCTTCTGAGACGCTGTGGCTGTGGCCAAACCCAGCTGATGATGATGATGATGATGATGAT 1048
 DB 2069 GCGCTTCTGAGACGCTGTGGCTGTGGCCAAACCCAGCTGATGATGATGATGATGATGATGAT 2128
 QY 1049 CCATGAGTACATCAGACCTGATCCGCAAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGG 1108
 DB 2129 CCATGAGTACATCAGACCTGATCCGCAAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGG 2188
 QY 1109 CATCGTGTCTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1168
 DB 2189 CATCGTGTCTCCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2248
 QY 1169 CTTCCTCTCCAGCAACCTCTGGAGCTGAGCAAGACTGTTTGGGCGCAAGCAACTGGG 1228
 DB 2249 CTTCCTCTCCAGCAACCTCTGGAGCTGAGCAAGACTGTTTGGGCGCAAGCAACTGGG 2308
 QY 1229 CAAGATGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1272
 DB 2309 CAAGATGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2352
 RESULT 11
 AAH14129
 ID AAH14129 standard; cDNA; 2392 BP.
 XX
 AC AAH14129;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human cDNA sequence SEQ ID NO:11329.
 XX
 KM Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN BP1074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

DR WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX Claim 8; SEQ ID NO 11329; 2537bp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX Sequence 2392 BP; 504 A; 774 C; 679 G; 435 T; 0 U; 0 Other;

Query Match 63.4%; Score 809.8; DB 4; Length 2392; Best Local Similarity 95.6%; Pred. No. 1.6e-183; Matches 844; Conservative 0; Mismatches 37; Indels 2; Gaps 1;

QY 392 AGAATCTACAGATCTCATGCACTCTCAACGGGCGGAGCCGATTCCTCTGGGCTC 451

DB 772 AGAATCTACAGATCTCATGCACTCTCAACGGGCGGAGCCGATTCCTCTGGGCTC 831

QY 452 CATGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 511

DB 832 CATGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 891

QY 512 AGGCTCTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 571

DB 892 AGGCTCTATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 951

QY 572 GAACCTGTTGATCGGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 631

DB 952 GAACCTGTTGATCGGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1011

QY 632 GCACAGTAAGTCCATGAGCTCTCAATGCGGAGATGTTTCCAGTGAAGATGAGGTTT 691

DB 1012 GCACAGTAAGTCCATGAGCTCTCAATGCGGAGATGTTTCCAGTGAAGATGAGGTTT 1071

QY 692 CCGGGGCTCCAGGCTCCAGAGTCCGAGGCTCCAGAGGCTCCAGAGGCTCCAGAGGCT 751

DB 1072 CCGGGGCTCCAGGCTCCAGAGTCCGAGGCTCCAGAGGCTCCAGAGGCTCCAGAGGCT 1131

QY 752 GAGGACACCAAGATGACGAGCTCAGAGAAACCAAGATGATGTCACAGGACACCTGTC 811

DB 1132 GAGGACACCAAGATGACGAGCTCAGAGAAACCAAGATGATGTCACAGGACACCTGTC 1191

QY 812 TGACCGGACGCGGCTCACTCTCCGGAATAGAGTCTCCAGAACTGTCG 871

DB 1192 TGACCGGACGCGGCTCACTCTCCGGAATAGAGTCTCCAGAACTGTCG 1251

QY 872 GAGGCTCTGTTCAACCAAGAGCTTAACTCAGGCTCCAGCTCAAGCTCCAGAC-AG 929

DB 1252 GAGGCTCTGTTCAACCAAGAGCTTAACTCAGGCTCCAGGCTCCAGGCTCCAGGCTCTT 1311

QY 930 CTGTGTGGGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 989

DB 1312 CTGTGTGGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1371

QY 990 CGCTTCCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1049

DB 1372 CGCTTCCTGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1431

QY 1050 CATGATGATCAATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1109

DB 1432 CATGATGATCAATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1491

QY 1110 ATCGTTGTCCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1169

DB 1492 ATCGTTGTCCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1551

QY 1170 TTCCGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1229

DB 1552 TTCCGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1611

QY 1230 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1272

DB 1612 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1654

RESULT 12

AA05842

ID AA05842 standard; cDNA; 2935 BP.

XX AA05842;

XX 15-JUN-1996 (first entry)

DE Calcium-independent cytosolic phospholipase-A2/B enzyme cDNA.

KW CHO; calcium-independent cytosolic phospholipase-A2/B; enzyme;

KW phospholipase-A2; phospholipase-B; drug screening; antiinflammatory;

KW antibody; ds.

XX Cricetulus griseus.

OS

XX Key Location/Qualifiers

FT CDS 96..2352

FT /+tag= a

PN US5466595-A.

PD 14-NOV-1995.

PF 27-JUL-1994; 94US-00281193.

PR 27-JUL-1994; 94US-00281193.

XX (GENE) GENETICS INST INC.

PA

XX Tang J, Jones S;

PI

XX WPI; 1996-009526/01.

DR P-PSDB; AAR83018.

XX

PT Isolated polynucleotide encoding cytosolic phospholipase A2/B - for

PT producing enzyme for use in screening anti-inflammatory agents and prodn.

PT of antibodies.

PS Claim 1; Col 15-22; 24pp; English.

XX This cDNA was prepared from RNA isolated from CHO-DUX cells. The cDNA may

XX be ligated into predigested lambda phage ZAP11/ScotI vector and packaged

XX into phage particles. The cDNA library was screened using oligonucleotide

XX probes based on peptide sequences of calcium-independent phospholipase-

XX A2/B. This polynucleotide may be operably linked to an expression control

XX sequence such as pMT2 or pED expression vectors in order to produce the

CC phospholipase enzyme recombinantly. Host cells include animal cells,
 CC insect cells, eukaryotes, prokaryotes, etc. The sequence may also be
 CC expressed in transgenic animals (e.g. milk of transgenic cow). The
 CC encoded protein is used to screen for agents which inhibit phospholipase
 CC activity for use as anti-inflammatory agents

XX Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 U; 0 Other;

Query Match 55.4%; Score 708; DB 2; Length 2935;
 Best Local Similarity 87.6%; Pred. No. 3.8e-159;
 Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 389 CACAGAACTACAGAGATTCATGCACATCTCACGGGCCCGAAGCCAGCTTCCTGGG 448
 DB 1277 CAAACAGCTTCAGAGACTTCATGCTCCCGAGCCCGGAACAGCATTCCTGAG 1336
 QY 449 CTCGATGAGGAGAGAGAGGAGCCACGACACTGCTGTGCTGTGATGAGAGAGAGT 508
 DB 1337 CTCGATGAGGAGAGAGAGGAGAAATCCATGATCACTGCTGTGCTGTGAGAGAGGAGGCT 1396
 QY 509 GAAAGCCTCATCATCATCATGCTCTCATGCTCATGCTCATGAGAGAGCCTCGGGTGTGGCAC 568
 DB 1397 GAAAGCCTGTGTATCATCATCACTCTCATGCTCATGAGAGAGCCTCAAGTGTGGCAC 1456
 QY 569 CAAAGACTGTGTGAGTGGTGGCGGACACAGCACTGAGAGGATCTGGCCCTGGCCAT 628
 DB 1457 CAAAGACTGTGTGAGTGGTGGCGGACACAGCACTGAGAGGATCTGGCCCTGGCCAT 1516
 QY 629 TCTGCAAGTAATGCTCATGCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 688
 DB 1517 TCTGCAAGTAATGCTCATGCTGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1576
 QY 689 GTTCCGGGCTCCAGAGCCTTACAGAGTGGGGCCCTGAGAGAGTCTTGAAGCGGAGTT 748
 DB 1577 GTTCCGGGCTCCAGAGCCTTACAGAGTGGGGCCCTGAGAGAGTCTTGAAGCGGAGTT 1636
 QY 749 TGGGAGACACACCAAGTACAGAGTGGAGAAACCAAGTGTGCTGACAGGACACT 808
 DB 1637 TGGGAGACACACCAAGTACAGAGTGGAGAAACCAAGTGTGCTGACAGGACACT 1696
 QY 809 GTCGACCGGACCGGCTGACCTTCCGGAATAGAGAGTCTGACAGAACTGT 868
 DB 1697 GTCGACCGGACCGGCTGACCTTCCGGAATAGAGAGTCTGACAGAACTGT 1756
 QY 869 CCGGAGCCTGCTTCAACAGACGTTAACTTCAAGCCTTCAAGCCTTCAAGACCA 928
 DB 1757 TCGGGAACCTCGCTTCAACAGACGTTAACTTCAAGCCTTCAAGCCTTCAAGACCA 1816
 QY 929 GCTGTGTGGCGGCGGCGGAGAGCGGCGGAGCTCTTACTTACTTCCGACCCCAATGG 988
 DB 1817 ACTGTATGGCGAGAGCGGCGGAGAGCTGCGGAGCGGCGGAGCTTACTTCCGCGCCCAATGG 1876
 QY 989 GCGCTTCTGGAAGGAGGAGGCTGTGGCAACACCCGAGCTGGATGCGATGACCGGAT 1048
 DB 1877 AGCTTCTGGAAGGAGGAGGCTGTGGCAACACCCGAGCTGGATGCGATGACCGGAT 1136
 QY 1049 CCATGATACATACAGAGACCTGATCCGCAAGGCTGAGGCCCAAGGTGAGAACTCTC 1108
 DB 1937 CCATGATACATACAGAGACATGATCCGCAAGGCGCAAGGCAAGGTGAGAACTCTC 1196
 QY 1109 CATGCTGTGTCTCTCTGGGAGACAGAGAGTCCCAAGTGCCTGTGACTGTGTGATGT 1168
 DB 1997 CATAGTGTGTCTCTCTGGGAGACAGAGAGTCCCTCAAGTCCCGGTAACTGTGTGATGT 2056
 QY 1169 CTCGCGGCGGAGAACCCCTGGGAGCTGGGCAAGACTGTTTGGGGCGCAAGAACTGGG 1228
 DB 2057 CTCGCGGCGGAGAACCCCTGGGAGCTGGGCAAGACTGTTTGGGGCGCAAGAACTGGG 2116
 QY 1229 CAAAGATGTGTGAGACTGTGCAACGATCCAGACGGGCGGCGCG 1272
 DB 2117 CAAAGATGTGTGAGACTGTGCAACGATCCAGATGCTGGGCGG 2160

RESULT 13
 AAT4578
 ID AAT44578 standard; cDNA; 2935 BP.
 XX
 XX AAT44578;

XX 25-MAR-2003 (revised)
 DT 11-FEB-1997 (first entry)
 XX
 DE Calcium-independent cytosolic phospholipase A2/B coding sequence.
 XX
 XX cPLA2/B; calcium-independent cytosolic phospholipase A2/B;
 KW arachidonic acid; 1-palmitoyl-2-[14C]-arachidonyl-phosphatidylcholine;
 KM anti-inflammatory; screen; rheumatoid arthritis; de.

OS Synthetic.

FN Key Location/Qualifiers
 FT CDS 96..2354
 FT /*tag= a

PN US5554511-A.

PD 10-SEP-1996.

XX 14-APR-1995; 95US-00422420.

XX 27-JUL-1994; 94US-00281193.

XX (GENE) GENETICS INST INC.

PI Tang J, Jones S;

XX WPI; 1996-424653/42.

DR P-PSDB; AAW01479.

XX

PT Prodn. of a Ca-independent cytosolic phospholipase A(2)/B - by culturing
 PT host cells contg. the phospholipase gene, useful for screening anti-
 PT inflammatory agents for treating e.g. rheumatoid arthritis.

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Db      1457 CAAGGACCTTTCAGCTGGGTGGGAGGACCAAGCACTGGGGGCACTCTGGCCAT 1516
Qy      629 TCTGCA CAGTAAGTCAATGCGCTTCACTATGCGGGCATGTACTTTCCATGAAAGATGAGT 688
Db      1517 TCTGCA CAGTAAGTCAATGCGCTTCACTATGCGGGCATGTACTTTCCATGAAAGATGAGT 1576
Qy      689 GTTCCGGGGCTCCAGGCGCTTCAAGATCGGGGCGCTTGAAGAGATTTCTTAAGGGGAGTT 748
Db      1577 GTTTCGGGGCTCAGGCGCTTATATGATCTGAGACCCCTGAGAGAGATTTCTTAAGGGGAGTT 1636
Qy      749 TGGGAGACACCAAGATGACGAGACGTCAAGAAACCAAGATGATGCTGACAGGACACT 808
Db      1637 TGGGAGACACCAAGATGACGAGATGCAAAAAACCAAGATGATGCTGACAGGACACT 1696
Qy      809 GTCTGACCCGAGCCGGCTGAACTCCACTCTTCCGGAACCTAGATGCTCCAGAACTGT 868
Db      1697 GTCTGACCCGAGCCGAGACGCTCCCACTGTTCGCAATTAAGATGCTCCAGAGGTCAAT 1756
Qy      869 CCGGAGACCTCTCTTCAACCAAGACCTTAACCTCAGGCTCCAGCTCCAGACCA 928
Db      1757 TCGGGAACCTCGCTTCAACCAAAACATTAACCTGAAGCCGCACTCAGCTGCAAGCA 1816
Qy      929 GCTGATGCGGCGGCGGCGGCGGAGACGCGGAGAGCTCTACTTACTTCCGACCAATGG 988
Db      1817 ACTGATATGGCGAGCAGCCGCGGAGCACTGGGGAGAGCCCACTTCCGGGCCAATGG 1876
Qy      989 GCGCTTCTTGACGCGTGGGCTGTTGGCAACACCCCAAGCTGATGCCATGACCAAT 1048
Db      1877 ACCTTTCCTGATGATGCGGCTGCTGGCCCAACCCCACTAGATGCCATGACTGAAT 1936
Qy      1049 CCATGATGTAACAACAGACCTGATCCGCAAGGTCAGGCGCAACCAAGTGAAGAACTTC 1108
Db      1937 CCATGATGTAACAACAGACCTGATCCGCAAGGTCAGGCGCAACCAAGTGAAGAACTTC 1996
Qy      1109 CATGCTTGTCTCCCTGCGGAGACAGGAGGTCCCAAGTCCCTGTCGCTGTGATGT 1168
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RESULT 14
AAT59199
ID      AAT59199 standard; cDNA; 2935 BP.
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AC      AAT59199;
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DT      17-OCT-2003 (revised)
DT      25-MAR-2003 (revised)
DT      20-MAY-1997 (first entry)
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DE      Ca-independent phospholipase A2/B gene.
XX
KW      Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;
KW      chromatography; DEAE anion exchange; hydrophobic interaction; lambda;
KW      heparin Toyopearl; chromatofocusing; eukaryotic expression vector; COS;
KW      CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade; ds.
XX
OS      Cricetus griseus; ovary cells.
XX
FH      Key
FT      CDS
FT      CDS
FT      CDS
XX
XX      Location/Qualifiers
XX      /tag= a
XX      /product= "ca-independent phospholipase A2/B"
XX
PN      US5589170-A.

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XX
PD      31-DEC-1996.
XX
PF      14-APR-1995; 95US-00422106.
XX
PR      27-JUL-1994; 94US-00281193.
XX
PA      (GEM ) GENETICS INST INC.
XX
PI      Tang J, Jones S;
XX
DR      WPI; 1997-076789/07.
XX
DR      P-PSDB; AAM13163.
XX
PT      Compden. comprising calcium-independent phospholipase enzyme - for
PS      screening for anti-inflammatory agents.
XX
PS      Claim 5; Col 15-22; 24pp; English.
XX
CC      This is the nucleotide sequence encoding the Ca-independent phospholipase
CC      A2/B from Chinese hamster ovary cells. The protein was isolated from
CC      these cells by conventional chromatographic methods e.g. DEAE anion
CC      exchange, hydrophobic interaction, heparin Toyopearl and Mono P 5/20
CC      chromatofocusing chromatography. The purified protein has mol. wt. of 86
CC      kD and an optimum pH 6. The protein was used for amino acid sequencing
CC      from which pools of degenerate probes were synthesised. The probes were
CC      used to screen a CHO cell cDNA library in lambda ZAPII vector. Of 40000
CC      recombinant phages screened, 12 positive plaques were isolated. One of
CC      these, designated clone 9, contained this sequence. The phospholipase
CC      gene can be inserted into eukaryotic vectors for expression in COS or CHO
CC      cells. The protein, or peptides derived from it e.g. AAM13164-76, can be
CC      used to identify phospholipase inhibitors that can be used as anti-
CC      inflammatory agents, esp. against components of the arachidonic acid
CC      cascade. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT
CC      -2003 to standardise OS field)
XX
SQ      Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 U; 0 Other;
XX
Query Match 55.4%; Score 708; DB 2; Length 2935;
Best Local Similarity 87.6%; Pred. No. 3,8e-159;
Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
Qy      389 CACGAGACTACAGGATCTCATGACATCTCAGGGGCGGGAAGCCGCTTACCTGGG 448
Db      1277 CAACAGCTTCAGAGACTATGCTCATCTCCGAGCCGGAAGCCAGCAATTCATCTGAG 1336
Qy      449 CTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 508
Db      1337 CTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1396
Qy      509 GAAAGGCTTCATCATATCATCATCTCTCATTCGCGATGAGAAAGGCTCGGGTGTGGCCAC 568
Db      1397 GAAAGGCTTCATCATATCATCATCTCTCATTCGCGATGAGAAAGGCTTCAGGTGTGGCCAC 1456
Qy      569 CAAGGACCTGTTGATGGGATGGGCGGAGACAGACATGAGAGGATCTGAGCCCTGGCCAT 628
Db      1457 CAAGGACCTTTCAGCTGGATGGGAGAGAAACAGACATGAGAGGATCTGAGCCCTGGCCAT 1516
Qy      629 TCTGCA CAGTAAGTCAATGCGCTTCACTATGCGGGCATGTACTTTCCATGAAAGATGAGT 688
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Qy      689 GTTCCGGGGCTCCAGGCGCTTCAAGATCGGGGCGCTTGAAGAGATTTCTTAAGGGGAGTT 748
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Qy      809 GTCTGACCCGAGCCGGCTGAACTCCACTCTTCCGGAACCTAGATGCTCCAGAACTGT 868
Db      1697 GTCTGACCCGAGCCGAGACGCTCCCACTGTTCGCAATTAAGATGCTCCAGAGGTCAAT 1756

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QY 869 CCGGAGACCTGTTTCACAGAACGTTAACTCAGGCTCCAGCTCAGGCTCAGACCA 928
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 DB 2117 CAAGATGTGTGTGACTGTTCACAGATCCAGATGGTGGGCGGCTG 2160
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RESULT 15

AAT68827
 ID AAT68827 standard; cDNA; 2935 BP.

AC AAT68827;

DT 27-AUG-2003 (revised)
 DT 07-AUG-1997 (first entry)

DE Hamster cytosolic phospholipase A2/B cDNA.

KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
 inflammation; inhibitor; antiinflammatory; CHO; ds.

OS Cricetus.

Location/Qualifiers
 96..2354
 /*tag= a

Key CDS

W09717448-A2.

15-MAY-1997.

07-NOV-1996; 96WO-US017794.

08-NOV-1995; 95US-00555568.

(GEMV) GENETICS INST INC.

Jones S, Tang J;

WPI; 1997-281037/25.

P-PSDB; AAW17849.

Calcium independent phospholipase A2/B - used to reduce inflammation in a
 mammalian subject.

Example 4; Page 33-36; 74BP; English.

A cDNA clone (AAT68827), deposited as ATCC 6969, codes for a cytosolic
 phospholipase A2/B (sPLA2/B) (AAW17849) that is thought to be involved in
 the arachidonic acid cascade. It was obtd. by screening a CHO-DUX cDNA

CC library with probes based on isolated peptides of the enzyme. Recombinant
 CC sPLA2/B was expressed in COS and CHO cells. Probes based on the hamster
 CC sPLA2/B clone were used to identify human sPLA2/B partial cDNA clones
 CC (see also AAT68823-26). (Updated on 27-AUG-2003 to correct OS field.)
 XX

SQ Sequence 2935 BP; 697 A; 856 C; 810 G; 572 T; 0 U; 0 Other;

Query Match 55.4%; Score 708; DB 2; Length 2935;
 Best Local Similarity 87.6%; Pred. No. 3.8e-159;
 Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 389 CACAGACTACAGGATCTCATGCACTTCAGGGGCGCCGAAAGCCAGGCTTACTCTGGG 448
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 DB 1277 CAACAGCTTCAGGACCTCATGCTCCATCTCCGAGCCCGAAGCCGCAATTACTCTGAG 1336
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 QY 449 CTCATGAGGGAACGAGACGGGACCAAGACCACTGTGTGCTGTGAGAGAGAGAT 508
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 DB 1337 CTCATGAGGAGATGAGAGGAGATCCATATCACTGTCTGTGCTGAGAGAGGGGCGT 1396
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Thu Dec 16 19:13:25 2004

us-10-612-668-18.rng

Page 15

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 11:27:19 ; Search time 128 Seconds
(Without alignments)
7091.230 Million cell updates/sec

Title: US-10-612-668-18

Sequence: 1 GAATTTGAGGGCCCCGAGGTC.....CAGACGGGGGCGCGAATTC 1277

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 1649014

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| 2 | 1277 | 100.0 | 1277 | 3 US-09-519-223-18 | Sequence 18, Appl |
| 3 | 1277 | 100.0 | 1277 | 4 US-09-927-180-18 | Sequence 18, Appl |
| 4 | 885.8 | 69.4 | 2112 | 2 US-08-555-568B-22 | Sequence 22, Appl |
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| 23 | 41.8 | 3.3 | 1866 | 1 US-08-336-408B-1 | Sequence 1, Appl |
| 24 | 41.8 | 3.3 | 1866 | 5 PCT-US91-00399-1 | Sequence 1, Appl |
| 25 | 41.8 | 3.3 | 5449 | 4 US-10-329-668-9 | Sequence 9, Appl |
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| 28 | 40.6 | 3.2 | 1984 | 4 US-09-377-466B-9 | Sequence 9, Appl |
| 29 | 40.6 | 3.2 | 1984 | 4 US-09-377-466B-11 | Sequence 11, Appl |
| 30 | 40.6 | 3.2 | 3039 | 4 US-09-377-466B-19 | Sequence 19, Appl |
| 31 | 40.6 | 3.2 | 3039 | 4 US-09-377-466B-21 | Sequence 21, Appl |
| 32 | 40.6 | 3.2 | 3450 | 4 US-09-377-466B-17 | Sequence 17, Appl |
| 33 | 40.6 | 3.2 | 3469 | 4 US-09-377-466B-23 | Sequence 23, Appl |
| 34 | 40.4 | 3.2 | 1614 | 4 US-09-409-778-2 | Sequence 2, Appl |
| 35 | 40.4 | 3.2 | 2338 | 1 US-08-425-069-1 | Sequence 1, Appl |
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| 37 | 39.8 | 3.1 | 927 | 4 US-09-252-991A-7387 | Sequence 7387, Ap |
| 38 | 39.8 | 3.1 | 978 | 4 US-09-252-991A-7319 | Sequence 7319, Ap |
| 39 | 39.8 | 3.1 | 1008 | 4 US-09-252-991A-7300 | Sequence 7300, Ap |
| 40 | 39.4 | 3.1 | 2514 | 3 US-09-144-914-3 | Sequence 3, Appl |
| 41 | 39.4 | 3.1 | 747 | 4 US-09-489-039A-5684 | Sequence 5684, Ap |
| 42 | 38.2 | 3.0 | 3001 | 4 US-09-620-312D-494 | Sequence 494, Ap |
| 43 | 38 | 3.0 | 1566 | 4 US-09-252-991A-1548 | Sequence 1548, Ap |
| 44 | 38 | 3.0 | 1611 | 4 US-09-252-991A-1569 | Sequence 1569, Ap |
| 45 | 38 | 3.0 | 2088 | 4 US-09-252-991A-1453 | Sequence 1453, Ap |

ALIGNMENTS

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RESULT 1
US-08-555-568B-18
; Sequence 18, Application US/08555568B
; Patent No. 597864
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1277 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 396..1271
; US-08-555-568B-18

Query Match      100.0%; Score 1277; DB 2; Length 1277;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-519-223-18

; Sequence 18, Application US/09519223

; Patent No. 6278140

; GENERAL INFORMATION:

; APPLICANT: Jones, Simon

; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/519,223

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/555,568

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Brown, Scott A.

; REGISTRATION NUMBER: 32,724

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1277 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 396..1271

; US-09-519-223-18

Query Match 100.0%; Score 1277; DB 3; Length 1277;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAATTTTGGGCCCCAGGTGGTATTATGACAGATCGGCTCCAGTCAGAAAGACATT 60
Db      1 GAATTTTGGGCCCCAGGTGGTATTATGACAGATCGGCTCCAGTCAGAAAGACATT 60
Qy      61 GTCTGAAGAGACACGCAAGGATATTATGCTTTGGGTTTCAAGAGAGATTAGG 120
Db      61 GTCTGAAGAGACACGCAAGGATATTATGCTTTGGGTTTCAAGAGAGATTAGG 120

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| | | | |
|----|------|--|------|
| OY | 121 | GGAACTGGGAGCTGGCTGGGAGGAGGTGGAGAGCCCTTCCAGAGAGAGGGGCCCCCTT | 180 |
| Db | 121 | GGAACTGGGAGCTGGCTGGGAGGAGGTGGAGAGCCCTTCCAGAGAGAGTGGGCCCCCTT | 180 |
| OY | 181 | TCCACTCCAGCCCATTTCTCTCTGTGGCTGTGGCTCAGCTTTCCTTGGGACAGAGTC | 240 |
| Db | 181 | TCCACTCCAGCCCATTTCTCTCTGTGGCTGTGGCTCAGCTTTCCTTGGGACAGAGTC | 240 |
| OY | 241 | CTTCTGTGGGGAAGGAGACAGATGACAGGGGGAGTGGGGGATGAGGGGCTGTGGCGTGGG | 300 |
| Db | 241 | CTTCTGTGGGGAAGGAGACAGATGACAGGGGGAGTGGGGGAGTGGGGGCTGTGGCGTGGG | 300 |
| OY | 301 | CGAGGCACAGCCCAAGTTTGATCTTGGGACCTCTGGGGTAGAGGGCTTGGGAGCCCAAC | 360 |
| Db | 301 | CGAGGCACAGCCCAAGTTTGATCTTGGGACCTCTGGGGTAGAGGGCTTGGGAGCCCAAC | 360 |
| OY | 361 | TGACCACAGATGCCCTGTCTGTGGCTCAGAGAACTACAGGATCTCATGCACTATCCAC | 420 |
| Db | 361 | TGACCACAGATGCCCTGTCTGTGGCTCAGAGAACTACAGGATCTCATGCACTATCCAC | 420 |
| OY | 421 | GGGCCCGGAAAGCAGCGTTCATCTGGGCTCCATGAGGAGCGAGAAAGCGGACCACAGCC | 480 |
| Db | 421 | GGGCCCGGAAAGCAGCGTTCATCTGGGCTCCATGAGGAGCGAGAAAGCGGACCACAGCC | 480 |
| OY | 481 | AACCTGTGGCTGGATGGAGGAGAGTGAAGGCTCATATCATTCAGCTCCATCAGC | 540 |
| Db | 481 | AACCTGTGGCTGGATGGAGGAGAGTGAAGGCTCATATCATTCAGCTCCATCAGC | 540 |
| OY | 541 | CCATCGAAGAGGCTCTGGGTGTGGCCACCAAGAGACTGTATTACCTGGGTGGGGACCA | 600 |
| Db | 541 | CCATCGAAGAGGCTCTGGGTGTGGCCACCAAGAGACTGTATTACCTGGGTGGGGACCA | 600 |
| OY | 601 | GCACTGAGGCACTCTGGCGCTTGGCCATTTCTGACAGTAAAGTCATAGCTTACATGCGCG | 660 |
| Db | 601 | GCACTGAGGCACTCTGGCGCTTGGCCATTTCTGACAGTAAAGTCATAGCTTACATGCGCG | 660 |
| OY | 661 | GCACTGAGGCACTCTGGCGCTTGGCCATTTCTGACAGTAAAGTCATAGCTTACATGCGCG | 720 |
| Db | 661 | GCACTGAGGCACTCTGGCGCTTGGCCATTTCTGACAGTAAAGTCATAGCTTACATGCGCG | 720 |
| OY | 721 | CCCTGAGAGAGTTCCTGAGACGGGAGTTTGGGGAGCAACACAAATGACAGGACTCAGGA | 780 |
| Db | 721 | CCCTGAGAGAGTTCCTGAGAGCGGAGTTTGGGGAGCAACACAAATGACAGGACTCAGGA | 780 |
| OY | 781 | AACCCAGGTGATCTGACAGGGAGACTGTCTGACCGGACGCGGCTGAACTCCACT | 840 |
| Db | 781 | AACCCAGGTGATCTGACAGGGAGACTGTCTGACCGGACGCGGCTGAACTCCACT | 840 |
| OY | 841 | TCGGGAATTAAGATCTCTCAGAAACTGTTCGGGAGCTCTGTTCAACCAAGACTTTAAC | 900 |
| Db | 841 | TCGGGAATTAAGATCTCTCAGAAACTGTTCGGGAGCTCTGTTCAACCAAGACTTTAAC | 900 |
| OY | 901 | TCAGGCTTCAGACTCAGGCTTCAGACAGAGCTGTGGCGGGCGGCGCCGAAGCACGGGG | 960 |
| Db | 901 | TCAGGCTTCAGACTCAGGCTTCAGACAGAGCTGTGGCGGGCGGCGCCGAAGCACGGGG | 960 |
| OY | 961 | CAGCTCTACTTACTTTCGAGCCCAATGAGGCGCTTCCTGAGCGGTGGGCTGTGGCAACA | 1020 |
| Db | 961 | CAGCTCTACTTACTTTCGAGCCCAATGAGGCGCTTCCTGAGCGGTGGGCTGTGGCAACA | 1020 |
| OY | 1021 | AACCCACGCTGGATGTCATGACCCGAGATTCATGAGTACATCAGAGCTGATCCGCAAGG | 1080 |
| Db | 1021 | AACCCACGCTGGATGTCATGACCCGAGATTCATGAGTACATCAGAGCTGATCCGCAAGG | 1080 |
| OY | 1081 | GTCAGGCGCAAGAGGTGAAGAACTCTCATGTGTCTCCCTGGGGACAGGAGAGTCTCC | 1140 |
| Db | 1081 | GTCAGGCGCAAGAGGTGAAGAACTCTCATGTGTCTCCCTGGGGACAGGAGAGTCTCC | 1140 |
| OY | 1141 | CACAAGTCTGTGACTGTGTGATGTCTTCCGTCCAGCAACCCCTGGAGCTGGGCCA | 1200 |
| Db | 1141 | CACAAGTCTGTGACTGTGTGATGTCTTCCGTCCAGCAACCCCTGGAGCTGGGCCA | 1200 |
| OY | 1201 | AGACTGTTTTGGGGCCAAAGAACTGGGCAAGATGTGTGTGAATCTGTTCACGCAATCCAG | 1260 |

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Db      1201 AGACTGTTTTGGGGCCCAAGCAATGGGCAAGATGTGTGACTGTTGCACGATCCAG 1260
Oy      1261 ACGGGCGGCCCGGAATTC 1277
Db      1261 ACGGGCGGCCCGGAATTC 1277

RESULT 3
US-09-927-180-18
; Sequence 18, Application US/09927180
; Patent No. 6645736
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 1277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEITICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 396..1271
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-927-180-18

Query Match      100.0%; Score 1277; DB 4; Length 1277;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1 GAATTCCTTAAGCCCCAGGTGTTATTGACAGCATCGGCTCCGATGCAAGAAAGCACTTT 60
Db      1 GAATTCCTTAAGCCCCAGGTGTTATTGACAGCATCGGCTCCGATGCAAGAAAGCACTTT 60

Oy      61 GTCTGAAGAGAGACACCGAAGGTATTCAATGACCTTTGGGGTTTCAAGAGGAAGAAATTGAGG 120
Db      61 GTCTGAAGAGAGACACCGAAGGTATTCAATGACCTTTGGGGTTTCAAGAGGAAGAAATTGAGG 120

Oy      121 GGAACCTGGAGCTGCTGGGCGAGGGGTGGGAGACCCCTTCCAGAGACAGTGGGCCCCCTTT 180
Db      121 GGAACCTGGAGCTGCTGGGCGAGGGGTGGGAGACCCCTTCCAGAGACAGTGGGCCCCCTTT 180

Oy      181 TCCACTCCAGCCCAATTTCTCTCCCTGTGGCCCTGTGGCTCAAGCTTTCTCTCGGACAAGATC 240
Db      181 TCCACTCCAGCCCAATTTCTCTCCCTGTGGCCCTGTGGCTCAAGCTTTCTCTCGGACAAGATC 240

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Db      181  TCCACTCCAGCCATTCTCTCTGTGCTCTGTGCTCAGCTTCTCTGAGCAGAGTC 240
Qy      241  CTTCTGTGGGGAAGGAGCAGATGACAGGGGAGTGGGGAGATGAGGGCTGTGGCCGTGGG 300
Db      241  CTTCTGTGGGGAAGGAGCAGATGACAGGGGAGTGGGGAGATGAGGGCTGTGGCCGTGGG 300
Qy      301  CGAGGACAGAGCCAGGTTTGTATCTAGGAGCTCTGGGGTGAAGAGGCTTGGGGAGCCACC 360
Db      301  CGAGGACAGAGCCAGGTTTGTATCTAGGAGCTCTGGGGTGAAGAGGCTTGGGGAGCCACC 360
Qy      361  TGACCAAGATGCGCTGTCTGTGCTTCAAGAACTACAGATCTCATATGCAATCTCAC 420
Db      361  TGACCAAGATGCGCTGTCTGTGCTTCAAGAACTACAGATCTCATATGCAATCTCAC 420
Qy      421  GGGCCGGAAGCCAGGCTTATCTCTGGGCTCTCAAGAGGAGAGAGGAGCCAGCCAGACC 480
Db      421  GGGCCGGAAGCCAGGCTTATCTCTGGGCTCTCAAGAGGAGAGAGGAGCCAGCCAGACC 480
Qy      481  ACCTGTGTGCTGTGATGAGAGAGAGAGAGGCTTATCTATCTCAGCTCTCTATCG 540
Db      481  ACCTGTGTGCTGTGATGAGAGAGAGAGAGGCTTATCTATCTCAGCTCTCTATCG 540
Qy      541  CCATCGAAGAGGCTCTGGGTTGTGGCCCAAGAGCTTGTGACTGGGTGGCGGAGCCA 600
Db      541  CCATCGAAGAGGCTCTGGGTTGTGGCCCAAGAGCTTGTGACTGGGTGGCGGAGCCA 600
Qy      601  GCACTGGAGGATCTGTGGCCCTGAGCCATTTGCAACAGTAACTGATGAGCTTATGCGCG 660
Db      601  GCACTGGAGGATCTGTGGCCCTGAGCCATTTGCAACAGTAACTGATGAGCTTATGCGCG 660
Qy      661  GCATGTATCTTTCGATGAGAGATGAGGTGTTCGGGGCTCCAGGCTTACAGAGTGGGGG 720
Db      661  GCATGTATCTTTCGATGAGAGATGAGGTGTTCGGGGCTCCAGGCTTACAGAGTGGGGG 720
Qy      721  CCTGTGAGAGGTTCTGGAAGCGGAGTTTGGGAGCAACAAGATGACGAGAGTGAAGA 780
Db      721  CCTGTGAGAGGTTCTGGAAGCGGAGTTTGGGAGCAACAAGATGACGAGAGTGAAGA 780
Qy      781  AACCAAGATGATGATGACAGAGCACTGTCTGACCGGAGCCGAGTGAATCCACTCT 840
Db      781  AACCAAGATGATGATGACAGAGCACTGTCTGACCGGAGCCGAGTGAATCCACTCT 840
Qy      841  TCCGGAACTAAGATCTCCAGAACTGTCCGGAGGCTCTGTTCAACAGAAAGTTAAC 900
Db      841  TCCGGAACTAAGATCTCCAGAACTGTCCGGAGGCTCTGTTCAACAGAAAGTTAAC 900
Qy      901  TCAAGGCTTCAAGCTCAGGCTTCAAGACCAAGCTGTGTGGCGGGCCCGAAGACGCGGG 960
Db      901  TCAAGGCTTCAAGCTCAGGCTTCAAGACCAAGCTGTGTGGCGGGCCCGAAGACGCGGG 960
Qy      961  CAGCTCTACTTACTTCCGACCCCATGTGGGCTTCTGAGACGCTGTGGGCTTGGCCAA 1020
Db      961  CAGCTCTACTTACTTCCGACCCCATGTGGGCTTCTGAGACGCTGTGGGCTTGGCCAA 1020
Qy      1021  ACCCAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db      1021  ACCCAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Qy      1081  GTGAGGCAACAGGTGAAGAACTCTCCATGCTGTGTCTCTGGGGAGAGGAGGTCC 1140
Db      1081  GTGAGGCAACAGGTGAAGAACTCTCCATGCTGTGTCTCTGGGGAGAGGAGGTCC 1140
Qy      1141  CACAAGTCTGTGATCTGTGTGATCTTCCGCTCCAGCAACCCCTGGGAGCTGGCCA 1200
Db      1141  CACAAGTCTGTGATCTGTGTGATCTTCCGCTCCAGCAACCCCTGGGAGCTGGCCA 1200
Qy      1201  AGACTGTGTTTGGGGCCAGAGAACTGGGCAAGATGTGTGTGATGATGATGATGAT 1260
Db      1201  AGACTGTGTTTGGGGCCAGAGAACTGGGCAAGATGTGTGTGATGATGATGATGAT 1260
Qy      1261  ACGGGCGCGCGGAAATTC 1277

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Db      1261  ACGGGCGCGCGGAAATTC 1277

RESULT 4
US-08-555-568B-22
; Sequence 22, Application US/08555568B
; Patent No. 597854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2112 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..2106
; US-08-555-568B-22

Query Match      69.4%; Score 885.8; DB 2; Length 2112;
Best Local Similarity 99.8%; Pred. No. 2.7e-233;
Matches 887; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      389  CACAGAACTACAGATCTCATGCAATCTCACAGGGCCCGGAAGCCAGCGTTCTGTGG 448
Db      1224  CACAGAACTACAGATCTCATGCAATCTCACAGGGCCCGGAAGCCAGCGTTCTGTGG 1283
Qy      449  CTCATGAGGAGAGAGAGGAGCCACAGACCACTGCTGTGCTGTGATGAGAGAGAT 508
Db      1284  CTCATGAGGAGAGAGAGGAGCCACAGACCACTGCTGTGCTGTGATGAGAGAGAT 1343
Qy      509  GAAAGGCTCATCATCATCAGCTCTCATGTGATGAGAGAGGCTCTGGGTGTGGCCAC 568
Db      1344  GAAAGGCTCATCATCATCAGCTCTCATGTGATGAGAGAGGCTCTGGGTGTGGCCAC 1403
Qy      569  CAGAGACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 628
Db      1404  CAGAGACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1463
Qy      629  TCTGCAAGTAATCTCATGTGCTTACATGCGCGGAGATGATCTTTCGATGAGAGAT 688
Db      1464  TCTGCAAGTAATCTCATGTGCTTACATGCGCGGAGATGATCTTTCGATGAGAGAT 1523
Qy      689  GTTCGGGGCTCAGAGCCCTTACAGAGTGGGGCCCTTGAAGAGTCTTCTGAAGCGGAG 748

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[illegible]

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Db      1974  ACAAGTGGCTGTGA CTTGTGTGATGTCTTCCTCCAGCAACCCCTGGAGCTGGCCAA 20333
Qy      1202  GACTGTTTTTGGGGCCAAAGAACTGGGCAAGATGCTGTGA CTTGTCAGGATCCAGA 12614
Db      2034  GACTGTTTTTGGGGCCAAAGAACTGGGCAAGATGCTGTGTGAC TTTGCAAGGATCCAGA 20933
Qy      1262  CGGGCGGGCCGAATTC 1277
Db      2094  CGGGCGGGCCGAATTC 2109

RESULT 8
US-09-519-223-20
; Sequence 20, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2109 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..2103
; US-09-519-223-20

Query Match      69.4%; Score 885.6; DB 3; Length 2109;
Best Local Similarity 97.9%; Pred. No. 3e-233;
Matches 897; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Db      422  GGCCCGAAGCAGCGTTCACTCTGGGCTCCATGAGGACGAGAACCCAGCACCA 481
Qy      422  GGCCCGAAGCAGCGTTCACTCTGGGCTCCATGAGGACGAGAACCCAGCACCA 481
Db      1254  GGCCCGAAGCAGCGTTCACTCTGGGCTCCATGAGGACGAGAACCCAGCACCA 1313
Qy      482  CCTGCTGTGCTGGATGAGAGAGAGGAAAGGCTCATCATATCCAGCTCTCATGCG 541

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Db 1314 CTTGCTGTGCTGATGAGAGAGAGTGAAGGCTCATCATCATCCAGCTCTCATGCG 1373
QY 542 CATCGAAGAGGCTCGGGGTGTGGCCACCAAGACCTGTTTGACTGGGTGGCGGGACACAG 601
Db 1374 CATCGAAGAGGCTCGGGGTGTGGCCACCAAGACCTGTTTGACTGGGTGGCGGGACACAG 1433
QY 602 CACTGAGGAGCTCTGGCCCTGGCCATTCTGACACAGTAAGTCCATGAGCTTACATGCGCGG 661
Db 1434 CACTGAGGAGCTCTGGCCCTGGCCATTCTGACACAGTAAGTCCATGAGCTTACATGCGCGG 1493
QY 662 CATGTACTTTCCGATGAAGATGAAGGTGTTCCGGGGCTCCAGGGCCCTCAAGATGCGGGCC 721
Db 1494 CATGTACTTTCCGATGAAGATGAAGGTGTTCCGGGGCTCCAGGGCCCTCAAGATGCGGGCC 1553
QY 722 CTTGAGAGAGTCTTGAAGCGGAGTTTGGGAGACACCAAGATGACGAGCTGAGAA 781
Db 1554 CTTGAGAGAGTCTTGAAGCGGAGTTTGGGAGACACCAAGATGACGAGCTGAGAA 1613
QY 782 ACCCAAGTATGTGTCAGAGGACACTGTGTGACCGGACCGGCTGAACTCCACTCTT 841
Db 1614 ACCCAAGTATGTGTCAGAGGACACTGTGTGACCGGACCGGCTGAACTCCACTCTT 1673
QY 842 CCGGAATACGATGCTCCAGAAACTGTCCGGGAGCTGTTTCAACCAAGCTTAACT 901
Db 1674 CCGGAATACGATGCTCCAGAAACTGTCCGGGAGCTGTTTCAACCAAGCTTAACT 1733
QY 902 CAGGCTCCAGCTCAGGCTCAGACCAAGCTGTGTGCGGGCGGCGGCGGAGAGCGGGGC 961
Db 1734 CAGGCTCCAGCTCAGGCTCAGACCAAGCTGTGTGCGGGCGGCGGCGGAGAGCGGGGC 1793
QY 962 AGCTCTACTTACTTCCGACCCCAATGGGGCTTCTGAGAGCTGTGGCTGTGGCCAA 1021
Db 1794 AGCTCTACTTACTTCCGACCCCAATGGGGCTTCTGAGAGCTGTGGCTGTGGCCAA 1853
QY 1022 CCCCAGCTGATGAGCTGAGACCAAGATCCATGAGTAATCAAGAACTGTATCCGCAAGG 1081
Db 1854 CCCCAGCTGATGAGCTGAGACCAAGATCCATGAGTAATCAAGAACTGTATCCGCAAGG 1913
QY 1082 TCAGGCAACAAAGTGAAGAACTCTCATGTTGTCTCCCTGGGAGCAGAGAGTCCG 1141
Db 1914 TCAGGCAACAAAGTGAAGAACTCTCATGTTGTCTCCCTGGGAGCAGAGAGTCCG 1973
QY 1142 ACAAGTGTCTGTGACCTGTGTGATGTCTTCCGTCCAGAGACCCCTGGAGCTGGCAA 1201
Db 1974 ACAAGTGTCTGTGACCTGTGTGATGTCTTCCGTCCAGAGACCCCTGGAGCTGGCAA 2033
QY 1202 GACTGTTTTGGGGCCCAAGAACTGGGCAAGATGTGTGAGACTGTTCACGATCCAGA 1261
Db 2034 GACTGTTTTGGGGCCCAAGAACTGGGCAAGATGTGTGAGACTGTTCACGATCCAGA 2093
QY 1262 CGGGCGGCGGAATTC 1277
Db 2094 CGGGCGGCGGAATTC 2109

RESULT 9
US-09-927-180-20

/ Sequence 20, Application US/09927180
/ Patent No. 6645736

/ GENERAL INFORMATION:

/ APPLICANT: Jones, Simon

/ Tang, Jim

/ TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

/ NUMBER OF SEQUENCES: 25

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Genetics Institute, Inc.

/ STREET: 87 Cambridgepark Drive

/ CITY: Cambridge

/ STATE: Massachusetts

/ COUNTRY: U.S.A.

/ ZIP: 02140

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/927, 180
/ FILING DATE: 09-Aug-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/519,223
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Brown, Scott A.
/ REGISTRATION NUMBER: 32,724
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 498-8224
/ TELEFAX: (617) 876-5851
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2109 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ HYPOTHETICAL: NO
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 43..2103
/ SEQUENCE DESCRIPTION: SEQ ID NO: 20:
/ US-09-927-180-20

Query Match 69.4%; Score 885.6; DB 4; Length 2109;
Best Local Similarity 97.9%; Pred. No. 3e-233;
Matches 897; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 362 GACCAAGATGCGCTCTGTGCTCTGCTCAAGAACTACAGATCTCATGACATCTCAGG 421
Db 1194 GACTCTTACATCTTCTGCTCTCAAAATGCGCAACTACAGATCTCATGACATCTCAGG 1253
QY 422 GCGCCGGAAGCCAGCTTATCTGTGGCTCATGAGGAGCAGAAAGCGGACCCAGACCA 481
Db 1254 GCGCCGGAAGCCAGCTTATCTGTGGCTCATGAGGAGCAGAAAGCGGACCCAGACCA 1313
QY 482 CTTGCTGTGCTGATGAGAGAGAGTGAAGGCTCATCATCATCTCCTCATGCG 541
Db 1314 CTTGCTGTGCTGATGAGAGAGAGTGAAGGCTCATCATCATCTCCTCATGCG 1373
QY 542 CATCGAAGAGGCTCGGGGTGTGGCCACCAAGACCTGTTTGACTGGGTGGCGGGACCA 601
Db 1374 CATCGAAGAGGCTCGGGGTGTGGCCACCAAGACCTGTTTGACTGGGTGGCGGGACCA 1433
QY 602 CACTGAGGAGCTCTGGCCCTGGCCATTCTGACACAGTAAGTCCATGAGCTTACATGCGCG 661
Db 1434 CACTGAGGAGCTCTGGCCCTGGCCATTCTGACACAGTAAGTCCATGAGCTTACATGCGCG 1493
QY 662 CATGTACTTTCCGATGAAGATGAAGGTGTTCCGGGGCTCCAGGGCCCTCAAGATGCGGGCC 721
Db 1494 CATGTACTTTCCGATGAAGATGAAGGTGTTCCGGGGCTCCAGGGCCCTCAAGATGCGGGCC 1553
QY 722 CTTGAGAGAGTCTTGAAGCGGAGTTTGGGAGACACCAAGATGACGAGCTGAGAA 781
Db 1554 CTTGAGAGAGTCTTGAAGCGGAGTTTGGGAGACACCAAGATGACGAGCTGAGAA 1613
QY 782 ACCCAAGTATGTGTCAGAGGACACTGTGTGACCGGACCGGCTGAACTCCACTCTT 841
Db 1614 ACCCAAGTATGTGTCAGAGGACACTGTGTGACCGGACCGGCTGAACTCCACTCTT 1673
QY 842 CCGGAATACGATGCTCCAGAAACTGTCCGGGAGCTGTTTCAACCAAGCTTAACT 901
Db 1674 CCGGAATACGATGCTCCAGAAACTGTCCGGGAGCTGTTTCAACCAAGCTTAACT 1733
QY 902 CAGGCTCCAGCTCAGGCTCAGACCAAGCTGTGTGCGGGCGGCGGCGGAGAGCGGGGC 961
Db 1734 CAGGCTCCAGCTCAGGCTCAGACCAAGCTGTGTGCGGGCGGCGGCGGAGAGCGGGGC 1793

| | | | | |
|----|------|--|---------------------|------|
| Qy | 962 | AGCTTCCTACTACTTCGCAACCCAAATGGGCGCTTCCTGCA | CGGTGGGCGTGTGGCCACA | 1021 |
| Db | 1794 | AGCTCTCACTTACTTCGCAACCCAAATGGGCGCTTCCTGCA | CGGTGGGCGTGTGGCCACA | 1853 |
| Qy | 1022 | CCCCACGCTGATGCGCATGACCCGAGATCATGAGTACAAATGAG | ACTGATCCGCAAGG | 1081 |
| Db | 1854 | CCCCACGCTGATGCGCATGACCCGAGATCATGAGTACAAATGAG | ACTGATCCGCAAGG | 1913 |
| Qy | 1082 | TCAGGCCAACAAGGTGAAGAACTCTCCATCGTGTCTCTCTGGGA | CAGGAGGTCCCTC | 1141 |
| Db | 1914 | TCAGGCCAACAAGGTGAAGAACTCTCCATCGTGTCTCTCTGGGA | CAGGAGGTCCCTC | 1973 |
| Qy | 1142 | ACAAGTGCCTGTGACCTGTGTGAGATGTTCCGTCCAGCAACCCCT | GGAGAGCTGGCCAA | 1201 |
| Db | 1974 | ACAAGTGCCTGTGACCTGTGTGAGATGTTCCGTCCAGCAACCCCT | GGAGAGCTGGCCAA | 2033 |
| Qy | 1202 | GACTGTTTTTGGGGGCAAGGAACGTGGGCAAGATGTGTGAGACTGT | TGCAAGGATCCAGA | 1261 |
| Db | 2034 | GACTGTTTTTGGGGGCAAGGAACGTGGGCAAGATGTGTGAGACTGT | TGCAAGGATCCAGA | 2093 |
| Qy | 1262 | CGGGCGGCGGAAATTC | 1277 | |
| Db | 2094 | CGGGCGGCGGAAATTC | 2109 | |

```

RESULT 10
US-09-851-896-10
; Sequence 10, Application US/09851896
; Patent No. 6410325
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freiler
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEPENDENT)
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0220
; CURRENT APPLICATION NUMBER: US/09/851, 896
; CURRENT FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 3240
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2770
; OTHER INFORMATION: unknown
; OTHER INFORMATION:
; NAME/KEY: CDS
; LOCATION: (137)...(2557)
; US-09-851-896-10

```

| | | | | | | | |
|-----------------------|-------|----------------------|----------------|---------------------|----------------------------|--------|------|
| Query Match | 68.6% | Score | 876.2 | DB | 4 | Length | 3240 |
| Best Local Similarity | 99.7% | Pred. No. | 1,4e-230 | | | | |
| Matches | 878 | Conservative | 0 | Mismatches | 3 | Indels | 0 |
| | | | | Gaps | 0 | | |
| QY | 392 | AGAACTACAGATCTCATGCA | CATCTCA | CGGCGCCGGAAGCAGCGTT | CATCTTGAGCTC | 451 | |
| Db | 1483 | AGAACTACAGATCTCATGCA | CATCTCA | CGGCGCCGGAAGCAGCGTT | CATCTTGAGCTC | 1542 | |
| QY | 452 | CATGAGGACGAGAAAGGGA | CCCAAGACA | CTGTGTGCTGTGATG | TGAGAGAGATGAA | 511 | |
| Db | 1543 | CATGAGGACGAGAAAGGGA | CCCAAGACA | CTGTGTGCTGTGATG | TGAGAGAGATGAA | 1602 | |
| QY | 512 | AGGCTTCATCATCA | CACTCTTCAT | GCCCATCGAAGGCTT | GAGTGTGACCACA | 571 | |
| Db | 1603 | AGGCTTCATCATCA | CACTCTTCAT | GCCCATCGAAGGCTT | GAGTGTGACCACA | 1662 | |
| QY | 572 | GGACCTGTTTGA | CTGGGTGTGGGGGA | CCACAGAC | CTGGAAGGCACTCTTGCGCCCATCTT | 631 | |
| Db | 1663 | GGACCTGTTTGA | CTGGGTGTGGGGGA | CCACAGAC | CTGGAAGGCACTCTTGCGCCCATCTT | 1722 | |

| | | | |
|----|------|---|------|
| QY | 632 | GCA CAGTAAAGCTCATGCGCTTACATGCCCGCATCTACCTTTGCAATGAAAGATGAGGTGTT | 691 |
| Db | 1723 | GCA CAGTAAAGCTCATGCGCTTACATGCCCGCATCTACCTTTGCAATGAAAGATGAGGTGTT | 1782 |
| QY | 692 | CCGGGGGCTCCAGGCGCTTACGAGTCGGGGCCCTTGAGGAGTTCCTGAAAGCGGAGTTTGG | 751 |
| Db | 1783 | CCGGGGGCTCCAGGCGCTTACGAGTCGGGGCCCTTGAGGAGTTCCTGAAAGCGGAGTTTGG | 1842 |
| QY | 752 | GGAGCACACCCAAAGATGACGGACGTCAGAGAAACCCAAAGGTATGCTGA CAGGGACACTGTC | 811 |
| Db | 1843 | GGAGCACACCCAAAGATGACGGACGTCAGAGAAACCCAAAGGTATGCTGA CAGGGACACTGTC | 1902 |
| QY | 812 | TGACCGGACGCGGCTGAACTTCCA CTTCTCCGAACTAGATGCTCCAGAACTGTCCG | 871 |
| Db | 1903 | TGACCGGACGCGGCTGAACTTCCA CTTCTCCGAACTAGATGCTCCAGAACTGTCCG | 1962 |
| QY | 872 | GGAGCCTCTGTTTCAACCAAGAACGTTTAACTTCAGGCTTCAGCTAGCTCAGACCAAGCT | 931 |
| Db | 1963 | GGAGCCTCTGTTTCAACCAAGAACGTTTAACTTCAGGCTTCAGCTAGCTCAGACCAAGCT | 2022 |
| QY | 932 | GGTGTGGCGGGCGGCGCCGAAGCAGCGGGGGGCGCTCTACTTACTTCCGACCCTTGAAGGCG | 991 |
| Db | 2023 | GGTGTGGCGGGCGGCGCCGAAGCAGCGGGGGGCGCTCTACTTACTTCCGACCCTTGAAGGCG | 2082 |
| QY | 992 | CTTCTCGGACGGTGGGCTGTTGGCCAA CAACCCACGCTGGATGCAATGACCGAGATCCA | 1051 |
| Db | 2083 | CTTCTCGGACGGTGGGCTGTTGGCCAA CAACCCACGCTGGATGCAATGACCGAGATCCA | 2142 |
| QY | 1052 | TGAGTAA CAA TCAAGACCTGTGATCCGCAAGGGTCAGGCCAA CAAGGTGAAAGAACTCTCAT | 1111 |
| Db | 2143 | TGAGTAA CAA TCAAGACCTGTGATCCGCAAGGGTCAGGCCAA CAAGGTGAAAGAACTCTCAT | 2202 |
| QY | 1112 | CGTGTGTCCTCTGGGGACAAGGAGAGTCCCCACAAGTGCCTGTGACTGTGTGATGTCCTT | 1171 |
| Db | 2203 | CGTGTGTCCTCTGGGGACAAGGAGAGTCCCCACAAGTGCCTGTGACTGTGTGATGTCCTT | 2262 |
| QY | 1172 | CCGTTCCACGCAACCCCTGGGAGCTGGCCCAAGACTGTTTTTGGGGCCAAAGAACTGGGCAA | 1231 |
| Db | 2263 | CCGTTCCACGCAACCCCTGGGAGCTGGCCCAAGACTGTTTTTGGGGCCAAAGAACTGGGCAA | 2322 |
| QY | 1232 | GATGTGTGTGACGTGTTGACCGATTCAGACCGGGCGGCGG | 1272 |
| Db | 2323 | GATGTGTGTGACGTGTTGACCGATTCAGACCGGGCGGCGG | 2363 |

```

      RESULT 11
US-08-281-193-1
; Sequence 1, Application US/08281193
; Patent No. 5466595
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0 , Version #1.25 (EPO)
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 1 :
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2935 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEITICAL: NO
; ANTI-SENSE: NO
; FEATURE:
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NAME/KEY: CDS
LOCATION: 96..2352
US-08-281-193-1

Query Match 55.4%; Score 708; DB 1; Length 2935;
Best Local Similarity 87.6%; Pred. No. 2e-184;
Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

389 CACAGACTACAGAGTCTGACATCTGACGGGCGGAGCGGACGCTTACCTGGG 448
1277 CAACAGCTTCAAGACCTTATGCCATCTCCGAGCCCGAGAGCGACATTCCTGAG 1336
449 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 508
1337 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1396
509 GAAAGGCTTATCATCTGACGCTCTGATGCGCATGAGAGGCTTGGGGTGGCCAC 568
1397 GAAAGGCTTATCATCTGACGCTCTGATGCGCATGAGAGGCTTGGGGTGGCCAC 1456
569 CAAGGACTTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 628
1457 CAAGGACTTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1516
629 TCTGCAAGTAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 688
1517 TCTGCAAGTAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1576
689 GTTCCGGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 748
1577 GTTCCGGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCA 1636
749 TGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 808
1637 TGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1696
809 GTTGAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 868
1697 GTTGAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1756
869 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 928
1757 TCGGGAACCTTCTGCAACCAAAACATTAACCTGAAACCGGAGGAGGAGGAGG 1816
929 GCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 988
1817 ACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1876
989 GCGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1048
1877 ACCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1936
1049 CCAATGAGTAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1108
1937 CCAATGAGTAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1996
1109 CATGCTTGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1168
1997 CATGCTTGTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2056
2057 CTTCCGCGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2116
1229 CAAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1272
2117 CAAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2160

RESULT 12
US-08-422-106-1
Sequence 1, Application US/08422106
Patent No. 5589170

GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,106
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE: 27-JUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 96..2352
US-08-422-106-1

Query Match 55.4%; Score 708; DB 1; Length 2935;
Best Local Similarity 87.6%; Pred. No. 2e-184;
Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

389 CACAGACTACAGAGTCTGACATCTGACGGGCGGAGCGGACGCTTACCTGGG 448
1277 CAACAGCTTCAAGACCTTATGCCATCTCCGAGCCCGAGAGCGACATTCCTGAG 1336
449 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 508
1337 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1396
509 GAAAGGCTTATCATCTGACGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 568
1397 GAAAGGCTTATCATCTGACGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTT 1456
569 CAAGGACTTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 628
1457 CAAGGACTTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1516
629 TCTGCAAGTAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 688
1517 TCTGCAAGTAACTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1576
689 GTTCCGGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGG 748
1577 GTTCCGGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGG 1636
749 TGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 808
1637 TGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1696
809 GTTGAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 868
1697 GTTGAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1756
869 CCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 928
1757 TCGGGAACCTTCTGCAACCAAAACATTAACCTGAAACCGGAGGAGGAGGAGGAG 1816
929 GCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 988

Db 1817 ACTGATGCGAGCAGCCCGGAGCAGTGGGGGAGCCCAACCTACTTCGGCCCAATGG 1876
QY 989 GCGCTTCCTGAGCGGTGGGCTGTTGGCCAAACCCCAACCGCTGATGCTGACCGAGAT 1048
Db 1877 ACCTTCTCTGAGATGGGGCTGGCTGGCCAAACCCCAACCTAGATGCTGATGAAAT 1936
QY 1049 CCATGATGAATCAGGACCTGATCCGCAAGGGGAGCCCAACAGGTGAAGAACTCTC 1108
Db 1937 CCATGATGAATCAGGACCTGATCCGCAAGGGGAGCCCAACAGGTGAAGAACTCTC 1996
QY 1109 CATGTTGTCTCCTGGGGGAGCAGGAGAGTCCCAACAGTCTGTGATGATGT 1168
Db 1997 CATAGTGTCTCTCTGGGGGAGCAGGAGAGTCCCTCAAGTCCGCTAATCTGTGATGT 2056
QY 1169 CTTCCTGCTCCAGCAACCTCTGGGAGCTGGCCAAAGACTGTTTGGGGCCAAAGACTGG 1228
Db 2057 CTTCCTGCTCCAGCAACCTCTGGGAGCTGGCCAAAGACTGTTTGGGGCCAAAGACTGG 2116
QY 1229 CAAGATGATGATGAGCTGTTGCAACGATTCAGACGCGGGGCGCG 1272
Db 2117 CAAGATGATGATGAGCTGTTGCAACGATTCAGATGATGATGATG 2160

RESULT 13

US-08-735-716-1
Sequence 1, Application US/08735716
Patent No. 5840511
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/735, 716
FILING DATE: 23-OCT-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE: 27-JUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 96..2352
US-08-735-716-1

Query Match 55.4%; Score 708; DB 2; Length 2935;
Best Local Similarity 87.6%; Pred. No. 2e-184;
Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
QY 389 CACGAACTACAGATCTCATGACATCTCAACGCGGCCGGAAGCCGTTTCACTGGG 448
Db 1277 CAAACAGCTTCAGAGACCTCATGCTCCATCTCCGAGCCCGGAAGCCCAATTCCTGAG 1336
QY 449 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 508
Db 1337 CTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1396
QY 509 GAAAGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 568
Db 1397 GAAAGGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1456

QY 569 CAGGACCTGTTTGAATGGGTTGGCGGGGCAACAGCACTGAGAGGATCTCTGGCCCTGGCCAT 628
Db 1457 CAGGACCTGTTTGAATGGGTTGGCGGGGCAACAGCACTGAGAGGATCTCTGGCCCTGGCCAT 1516
QY 629 TCTGCAAGTAAAGTCCATGAGCTCAATGAGCGGATGATCTTTCGATGAGAGGATGAGT 688
Db 1517 TCTGCAAGTAAAGTCCATGAGCTCAATGAGCGGATGATCTTTCGATGAGAGGATGAGT 1576
QY 689 GTTCCGGGCTCAGGACCTCAAGTGGGAGGCTTGAAGAGTCTTGAAGCGGAGT 748
Db 1577 GTTCCGGGCTCAGGACCTCAAGTGGGAGGCTTGAAGAGTCTTGAAGCGGAGT 1636
QY 749 TGGGAGGAGCAGCAAGATGACGAGCTGAGGAAACCAAGGTGATGATGAGGAGGAGT 808
Db 1637 TGGGAGGAGCAGCAAGATGACGAGCTGAGGAAACCAAGGTGATGATGAGGAGGAGT 1696
QY 809 GTCTGACCGGAGCGGCTGAACTCCAGCTCTTCCGGAATCAAGATGCTCAAGAACTGT 868
Db 1697 GTCTGACCGGAGCGGCTGAACTCCAGCTCTTCCGGAATCAAGATGCTCAAGAACTGT 1756
QY 869 CCGGAGGCTCTGTTTCAACCAAGCTTAACTCAGGCTCCAGCTCAGCTCAGACCA 928
Db 1757 TCGGAACTCTGCTTCAACCAAGCTTAACTCAGGCTCCAGCTCAGACCA 1816
QY 929 GCTGATGAGCGGCGCGCGCGGAGCAGCGGCGGAGCTCTTACTTCCGACCAATGG 988
Db 1817 ACTGATGAGCGGAGCGCGCGGAGCAGCGGCGGAGCTCTTACTTCCGACCAATGG 1876
QY 989 GCGCTTCCTGAGCGGTGGGCTGTTGGCCAAACCCCAACCGCTGATGCTGATGATGATG 1048
Db 1877 ACCTTCTCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1936
QY 1049 CCATGATGAATCAGGACCTGATCCGCAAGGGTCAAGGCCAAGGTGAAGAACTCTC 1108
Db 1937 CCATGATGAATCAGGACCTGATCCGCAAGGGTCAAGGCCAAGGTGAAGAACTCTC 1996
QY 1109 CATGTTGTCTCCTGGGGGAGCAGGAGAGTCCCAACAGTCTGTGATGATGT 1168
Db 1997 CATAGTGTCTCTCTGGGGGAGCAGGAGAGTCCCTCAAGTCCGCTAATCTGTGATGT 2056
QY 1169 CTTCCTGCTCCAGCAACCTCTGGGAGCTGGCCAAAGACTGTTTGGGGCCAAAGACTGG 1228
Db 2057 CTTCCTGCTCCAGCAACCTCTGGGAGCTGGCCAAAGACTGTTTGGGGCCAAAGACTGG 2116
QY 1229 CAAGATGATGATGAGCTGTTGCAACGATTCAGACGCGGGGCGCG 1272
Db 2117 CAAGATGATGATGAGCTGTTGCAACGATTCAGATGATGATGATGATG 2160

RESULT 14

US-08-555-568B-1
Sequence 1, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2935 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 96..2352
US-08-555-568B-1

Query Match 55.4%; Score 708; DB 2; Length 2935;

Best Local Similarity 87.6%; Pred. No. 2e-184; Mismatches 110; Indels 0; Gaps 0;

Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

389 CACAGACTACAGAGTCTCATGACATCTCACGGGCCCGGAGCCAGCGTTTCATCTGG 448
1277 CAAACAGCTTCAGAGACTCATGCGCATCTCCGAGCCCGGAGCGAGCATTCCTGAG 1336
449 CTCCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 508
1337 CTCCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1396
509 GAAAGGCTCAT 568
1397 GAAAGGCTCAT 1456
569 CAAAGACTCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 628
1457 CAAAGACTCTTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1516
629 TCTGCAAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 688
1517 TCTGCAAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1576
689 GTTCGGGGGCTTCAGAGGCTTACGAGTGGGGGCTTCGAGAGTTCCTGAAGGGGAGTT 748
1577 GTTCGGGGGCTTCAGAGGCTTACGAGTGGGGGCTTCGAGAGTTCCTGAAGGGGAGTT 1636
749 TGGGAGACACCAAGATGACGAGCTCAGAGAAACCAAGATGATGCTGACAGGAGACT 808
1637 TGGGAGACACCAAGATGACGAGCTCAGAGAAACCAAGATGATGCTGACAGGAGACT 1896
809 GTCTGACCGGACCGGCTGATCTCCACTCTTCCGGAATAGATGCTCCAGAAACTGT 868
1697 GTCTGACCGGACCGGCTGATCTCCACTCTTCCGGAATAGATGCTCCAGAGGCTCAT 1756
869 CCGGAGGCTCGTTTCAACAGAAAGTTAAGCTCAGAGGCTCAGAGGCTCAGAGCA 928
1757 TCGGGAACCTCGCTTCAACAGAAAGTTAAGCTCAGAGGCTCAGAGGCTCAGAGCA 1816
929 GCTGATGTGGCGGGCCCGGAGACGCGGAGGAGCTCTACTTCTTCGAGCCCATGG 988
1817 ACTGATGTGGCGGGCCCGGAGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1876
989 GCGCTTCTTGAAGGCTGTTGGCTGTTGGCTGTTGGCTGTTGGCTGTTGGCTGTTGGCT 1048
1877 ACCTTTCTTGAAGGCTGTTGGCTGTTGGCTGTTGGCTGTTGGCTGTTGGCTGTTGGCT 1936
1049 CCAATGATACATCAGGAGCTGATCCGCAAGGAGGCTCAGAGCAAAAGGATGAAGAACTCTC 1108
1937 CCAATGATACATCAGGAGCTGATCCGCAAGGAGGCTCAGAGCAAAAGGATGAAGAACTCTC 1996

1109 CATGTTGTTCTCCCTGGGAGACAGGAGGATGCCCAAGTGCTGTGATGATGT 1168
1997 CATAGTGTCTCTCTGGGAGACAGGAGGATGCCCAAGTGCTGTGATGATGT 2056
1169 CTTCGGTCCAGAACCCCTGGGAGGCTGGCCAAAGATCTTTTGGGCGCAAGAACTGGG 1228
2057 CTTCGGGCGGAGAACCCCTGGGAGGCTGGCTAAGATCTTTTGGAGCCAAAGAACTGGG 2116
1229 CAAGATGTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1272
2117 CAAGATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160

RESULT 15

US-09-519-223-1

Sequence 1, Application US/09519223

Patent No. 6274140

GENERAL INFORMATION:

APPLICANT: Jones, Simon

APPLICANT: Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/519,223

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/555,568

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2935 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 96..2352

US-09-519-223-1

Query Match 55.4%; Score 708; DB 3; Length 2935;

Best Local Similarity 87.6%; Pred. No. 2e-184; Mismatches 110; Indels 0; Gaps 0;

Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

389 CACAGACTACAGAGTCTCATGACATCTCACGGGCCCGGAGCCAGCGTTTCATCTGG 448
1277 CAAACAGCTTCAGAGACTCATGCGCATCTCCGAGCCCGGAGCGAGCATTCCTGAG 1336
449 CTCCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 508
1337 CTCCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1396

QY 509 GAAAGGCTCATCATCATCCAGCCTCATGCGCATGAGAGGCTCGGGTGTGGCCAC 568
DB 1397 GAAAGGCTGTGCTATCCAACTCTCATTTGCCATGAGAGGCTTCAGAGTGTGGCCAC 1456
QY 569 CAAGACCTGTTTGAAGTGGGTGGCGAGCACAGCATGAGAGCATCTGGCCCTGGCCAT 628
DB 1457 CAAGACCTTGTGACTGGGTGGCAGGAAACAGCATGGGGGCACTCTGGCCCTGGCCAT 1516
QY 629 TCTGCACAGTAAGTCCATGGGCTTACATGGCGGCGCATGACTTTCGCATGAAGAGTAGT 688
DB 1517 TCTGCACAGTAAGTCCATGGGCTTATATGCGTGGTGTACTTCCGTATGAAGAGTAGT 1576
QY 689 GTTCCGGGGCTCCAGAGGCTTACGAGTGGGGCCCTGAGAGAGTTCCTGAAGCGGAGTT 748
DB 1577 GTTCCGGGGCTCCAGAGGCTTATGATGTGAACCCCTGAGAGAGTTCTGAAGCGGAGTT 1636
QY 749 TGGGAGCACACCAAGATGACGACGTCAAGAAAACCAAGGTGATGCTGACAGGACACT 808
DB 1637 TGGGAGCACACCAAGATGACGATGTCAAAAAACCAAGGTGATGCTGACAGGACACT 1696
QY 809 GTCTGACCGGAGCGGCTGAACTCCACTCTTCCGGAATAGATGCTCCAGAACTGT 868
DB 1697 GTCTGACCGGAGCGGCTGAACTCCACTCTTCCGGAATAGATGCTCCAGAGGTCTAT 1756
QY 869 CCGGGAGGCTCGTTTCAACAGAACGTTAACTCAAGGCTCCAGGCTCAGGCTCAGACCA 928
DB 1757 TCGGGAACCTCGCTTCAACCAAAACATTAACCTGAAGCGGCAACCTCAGGCTCAGACCA 1816
QY 929 GCTGTGTGGCGGGCGGCGGAGCAGCGGGGAGCTCTACTTACTTCCGACCAATGG 988
DB 1817 ACTGTATGGCGAGCAGCGGCGGAGCACTGGGGCAGCCCAACTTCCGGCCCAATGG 1876
QY 989 GCGCTTCTTGAAGTGGGCTGTGGCCAAACAACCCCAAGCTGATGCCATGACCGAGAT 1048
DB 1877 ACGTTTCTTGAAGTGGGCTGTGGCCAAACAACCCCAAGCTGATGCCATGACCGAGAT 1936
QY 1049 CCATGAGTACAATCAAGGACCTGATCCGCAAGGGTCAAGGCAACAAGGTGAAGAACTCTC 1108
DB 1937 CCATGAAATACATCAAGGACATGATCCGCAAGGGTCAAGGCAACAAGGTGAAGAACTCTC 1996
QY 1109 CATGTTGTCTCCCTGGGGAACAGGAGGTCCCAACAATGCTGTGATGATGT 1168
DB 1997 CATAGTGTCTCTCTGGGGAACAGGAGGTCCCTCAAGTGCCTGTAGATGT 2056
QY 1169 CTTCCGTCCAGCAACCTCTGGGAGCTGSCCAAGACTGTTTGGGCAAGAACTGGG 1228
DB 2057 CTTCCGCCCCAGCAACCTCTGGGAACTGGCTAAGACTGTTTGGAGCCAAAGAACTGGG 2116
QY 1229 CAAGATGTGTGAGACTGTTGCAAGGATCCAGACGGGCGGCGG 1272
DB 2117 CAAGATGTGTGAGACTGTTGCAAGGATCCAGATGTGGGCTG 2160

Search completed: December 16, 2004, 13:56:25
Job time : 131 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 12:10:46 ; Search time 728 Seconds

(Without alignments)
9684.217 Million cell updates/sec

Title: US-10-612-668-18

Sequence: 1 GAATTTTGGGCCCCGAGGCG.....CAGACGGGGGGCCGAATTC 1277

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 276041825 residues

Total number of hits satisfying chosen parameters: 8186004

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*

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20: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*

21: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 885.6 | 69.4 | 2112 | 9 | US-09-927-180-22 |
| 3 | 885.6 | 69.4 | 2109 | 9 | US-09-927-180-20 |
| 4 | 876.2 | 68.6 | 2755 | 16 | US-10-108-260A-1335 |
| 5 | 876.2 | 68.6 | 3240 | 18 | US-10-476-991-10 |
| 6 | 708 | 55.4 | 2935 | 9 | US-09-927-180-1 |
| 7 | 472.2 | 37.0 | 70000 | 18 | US-10-476-991-3 |
| 8 | 268 | 21.0 | 411 | 10 | US-09-918-995-35047 |
| 9 | 60 | 4.7 | 60 | 10 | US-09-908-975-9474 |
| 10 | 60 | 4.7 | 60 | 10 | US-09-908-975-31864 |
| 11 | 50 | 3.9 | 3798 | 9 | US-09-938-842A-1043 |
| 12 | 50 | 3.9 | 3798 | 11 | US-09-938-842A-1043 |

| 13 | 48.8 | 3.8 | 1065 | 15 | US-10-369-493-42988 | Sequence 42988, A |
|----|--|-----|---------|----|---------------------|-------------------|
| 14 | 48.4 <td>3.8</td> <td>1515</td> <td>18</td> <td>US-10-411-910A-276</td> <td>Sequence 276, App</td> | 3.8 | 1515 | 18 | US-10-411-910A-276 | Sequence 276, App |
| 15 | 46.6 | 3.6 | 1009 | 17 | US-10-369-493-32157 | Sequence 32157, A |
| 16 | 45.2 | 3.5 | 1617 | 17 | US-10-437-963-32157 | Sequence 9028, Ap |
| 17 | 45 | 3.5 | 1836 | 15 | US-10-156-761-2659 | Sequence 2659, Ap |
| 18 | 45 | 3.5 | 9025608 | 15 | US-10-156-761-1 | Sequence 1, Appl |
| 19 | 44.8 | 3.5 | 2370 | 15 | US-10-156-761-4813 | Sequence 4813, Ap |
| 20 | 44.4 | 3.5 | 919 | 15 | US-10-424-539-32102 | Sequence 32102, A |
| 21 | 44.4 | 3.5 | 1256 | 17 | US-10-437-963-85239 | Sequence 85239, A |
| 22 | 44.2 | 3.5 | 1332 | 15 | US-10-369-493-35811 | Sequence 35811, A |
| 23 | 43.6 | 3.4 | 3529 | 18 | US-10-425-115-11861 | Sequence 11861, A |
| 24 | 43.2 | 3.4 | 2337 | 9 | US-09-969-347-317 | Sequence 317, App |
| 25 | 42.8 | 3.4 | 3916 | 17 | US-10-437-963-67100 | Sequence 67100, A |
| 26 | 42.6 | 3.3 | 654 | 16 | US-10-425-114-18925 | Sequence 18925, A |
| 27 | 42.6 | 3.3 | 1122 | 16 | US-10-425-114-1056 | Sequence 1056, Ap |
| 28 | 42.6 | 3.3 | 1247 | 16 | US-10-425-114-14342 | Sequence 14342, A |
| 29 | 42.6 | 3.3 | 2718 | 15 | US-10-132-350-47 | Sequence 47, Appl |
| 30 | 42.6 | 3.3 | 3074 | 15 | US-10-132-350-45 | Sequence 273, Ap |
| 31 | 42.4 | 3.3 | 765 | 15 | US-10-369-493-30552 | Sequence 30552, A |
| 32 | 42.4 | 3.3 | 1342 | 15 | US-10-200-562-180 | Sequence 180, App |
| 33 | 42.4 | 3.3 | 9369 | 15 | US-10-237-551-190 | Sequence 190, App |
| 34 | 42.4 | 3.3 | 9369 | 15 | US-10-237-551-247 | Sequence 247, App |
| 35 | 42.4 | 3.3 | 154746 | 10 | US-09-827-688-8 | Sequence 8, Appl |
| 36 | 42.4 | 3.3 | 9025608 | 15 | US-10-156-761-1 | Sequence 1, Appl |
| 37 | 42.4 | 3.3 | 670 | 9 | US-09-965-703-29 | Sequence 29, Appl |
| 38 | 41.8 | 3.3 | 670 | 16 | US-10-239-134-29 | Sequence 29, Appl |
| 39 | 41.8 | 3.3 | 672 | 9 | US-09-965-703-30 | Sequence 30, Appl |
| 40 | 41.8 | 3.3 | 672 | 16 | US-10-239-134-30 | Sequence 30, Appl |
| 41 | 41.8 | 3.3 | 850 | 9 | US-09-965-703-28 | Sequence 28, Appl |
| 42 | 41.8 | 3.3 | 850 | 16 | US-10-239-134-28 | Sequence 28, Appl |
| 43 | 41.8 | 3.3 | 850 | 16 | US-10-468-199-12 | Sequence 12, Appl |
| 44 | 41.8 | 3.3 | 925 | 9 | US-09-965-703-27 | Sequence 27, Appl |
| 45 | 41.8 | 3.3 | 925 | 16 | US-09-965-703-27 | Sequence 27, Appl |

ALIGNMENTS

RESULT 1

US-09-927-180-18

Sequence 18, Application US/09927180

Patent No. US20020106364A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 CambridgePark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1277 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 396..1271
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-09-927-180-18

Query Match 100.0%; Score 1277; DB 9; Length 1277;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 GAATTTCTAGGCCCCAGGTGTTATTCAGCATCGCTCCGATGCAAGAAAGCACTTT 60
 QY 61 GTCGAAAGAGACACGCAAGGTTATTCATGCTTGGGGTTCAAGAGAAAGATTGAG 120
 DB 61 GTCGAAAGAGACACGCAAGGTTATTCATGCTTGGGGTTCAAGAGAAAGATTGAG 120
 QY 121 GGAACCTGGAGCTGGCTGGGCAAGGTGGAGGACCTTCCAGAGCAGTGGCCCCCTT 180
 DB 121 GGAACCTGGAGCTGGCTGGGCAAGGTGGAGGACCTTCCAGAGCAGTGGCCCCCTT 180
 QY 181 TCCATCTCAGACCCATTTCTCTCTGTGGCTGTGGCTCAAGCTTTCTCTGGGACAGATC 240
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 QY 241 CTTCTGTGGGGAAGGGAAGATGACAGGGGAGTGGGGGAGATGAGGGGCGTGGCGTGG 300
 DB 241 CTTCTGTGGGGAAGGGAAGATGACAGGGGAGTGGGGGAGATGAGGGGCGTGGCGTGG 300
 QY 301 CGAGGACAGCCAGGTTTATCTAGGACCTCTGGGTTAGCAGGGCTTGGGACCCACC 360
 DB 301 CGAGGACAGCCAGGTTTATCTAGGACCTCTGGGTTAGCAGGGCTTGGGACCCACC 360
 QY 361 TGACCAAGATGCTCTGTCTGTGCTCAAGAACTCAAGATCTCATGACATCTCAC 420
 DB 361 TGACCAAGATGCTCTGTCTGTGCTCAAGAACTCAAGATCTCATGACATCTCAC 420
 QY 421 GGGCCCGGAAGCCAGGCTTATCTGTGGGCTCCATGAGGAGGAGAGCCGACGACC 480
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 QY 541 CCATCGAAGAGGCTCGGGGTGTGGCCCAAGAGACTTGTGATGGGTGGGGACCA 600
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 QY 601 GCACTGAGAGGCTCGGGGCTTCTGCAAGGACTTGTGACTGGGTGGCGGACCA 660
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 QY 661 GCATGATCTTTCGATGAGAGATGAGGTGTTCCGGGGCTCCAGGCTTACGATCGGGG 720
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 QY 721 CCTCGAAGAGTTCCTGAAGCGGAGTTTGGGAGACACCAAGATGACGAGCTGAG 780
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QY 841 TCCGAAGTACGATGCTCCAGAACTGTCGGGAGCTTGTTCACACAGACGTTAAAC 900
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 DB 901 TCAGGCTCCAGTCAAGCCCTCAGACCACTGTTGGGGGGGGGGGCGGAGGAGGG 960
 QY 961 CAGCTCTACTTACTTCCGACCCCAATGGGCGCTTCTGGAGCGGTGGTGGCCACA 1020
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 QY 1141 CACAATGCTGTGATCTGTGTGATGTTCCGTCACAGCAACCCCTGGAGCTGGCA 1200
 DB 1141 CACAATGCTGTGATCTGTGTGATGTTCCGTCACAGCAACCCCTGGAGCTGGCA 1200
 QY 1201 AGACTGTTTGGGGCAAGAACTGGGCAAGATGATGATGATGATGATGATGATG 1260
 DB 1201 AGACTGTTTGGGGCAAGAACTGGGCAAGATGATGATGATGATGATGATGATG 1260
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 DB 1261 ACGGGGCGCGGAATTC 1277

RESULT 2

US-09-927-180-22
 Sequence 22, Application US/09927180
 Patent No. US20020106364A1

GENERAL INFORMATION:
 APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSER: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 876-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 2112 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear


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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2770
; OTHER INFORMATION: unknown
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (137)...(2557)
; US-10-476-991-10

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Query Match      68.6%; Score 876.2; DB 18; Length 3240;
Best Local Similarity 99.7%; Pred. No. 2.4e-240;
Matches 878; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1483 AGAAGTACAGAGATCTCATGACATCTTCAGCGGCGCCGGAAGCCAGCGTTACTCTGCGCTC
QY 452 CATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
DB 1543 CATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY 512 AGGAGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT
DB 1603 AGGAGCTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT
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QY 872 GAGAGCTCGTTTCAACAGAGAGTGAACCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAG
DB 1963 GAGAGCTCGTTTCAACAGAGAGTGAACCTCAAGGCTCAAGGCTCAAGGCTCAAGGCTCAAG
QY 932 GATGTGGCGGCGGCGGCGGAGAGCGGAGCGGAGCTCTACTTACTTCCAGCCCAATGGGCG
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DB 2203 CGTTGTCTCTCGGAGAGAGAGTCCCAAGAGTCTGTGTGATGTGTCTT
QY 1172 CCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
DB 2263 CCGTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
QY 1232 GATGTGTGAGAGTGTGACAGAGTCCAGAGCGGCGGCGG 1272

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DB 2323 GATGTGTGAGAGTGTGACAGAGTCCAGAGCGGCGGCGGCTG 2363

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RESULT 6
US-09-927-180-1
; Sequence 1, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2935 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 96..2352
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; US-09-927-180-1
Query Match      55.4%; Score 708; DB 9; Length 2935;
Best Local Similarity 87.6%; Pred. No. 3.2e-192;
Matches 774; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

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Query Match 3.9%; Score 50; DB 11; Length 3798;
Best Local Similarity 58.9%; Pred. No. 0.00066;
Matches 86; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

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DB 1364 TACTCACCAATGATGAGGAGATGATGAAGTCTTGCAAGCGTGCAGATTCTTAAGAGA 1423
QY 544 TCGAGAGGCGCTCGGGGTGCGCCACCAAGAGCCTGTTGACTGGGTGCGGACAGCA 603
DB 1424 TTGAGAGGAGAAAGTGCAGACCTTATTCATGATGATTCGACTTATATGAGCATCAA 1483
QY 604 CTGAGAGCATCTGCGCCCTGGCCATT 629
DB 1484 CAGAGGAATGCTAGCTATTGCCCTT 1509

RESULT 13

US-10-369-42988
Sequence 42988, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 42988
LENGTH: 1065
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-10-369-493-42988

Query Match 3.8%; Score 48.8; DB 15; Length 1065;
Best Local Similarity 55.2%; Pred. No. 0.0012;
Matches 95; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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DB 663 CCGGATCTGTCTCCCGAGGAGTGCAGAGTGTGATGTGCGCGGCCCAAGACT 722
QY 434 AGCGTTCATCTGGCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 493
DB 723 CGCGGCTCATCTGCAGCAACACCGTGGCCGCGCTTGGAGCATCCCTGGGGAA 782
QY 494 GATGAGAGGAGGAGTGAAGGCTCATCATCATCTCACTCTCTGCGCATC 545
DB 783 GGAAGCGCGGCGCTGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 834

RESULT 14

US-10-411-910A-276
Sequence 276, Application US/10411910A
Publication No. US20040209256A1
GENERAL INFORMATION:
APPLICANT: Dillon, Harrison F.
TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
FILE REFERENCE: H2041203-P
CURRENT APPLICATION NUMBER: US/10/411,910A
CURRENT FILING DATE: 2003-04-12
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PatentIn version 3.2
SEQ ID NO 276
LENGTH: 1515

TYPE: DNA
ORGANISM: Entamoeba histolytica
US-10-411-910A-276

Query Match 3.8%; Score 48.4; DB 18; Length 1515;
Best Local Similarity 46.2%; Pred. No. 0.0016;
Matches 160; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

QY 406 TCATGACATCTCCAGGCGCGGAGCCAGACCTTCATCTCTGGCTTCATGAGGAGAG 465
DB 1019 TCATGGCCCTTCAGACGCGCAAGCGTGGAGAGCCTTGAGAGACACACCAAGTACT 1078
QY 466 AGCGACCCACGACCACTCTGCTGCTGATGAGAGAGATGAAAGCCTCATATCA 525
DB 1079 GCGTGAATCTTCAGAGATCTTCGCGCTTTCAGAGGAGCGGACATGACATGAGCA 1138
QY 526 TCCAGCTCTCATTCGACATGAGAGGCGCTGGGTGAGCCACCAAGACCTGTTGACT 585
DB 1139 TGCAGCCCTTACACTTCTGTGACAGAGCCCAAGAGGAGAGATCTTCCCTGAGCG 1198
QY 586 GGGTGGCGGACACAGCACTGAGGATCTGGCCCTGCGCATTTGCAAGTAAGTCA 645
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QY 706 CTTAGAGTGGGGGCGCTGAGAGATCTCTGAAGCGGAGTTTG 751
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RESULT 15

US-10-369-493-32157
Sequence 32157, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 32157
LENGTH: 1009
TYPE: DNA
ORGANISM: Ralstonia metallidurans
US-10-369-493-32157

Query Match 3.6%; Score 46.6; DB 15; Length 1009;
Best Local Similarity 46.5%; Pred. No. 0.005;
Matches 151; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 520 TCATCATCAAGCTCTCATTCGATGAGAGGCTTGGGTGCGCCACCAAGAGCTCT 579
DB 62 TCAGTTTCCTTCACTTCGCGACGAGAAACGCGCCCGCGGTGGCATCAAGAGATACC 121
QY 580 TTGACGTGGGTGGGAGACAGACATGAGGAGATCTGCGCTGGCATTCGACAGTA 639
DB 122 TGGCGTGTCACTGGGCGCGCGAGTCCCGGAGCTGATCCGGTGTTCGGAGAGAA 181
QY 640 AGTCATGCGCTTACATGCGCGGATGATCTTTCGATGAAGATGAGTGTTCGGGGCT 699
DB 182 ACCTGCGCTTATTCGCGCTTGGCTGAGATATTCTTCAGAGAGAGACGCTGCTGGCC 241

```

Qy      700 CCAGGCCCTACGAGTCGGGGCCCTGGAGGAGTTCTGAAAGCGGAGTTGGGAGCACA 759
Db      242 GTATTTCGACCCCAAGCTGTCCGCTGTGAATTTCTTCCCGAGAAATTCACGCTCT 301
Qy      760 CCAAGATGACGACGTCACGGAACCCAAAGGTGATGCTGACAGGAGACATGTCTGACCGGC 819
Db      302 ACATGTGTATGAACTACGAGCTGGGCAAGACGCTGACAGAGCATATCTCTGACAGCCCGGC 361
Qy      820 AGCCGGCTGAACCTCCACCTTCTCG 844
Db      362 AGCAGGGCAAGGCCAAAGTCTCTCG 386

```

Search completed: December 16, 2004, 15:22:16
 Job time : 739 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:52:55 ; Search time 13.1857 Seconds
(without alignments)
2130.736 Million cell updates/sec

Title: US-10-612-668-19
Perfect score: 1531
Sequence: 1 LQDLMHISRRARKPATLGSW.....GAKELGMVVDCTDPDGR 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR:79:1*
2: PIR:1:1*
3: PIR:3:1*
4: PIR:4:1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1524 | 99.5 | 851 | 2 | T12503 |
| 2 | 456.5 | 29.8 | 1071 | 2 | T22327 |
| 3 | 419 | 27.4 | 1023 | 2 | T26261 |
| 4 | 261 | 17.0 | 468 | 2 | T33857 |
| 5 | 255 | 16.7 | 1265 | 2 | T02131 |
| 6 | 253.5 | 15.6 | 456 | 2 | T24442 |
| 7 | 235.5 | 15.4 | 355 | 2 | E82354 |
| 8 | 213.5 | 13.9 | 679 | 2 | G71615 |
| 9 | 211.5 | 13.8 | 782 | 2 | UC7284 |
| 10 | 201 | 13.1 | 382 | 2 | T48109 |
| 11 | 198 | 12.9 | 390 | 2 | AG2093 |
| 12 | 182 | 11.9 | 414 | 2 | G85437 |
| 13 | 179 | 11.7 | 428 | 2 | T52294 |
| 14 | 176 | 11.5 | 410 | 2 | P85437 |
| 15 | 176 | 11.5 | 414 | 2 | H85437 |
| 16 | 174.5 | 11.4 | 439 | 2 | T03841 |
| 17 | 164 | 10.7 | 499 | 2 | T02580 |
| 18 | 163 | 10.6 | 405 | 2 | T10260 |
| 19 | 161 | 10.5 | 407 | 2 | T00989 |
| 20 | 158.5 | 10.4 | 388 | 2 | T10770 |
| 21 | 158.5 | 10.4 | 490 | 2 | B97815 |
| 22 | 151.5 | 9.9 | 388 | 2 | T10765 |
| 23 | 151.5 | 9.9 | 388 | 2 | T10763 |
| 24 | 150.5 | 9.8 | 494 | 2 | T16655 |
| 25 | 147 | 9.6 | 526 | 2 | T08541 |
| 26 | 146 | 9.5 | 386 | 2 | T07932 |
| 27 | 140 | 9.1 | 386 | 2 | A29810 |
| 28 | 139 | 9.1 | 386 | 2 | A26017 |
| 29 | 138 | 9.0 | 377 | 2 | S05593 |

| | | | | | | |
|----|-------|-----|-----|---|--------|--------------------|
| 30 | 138 | 9.0 | 386 | 2 | S51596 | patacin precursor, |
| 31 | 137 | 8.9 | 320 | 2 | F70034 | conserved hypothe |
| 32 | 137 | 8.9 | 384 | 2 | A24142 | patacin precursor |
| 33 | 134 | 8.8 | 386 | 2 | S05592 | patacin precursor |
| 34 | 134 | 8.8 | 386 | 2 | B26017 | patacin T58 precu |
| 35 | 129.5 | 8.5 | 488 | 2 | T06725 | hypotheical prote |
| 36 | 124 | 8.1 | 318 | 2 | S24923 | TEG protein - Bac |
| 37 | 116 | 7.6 | 324 | 2 | D70943 | hypotheical prote |
| 38 | 112 | 7.3 | 473 | 2 | T28118 | hypotheical prote |
| 39 | 108 | 7.1 | 329 | 2 | A87087 | conserved hypothe |
| 40 | 103 | 6.7 | 610 | 2 | B87518 | conserved hypothe |
| 41 | 96.5 | 6.3 | 296 | 2 | E84000 | hypotheical prote |
| 42 | 95 | 6.2 | 598 | 2 | E71657 | hypotheical prote |
| 43 | 94 | 6.1 | 314 | 2 | AF3365 | serine proteinase |
| 44 | 91 | 5.9 | 260 | 2 | H69874 | conserved hypothe |
| 45 | 90.5 | 5.9 | 254 | 2 | G72343 | conserved hypothe |

ALIGNMENTS

RESULT 1
T12503
hypotheical protein DKFZp434A102.1 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C:Accession: T12503
R:Amstrong, W.; Winkler, U.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17527
A:Accession: T12503
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <ANS>
A:Cross-references: EMBL:AL080187
A:Experimental source: adult testis; clone DKFZp434A102
C:Genetics:
A>Note: DKFZp434A102.1

Query Match 99.5%; Score 1524; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 7.8e-130;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | LQDLMHISRRARKPATLGSWDEKRTDHLCDGGGVGGLIIQLLIATEKSGVATKD | 60 |
| DB | 496 | LQDLMHISRRARKPATLGSWDEKRTDHLCDGGGVGGLIIQLLIATEKSGVATKD | 555 |
| QY | 61 | LFDWVAGTSTGGILALALILHSKSMAYWGMVFRKDEVFRRGSRPYESGPLEEFKGEFGE | 120 |
| DB | 556 | LFDWVAGTSTGGILALALILHSKSMAYWGMVFRKDEVFRRGSRPYESGPLEEFKGEFGE | 615 |
| QY | 121 | HTKTDVRRKRWMLTGLTSRQPAELHLPRNYDAPETVRPRPNQVNLAPPQPSDQV | 180 |
| DB | 616 | HTKTDVRRKRWMLTGLTSRQPAELHLPRNYDAPETVRPRPNQVNLAPPQPSDQV | 675 |
| QY | 181 | WRARSSGAAPYFRPNRGRPLDGLLANNPTLDAMTEIHEYNODLIRKQGANVKKLSIV | 240 |
| DB | 676 | WRARSSGAAPYFRPNRGRPLDGLLANNPTLDAMTEIHEYNODLIRKQGANVKKLSIV | 735 |
| QY | 241 | VSLGTGRSPQVPYTCVDFRPSNPWEIAKTVFAGKEIGKRVVDDCTDPDGR | 291 |
| DB | 736 | VSLGTGRSPQVPYTCVDFRPSNPWEIAKTVFAGKEIGKRVVDDCTDPDGR | 786 |

RESULT 2
T22327
hypotheical protein F47A4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T22327
R:Mortimore, B.
Submitted to the EMBL Data Library, June 1995
A:Reference number: Z19549

A/Accession: T22237
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1071 <WIL>
 A/Cross-references: UNIPROT:Q20500; EMBL:Z49888; PIDN:CAA90061.1; GSPDB:GN00028; CESP:F4
 A/Experimental source: clone F47A4
 C/Genetics:
 A/Gene: CESP:F47A4.5
 A/Map position: X
 A/Introns: 27/1; 59/2; 134/1; 199/2; 402/2; 460/3; 591/3; 634/3; 665/2; 1018/3

Query Match 29.8%; Score 456.5; DB 2; Length 1071;
 Best Local Similarity 34.8%; Pred. No. 7.4e-33;
 Matches 102; Conservative 62; Mismatches 97; Indels 35; Gaps 8;

QY 1 LODLMSRKARAFILGSRDEKTHDHLCLDGGVKGIIITQLIAIEKSGVATKD 60
 DB 730 IQDTLDSGRKGAKV-----NLSMDGGIRGLVITQLIAIEKLGDDIFK 777
 QY 61 LFDVAGTSTGILALAILHKSMAVNRGMYFRKDEVEFRG-SRPESGLEEFLEKREFG 119
 DB 778 YFDMAGTSTGSLIMGLATGKSLREMQYLLKORFVGIMPEYDTVGLKFTIQDFG 837
 QY 120 EHTKMTDKRKPKWLTSTLSDROPALHLFRNVDAPETVREPRNQVNLPPAOPSDEL 179
 DB 838 TGT-VWEIPIPRMISAVNSEKLPVRLEMAKRYKPAQV-----AETPREMP 884
 QY 180 VWRARSSGAPTYFRPN-GRFLDGLANPTLDAMTEIHEYNQDLIRKQANKVKLS 238
 DB 885 LMMALRSTAPLPVLFKSEPRYIDGGITSNPDLMSBHAYNRELQLSGRSADVQNM 944
 QY 239 IVVSLGTGRSPQVPTCVDFR--PSNPWEIAKTVFGAKELGKVVVDCCTPDGRP 292
 DB 945 VLVSFGTG--QIPSTVIERLSIDSNPLQSIKTI---KULAMFIDQATASGAP 994

RESULT 3

T26261
 hypothetical protein W07A8.2 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T26261; T26892

R/Hasham, V.
 submitted to the EMBL Data Library, November 1996
 A/Reference number: Z20184
 A/Accession: T26261
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1023 <WIL>
 A/Cross-references: UNIPROT:O62398; EMBL:Z82075; PIDN:CA804932.1; GSPDB:GN00023; CESP:W0
 A/Experimental source: clone W07A8
 R/Hasham, V.
 submitted to the EMBL Data Library, January 1998
 A/Reference number: Z20281
 A/Accession: T26892
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1023 <WIL>
 A/Cross-references: EMBL:AI021489; PIDN:CAA16371.1; GSPDB:GN00023; CESP:W07A8.2
 A/Experimental source: clone Y44AC
 C/Genetics:
 A/Gene: CESP:W07A8.2
 A/Map position: 5
 A/Introns: 32/1; 83/2; 155/3; 202/2; 240/3; 264/1; 331/2; 411/1; 479/3; 534/3; 571/2; 70

Query Match 27.4%; Score 419; DB 2; Length 1023;
 Best Local Similarity 33.9%; Pred. No. 1.8e-29;
 Matches 95; Conservative 61; Mismatches 110; Indels 14; Gaps 7;

QY 17 LGSMDKERTHD-LLCLDGGVKGIIITQLIAIEKSGVATKDLFDVWAGTSGIL 74
 DB 678 LKELVEKKSINVINVLGGGGIRGLVTVQMLICLFAFDRLPIDVDFWIGATISGCIY 737

QY 75 ALAILHKSMAVNRGMYFRKDEVEFRG-SRPESGLEEFLEKREFGENTHMDVRKPKVM 133
 DB 738 MSTMTGSLRKQRYYLMFKDQLFDSMTFRPYDTKLTETFIQAFAGADRLMGDIKYPRFF 797
 QY 134 LTGTLSDROPALHLFRNVDAPETVREPRNQVNLPPAOPSDELVWRARSSGAPTY 193
 DB 798 CTVRADTFPPVQLELRNRLPLSEKE--NNDLGF--TDPELTIWKATRRSSAPTY 851
 QY 194 FRPN-GRFLDGLANPTLDAMTEIHEYNQDLIRKQANKVKLSIVVSLGTGRSPQV 252
 DB 852 FSASBEKFTIDGMISNNPVLDMSDIGFNTTCQKRIEPRKVDMGCVLSVGTGIRPICP 911
 QY 253 VTCVDFRSPNPWEIAKTVFGAKELGKVVVDCCTPDGRP 292
 DB 912 VD-PSVFEMNDLFGMLR--GKMLSLVVIDQATATEGAP 947

RESULT 4

T33857
 hypothetical protein D1037.5 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

A/Accession: T33857
 R/Bedwith, J.; Biewald, T.
 submitted to the EMBL Data Library, November 1998
 A/Description: The sequence of C. elegans cosmid D1037.
 A/Reference number: Z21424

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Accession: T33857
 A/Molecule type: DNA
 A/Residues: 1-468 <LED>
 A/Cross-references: EMBL:AF106592; PIDN:AC78490.1; GSPDB:GN00019; CESP:D1037.5
 A/Experimental source: strain Bristol N2; clone D1037
 C/Genetics:
 A/Gene: CESP:D1037.5
 A/Map position: 1
 A/Introns: 66/3; 89/3; 113/3; 151/2; 247/1; 354/2

Query Match 17.0%; Score 261; DB 2; Length 468;
 Best Local Similarity 29.8%; Pred. No. 1.3e-15;
 Matches 78; Conservative 54; Mismatches 100; Indels 30; Gaps 10;

QY 16 ILGSRDEKERTHDH-LLCLDGGVKGIIITQLIAIEKSGVATKDLFDVWAGTSGIL 74
 DB 180 VLASEKKQWKPBEVRVLALDGGGIRAVITQMLIHIDVLLGKLVKLDIACTSGGYI 239
 QY 75 ALAI-LHKSMAVNRGMYFRKDEVE-RGSR--PYESGPLEEFLEKREF--GEHTQWTVV 127
 DB 240 TLLSTNNRRIETRKLLDMRVRIRGADKAVPKYSNGMEYIARHVTTWEDSKMSI 299
 QY 128 RKPKWLTGTLSDROPALHLFRNY--DAPETVREPRNQVNLPPAOPSDELVWRAA 184
 DB 300 KRRRAIVTVADTMVPPQLLFRSYRPEMEBEACEHYK-----LDPTVLELTKTL 350
 QY 185 RSSGAAPTYFRPNRGRFLDGLANPTLDAMTEIHEYNQDLIRKQANKV-----K 236
 DB 351 RCTTAAPYFESEFNGSLDGLANPTLALISDFPLTK--LEKSPAKSSSERENGNWK 408
 QY 237 LSVSLGTGRSPQVPTCVDF 258
 DB 409 IGCVISLGTGVFTEKIDIDL 430

RESULT 5

T02131
 hypothetical protein F8K4.6 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
 A/Accession: T02131

R/Vyotskaja, V.S.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, O.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Becker, J.R.; Federspiel, N.
 submitted to the EMBL Data Library, August 1998
 A/Description: Arabidopsis thaliana chromosome 1 BAC F8K4 sequence.

A:Reference number: 214574
A:Accession: T02131
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1265 <YYS>
A:Cross-references: UNIPROT:O80693; EMBL:AC004392; NID:g3282170; PID:g3367519; GSPDB:GNC
C:Genetics:
A:Gene: ATSP.F8K4.6
A:Map position: 1
A:Introns: 146/3; 196/1; 229/3; 379/3; 434/1; 521/1; 561/3; 615/3; 683/1; 728/3;
C:Superfamily: Arabidopsis thaliana hypothetical protein F8K4.6

Query Match 16.7%; Score 255; DB 2; Length 1265;
Best Local Similarity 28.7%; Pred. No. 1.8e-14;
Matches 81; Conservative 39; Mismatches 90; Indels 72; Gaps 8;

QY 30 LCLDGGGVKGLIIQLLAIKASGATDLPFWAGTGTGILALAI-LHSKSMAYMR 88
DB 455 ILTMDGGMKGLATVQILKEIKSGKPIHLPDLIGTGTGMLALALGVKMLTLEQCE 514
QY 89 GMYFRMKDEVGRSRP-----YESGP-----LEEF 113
DB 515 EIKKNLGLVPAASVPPDNEPAASREKLDLYSSQSFVAVIHGSHANEFRLKEM 574
QY 114 LKKEFGHTKMTDVRK-PKVMLTGTLSDROPALHLFRNYDAETVREPRF---NONVN 168
DB 575 CAEDDGLLESANVKNPKFVSVTLVSVPAPGPIFRNQQYPTGTGEMGVAASDHSGS 634
QY 169 LRPPADPSDL-----VWRASSGAAPTYF-----RPNGRFLDGLLA 207
DB 635 TLTSSTASDAGYKQSAFMSGCHGQWQAIRASSAPYLDLDFSVGTNSYFMODGAI 694
QY 208 NNPTLAMEIHEYNODLIRKGAANKKXLSIVSLGTGSRP 249
DB 695 NNPTLAIKRAQLMPD-----TKIDCLVSISSGSVP 726

RESULT 6

T24442
hypothetical protein T04B2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24442; T26042
R:Colles, L.
submitted to the EMBL Data Library, December 1995
A:Reference number: 219890
A:Accession: T24442
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-456 <WTL>
A:Cross-references: UNIPROT:Q22152; EMBL:Z68299; PIDN:CAA92615.1; GSPDB:GN00022; CESP:TO
A:Experimental source: clone T04B2
R:Colles, L.
submitted to the EMBL Data Library, December 1995
A:Reference number: 220141
A:Accession: T26042
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-456 <W12>
A:Cross-references: EMBL:Z68301; PIDN:CAA92628.1; GSPDB:GN00022; CESP:T04B2.5
A:Experimental source: clone W01B6
C:Genetics:
A:Gene: CESP.T04B2.5
A:Map position: 4
A:Introns: 48/3; 104/3; 139/1; 424/3
C:Superfamily: patatin

Query Match 16.6%; Score 253.5; DB 2; Length 456;
Best Local Similarity 32.3%; Pred. No. 5.9e-15;
Matches 86; Conservative 41; Mismatches 76; Indels 63; Gaps 14;
QY 5 WHISRAKPAFIIGSMDEKRTDHLCLDGGGVKGLI-IIOQLIAEKASGVAT-KDLF 62
DB 111 LCLDGGGVKGLIIQLLAIKASGATDLPFWAGTGTGILALAI-LHSKSMAYMR 88

DB 112 IQINRSKVDGVNA-----LCLDGGMGRLVSVVCLLYASRRLLGDETLPNLF 159
QY 63 DWVAGTGTGILALAIKASGAMVGRMDVFP-AGSRVYESGPLEEFLKRGHEH 121
DB 160 DWPIGTGTGMLALSMVKNKISISECFQYWDMSQILFRST-----VKRLIGDQ 209
QY 122 TKMTDVRKPKVM-----LTGTLSD-----ROPALHLFRNYDAETVREPRFN 164
DB 210 VAVQTNIDKVLDDCEPTQTLQCEPRLRLTIPALDISTAPARLHVFNYSFTKPFQAP-LN 268
QY 165 QVNLNPPAQPDSQLVWRASSGAAPTYFRP---NGRFLDGLLANPTLDAMTEIHE 220
DB 269 ED-----QVLFREARASSAAPTYFEFPFIYGNKVLVDGSFVANYP-LNVL--FKX 316
QY 221 YNODLIRKGAANKKXLSIVSLGTG 246
DB 317 Y--DSFSKQD--OPIHAGVLSIGTG 338

RESULT 7

E82354
patatin-related protein VC0178 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: E82354
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermlaeva, M.D.; Yamatevian, J.; Baas, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: E82354
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-355 <HEI>
A:Cross-references: UNIPROT:Q9RVG8; GB:AE004108; GB:AE003852; NID:99654578; PIDN:AAF9335,
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0178
A:Map position: 1
C:Superfamily: patatin

Query Match 15.4%; Score 235.5; DB 2; Length 355;
Best Local Similarity 29.2%; Pred. No. 1.8e-13;
Matches 75; Conservative 38; Mismatches 83; Indels 61; Gaps 9;

QY 27 HDHL-----LCLDGGGVKGLIIQLLAIK-----ASGVATDLPFWAGTGTG 73
DB 7 YHLLKNQVRLISLNGGARGLFTISLAETRIIEKQINGKVDLPDLTGTSTIGI 66
QY 74 LALAIHSKSMAYMRGMV-----FMKDEVFRGSRPYEGPLEEFL 114
DB 67 LALGLAVGKSARELEVFRRQAGYIPPEQKYPRFPFRRRYKLAGPL-YDSKPLAKTI 125
QY 115 KREFGHTKMTDVRKVMLTGTLSDROPALHLFRNYDAETVREPRFNQVNLNPPAQ 174
DB 126 ASNVGSESTPNDLCKVLIPTVNLSTGKP---QFRTPIHPERHGRGRIK----- 172
QY 175 PSDQVWRASSGAAPTYFRP-----NGRFLDGLLANPTLDAMTEIHEYNODLIRK 228
DB 173 -----LIDALATSAAPTYFAPHYCVLDLSYFADGGLVANNP---SFIGLHEVFRDMATD 224
QY 229 GQANKVKKXLSIVSLGT 245
DB 225 FPEAKVSDVKI-LNVGT 240

RESULT 8

G71615
phospholipase A2-like a/b fold hydrolase PFB0410c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C:Accession: G71615

R:Gardner, M.J.; Tetteijn, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
 ; Perera, M.; Salizberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
 Science 282, 1126-1132, 1998
 A>Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
 A:Accession: A71600; MIMD:99021743; PMID:9804551
 A:Accession: G71615
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-679 <GAR>
 A:Cross-references: UNIPROT:Q96176; GB:AE001393; GB:AE001362; MIMD:93845175; PIDN:AC7187
 A:Experimental source: clone 3D7
 A:Genetic: PFB0410C

Query Match 13.9%; Score 213.5; DB 2; Length 679;
 Best Local Similarity 27.7%; Pred. No. 4,3e-11;
 Matches 71; Conservative 37; Mismatches 95; Indels 53; Gaps 8;
 QY 30 LCLDGGVKGKLIITQLLIAEKASGVATK-----DLPDVAAGTSTGGIATLAIL 79
 DB 337 ILSDGGGI---LTISLVLVNLRLAEARKIGSDIKLIDCFDVGCTAGGLISLAIL 393
 QY 80 HSSMAVMKMYFRMKDEVKRGSRPYSGPLE-----FLKREGEHTKMTDVK 129
 DB 394 REIDLDDVSNMWSPTIKKVEGNRNIIISGIFFGYDVNNVKDVFLEMGKRF--MSSYKK 451
 QY 130 PKVMLTGLSDRQPAELHLFRNYDAPETVREPRNQVNLPRPAQPSDQLVMPAASSGA 189
 DB 452 FYCFVATVDVKKHFKYKFLIRNTHTKNSINASSYDGINVP-----LWLAAMATAS 503
 QY 190 APFY-----FRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKQANKV 234
 DB 504 APFYLKGPSAEDIKLGINKIPETIHLDGALKASNPALILAECCARLIN---NKNLSTFI 559
 QY 235 KK-LSTIVSLGTGRSP 249
 DB 560 KEDLDTLVSLGTQVP 575

RESULT 9

JC7284
 phospholipase A2 (EC 3.1.1.4) 2, calcium-independent - human
 N:Alternate names: membrane-associated calcium-independent phospholipase A2
 C:Species: Homo sapiens (man)
 C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
 C:Accession: J07284
 R:Tanaka, H.; Takeya, R.; Sumimoto, H.
 Biochem. Biophys. Res. Commun. 272, 320-326, 2000
 A>Title: A novel intracellular membrane-bound calcium-independent phospholipase A2.
 A:Reference number: J07284
 A:Accession: J07284
 A:Molecule type: mRNA
 A:Residues: 1-782 <TAN>
 A:Cross-references: UNIPROT:Q9NP80; DDBJ:AB041261
 C:Genetic:
 A:Gene: dila2-2
 A:Map position: 7q31
 C:Keywords: carboxylic ester hydrolase; membrane-associated protein

Query Match 13.8%; Score 211.5; DB 2; Length 782;
 Best Local Similarity 28.5%; Pred. No. 8e-11;
 Matches 72; Conservative 33; Mismatches 107; Indels 41; Gaps 8;
 QY 16 ILGSMDEKTHHLLCLDGGVKGKLIITQLLIAEKASGVATKDLPDVAAGTSTGGIILA 75
 DB 430 LIGVDPVYKRGIRILSIDGGTRGVVALQTLKLVLTQKPVHQLFDYICVSTGAILA 489
 QY 76 LAI-LHSKSNAYKMGYFRMKDEVF-----GSRPYSGPLEEFLKRGFENT 122
 DB 490 FMGLGFMPDLDECELETRKIGSDVFSQNVIVGVKMSWASHAFQSCWENILDKRMGSA 549
 QY 123 KMTDVK--PKVMLTGLSDRQ-PAELHLFRNYDAPETVREPRNQVNLPRPAQPSDQ 178

DB 550 MIETANPTCPKVAASVTINRGITPKAFVFRNYG-----HPPGINSY-----LGGCQY 599
 QY 179 LWMRAARSSGAAPTYFRP-----NGRFLDGLLANNPTLDAMTEIHEYNODLIRKQANKV 234
 DB 600 KMWQARASSANAPGYAEALGNLDHQDGLLNNPSALAMHECKLWPDV----- 650
 QY 235 KKLSTIVSLGTGR 247
 DB 651 -PLECIVSLGTGR 662

RESULT 10

T48109
 hypothetical protein F16M2.50 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C:Accession: T48109
 R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Scheifer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z24459
 A:Accession: T48109
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-382 <RIE>
 A:Cross-references: UNIPROT:Q9M1W9; EMBL:AL136648
 A:Experimental source: cultivar Columbia; BAC clone F16M2
 C:Genetic:
 A:Map position: 3
 A:Introns: 313/3
 A>Note: F16M2.50
 C:Superfamily: patactin

Query Match 13.1%; Score 201; DB 2; Length 382;
 Best Local Similarity 26.7%; Pred. No. 2.7e-10;
 Matches 75; Conservative 38; Mismatches 94; Indels 74; Gaps 12;

QY 4 LMAHSRARKPAFLGSMRDEKTHHLLCLDGGVKGKLIITQLLIAEKASGVAT----- 58
 DB 19 LSHCDSSRK-----TRILSIDGGTGIIVAAASILHLHQIRLQTDPPHA 63
 QY 59 --KDLFDVAAGTSTGGIATLAILHS-----KSMAYKMGYFRMK-DEVFRG 101
 DB 64 HSDFDIYAGTIGGILALVADDGSRPMTADAVKFAEKSELPETRIYTGVER 123
 QY 102 SRPYSGPLEEFL-----KKEFGHTKMTDVKRKVWLITGLSDRQPAELHLFRNYDAPET 157
 DB 124 NKRYSGKSMERVLFTFRREDGKVLMTKTCRPLVPCVDLTSAP---FVPSRAGASBS 180
 QY 158 VREPRNQVNLPRPAQPSDQLVMPAARSSGAAPTYFRP-----NGR-----FLDGLLA 207
 DB 181 ---PSP-----DFELMKVCRAVTSATPSLFKPFSSVSVSDGKTSQSAVDGLVW 224
 QY 208 NNPTLDAMTEIHEYNODLIRKQANKVKKLSTIVSLGTGRS 248
 DB 225 NNPTAAAVTHVLAHNRKF---PSVNGVDL-LVLSLGNPS 261

RESULT 11

AG2093
 patactin-like protein [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120
 A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AG2093
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matsumoto, A.; Iriyuch, N.; Shimizu, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
 A:Reference number: AB1807; MIMD:21595285; PMID:11759840
 A:Accession: AG2093
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-390 <KUR>

A:Cross-references: UNIPROT:O8YUN7; GB:BA000019; PIDN:BA874001.1; PID:G17131394; GSPDB:C
A:Experimental source: strain PCC 7120
A:Gene: all2302
C:Superfamily: patatin

Query Match 12.9%; Score 198; DB 2; Length 390;

Best Local Similarity 24.3%; Pred. No. 5.1e-10;
Matches 68; Conservative 40; Mismatches 78; Indels 94; Gaps 10;

QY 30 LCLDGGGVKGLIITQLIAIEK---ASGVATKDLFDWVAGTSGTGLALALAIHSKSMA 85
DB 5 ILSLDGGGIRGIVTARILQGEVERQIQQQQKSLHEVYDILAGTSGTGLIAGIAAKNNS 64
QY 86 YNKGATFRMKDEVFRGSRP---YESGP-----LEEF-----LKREFGERTKM 124
DB 65 ELVQLVQOEQKQIFPERKERKYSFLOPLLEAFSLPKYSHQGLINLVKLVGD-TRI 123
QY 125 TDVKKPKVMTG-----TSDROPALHLFRNYDAPETVREPRENQNVN 168
DB 124 KDVESPLMLIAYDTLYRNTTPTNCHPDGDRMYDDCHL----- 163
QY 169 LRPPAPSDQLVWRARSSGAAPTYFRP-----NGRP--LDGGLANPTLDA 214
DB 164 -----WEICTAATAPFPFPYKLEPVNKEKYNWVFPHIDGVAANNPALAA 211
QY 215 MTEIHYNQDLIRKGAANKYKXLSI-----VVSIGTGRS 248
DB 212 LSLVRLSSGSVSAIKQKYNLDGINDIADIALISIGTGT 251

RESULT 12

patatin-like protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G85437
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: G85437
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-414 <STO>
A:Cross-references: UNIPROT:O23180; GB:NC_001268; NID:G7270655; PIDN:CA80372.1; GSPDB:C
C:Gene: AT4G37060
A:Map position: 4
C:Superfamily: patatin

Query Match 11.9%; Score 182; DB 2; Length 414;
Best Local Similarity 27.3%; Pred. No. 1.6e-08;
Matches 73; Conservative 34; Mismatches 84; Indels 76; Gaps 13;

QY 30 LCLDGGGVKGLIITQLIAIEK---ASGVATKDLFDWVAGTSGTGLALALAIHSKS 83
DB 21 ILSLDGGGIRGIVTARILQGEVERQIQQQQKSLHEVYDILAGTSGTGLIAGIAAKNNS 64
QY 84 MAYMR-----GMVFRMKDEVFRGSRPYESGPLE-----EFKREFGE 120
DB 81 NGRRPRAKRIIVFPYLEHCKRIF---PQRTGVALLPKPKLSGPKSGNVIKRTLLGK 136
QY 121 ---HTTKTVDRKPKVMTGLTSLDRQPAELHLFRNYDAPETVREPRENQNVNLRPPAPSD 177
DB 137 ILGETKLKQTLTNVNIPTPDIKTLQPT---IFSSYQA---LTDPSSLVVKY-----SD 182
QY 178 QLVWRARSSGAAPTYFRP-----NGRFPDGLANPTLDMT-----RIHE 220
DB 183 TCI---GTSAAPTYPFPYFSNEDSGKTRHFNPLVDGVANPTLVAMTAVTKQIVN 237
QY 221 YNODLIRKGAANKY-KKLSIVSLGSGT 246

DB 238 NNPDW---GTINPLAGYDQFLVISIGTG 261

RESULT 13

patatin-like protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: F85437

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

Nature 402, 769-777, 1999

A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: F85437

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-428 <STO>

A:Cross-references: UNIPROT:O23181; GB:NC_001268; NID:G7270654; PIDN:CA80371.1; GSPDB:C

C:Gene: AT4G37050

A:Map position: 4

C:Superfamily: patatin

Query Match 11.7%; Score 179; DB 2; Length 428;

Best Local Similarity 26.5%; Pred. No. 3.1e-08;
Matches 72; Conservative 41; Mismatches 81; Indels 78; Gaps 14;

QY 30 LCLDGGGVKGLIITQLIAIEKSGVATK--DLFDWVAGTSGTGLALALAIHSK 82
DB 37 ILSLDGGGIRGIIPTITLAVLESQLOLDEGEARLVDPVISTGSLIVAMTLRAOQ 96
QY 83 SMAYMRG-----MYFRMKDEVFRGSR-----PYSSGLEER 113
DB 97 SGCHSNNSRPLFEAKIYPTFKHSFKIFPQPRGIFCGWGETIYVLVGSPKNGKYLND 156
QY 114 LKREFGERTKMTDVRKPKVMTGLTSLDRQPAELHLFRNYDAPETVREPRENQNVNLRPPA 173
DB 157 LVGFGIDGKTLNGLNVIIPCDIKKLQPV---IFSSYQAVN-----NQAMN-----A 202
QY 174 QPSDQLVWRARSSGAAPTYFRPNRPF-----LDGGLANPTLDMTTEH 219
DB 203 KSDICI-----STSAAPTFP--PAHRFTMEDSGIRGHEFNLLIDGIAANNPTLCAIAEV- 255
QY 220 EYNQDLIRKGAANKYKXLSI-----VVSIGTGT 246
DB 256 --TKQIKKPNVWGDISPDLFTFLVISIGTG 285

RESULT 14

patatin-like protein [imported] - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004

C:Accession: T52294

R:Terryn, N.; Heijnen, L.; De Keyser, A.; Van Asseltonck, M.; De Clercq, R.; Verbaekel, H

Weller, C.; Mayer, K.; Dehais, P.; Rombaut, S.; Van Montagu, M.; Rouse, P.; Vos, P.

FEBS Lett. 445, 237-245, 1999

A>Title: Evidence for an ancient chromosomal duplication in Arabidopsis thaliana by seq

A:Reference number: Z26022; MUID:99192287; PMID:10094464

A:Accession: T52294

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-410 <TER>

A:Cross-references: UNIPROT:O23148; EMBL:AJ002596; PIDN:CA05628.1

C:Gene: AT4G37060

A:Map position: 4

C:Superfamily: patatin

Query Match 11.5%; Score 176; DB 2; Length 410;
Best Local Similarity 26.6%; Pred. No. 5.4e-08;
Matches 74; Conservative 36; Mismatches 70; Indels 98; Gaps 15;

QY 30 LCLDGGGVKGLIITQLIAIEK---ASGVATKDLFDWVAGTSGTGLALALAIHSKS 83

```
Db      17 ILSDGGGVAGIAGVILAFLEKQLOELDGEARLADYFDVIAGTGTGILVMTLVDPDE 76
QY      84 MAYMRGMYFRMKDEVFRGSRPYE-----SGP-----LEE 112
Db      77 TG---RPHFAKDIY-----PFYLEHCPKIFPOPTGVALLPKLPKLLSGPKYSGKYL RN 128
QY      113 FLKRRGE---HTKMTDVRRPKYMLTGLSDRQPAELHLFRNYDAPETVREPRFNQVNL 169
Db      129 LLSKLTGETRLHQTLTNI-----VLPFDIKKLOPT--IFSSY---QLVDPSLDVKV-- 176
QY      170 RPPAOPSDDLVMRAASSGAPTYFRPN-----GRFLDGLIANNPTLDAMT 216
Db      177 -----SDICI-----GTSAAPTFFPPHYFSNEDSQGNKTEFNLVDGAVTANNPTLVAMT 225
QY      217 ---EIHEVYNQDLIRKQANKVKKS---IVVSLGTG 246
Db      226 AVSKQIVKNNPDM-----GKLKPLGPRFLVVISIGTG 257
```

RESULT 15

```
H85437
patatin-like protein (imported) - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: H85437
R: anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A/Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A/Reference number: A85001; MUID:20083486; PMID:10617198
A/Accession: H85437
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-414 <STO>
A/Cross-references: UNIPROT:O23179; GB:NC_001268; NID:g7270656; PIDN:CA80373.1; GSPDB:C
C/Genetics:
A/Gene: AT4g37070
A/Map position: 4
C/Superfamily: patatin
```

```
Query Match      11.5%; Score 176; DB 2; Length 414;
Best Local Similarity 26.6%; Pred. No. 5.5e-08;
Matches 74; Conservative 36; Mismatches 70; Indels 98; Gaps 15;

QY      30 ILCLDGGGVAGIAGVILAFLEK-----ASGVATKDLFDMVAGTGTGILALAILHSKS 83
Db      21 ILSDGGGVAGIAGVILAFLEKQLOELDGEARLADYFDVIAGTGTGILVMTLVDPDE 80
QY      84 MAYMRGMYFRMKDEVFRGSRPYE-----SGP-----LEE 112
Db      81 TG---RPHFAKDIY-----PFYLEHCPKIFPOPTGVALLPKLPKLLSGPKYSGKYL RN 132
QY      113 FLKRRGE---HTKMTDVRRPKYMLTGLSDRQPAELHLFRNYDAPETVREPRFNQVNL 169
Db      133 LLSKLTGETRLHQTLTNI-----VLPFDIKKLOPT--IFSSY---QLVDPSLDVKV-- 180
QY      170 RPPAOPSDDLVMRAASSGAPTYFRPN-----GRFLDGLIANNPTLDAMT 216
Db      181 -----SDICI-----GTSAAPTFFPPHYFSNEDSQGNKTEFNLVDGAVTANNPTLVAMT 229
QY      217 ---EIHEVYNQDLIRKQANKVKKS---IVVSLGTG 246
Db      230 AVSKQIVKNNPDM-----GKLKPLGPRFLVVISIGTG 261
```

Search completed: December 15, 2004, 13:14:17
Job time : 15.1857 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 12:52:25 ; Search time 63.5892 Seconds
(without alignments)
2642.105 Million cell updates/sec

Title: US-10-612-668-19
Perfect score: 1531
Sequence: 1 LODMHISARKKPAFLISM.....GAKELKRVVDCCTDPDGRP 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 segs, 57537466 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1524 | 99.5 | 806 | 1 | PA26 HUMAN |
| 2 | 1524 | 99.5 | 806 | 1 | CAG30429 |
| 3 | 1463 | 95.6 | 752 | 1 | PA26 MOUSE |
| 4 | 1463 | 95.6 | 752 | 2 | Q7TPX2 |
| 5 | 1463 | 95.6 | 807 | 2 | Q9JKE1 |
| 6 | 1463 | 95.6 | 807 | 2 | AAH57209 |
| 7 | 1454 | 95.0 | 751 | 1 | PA26 RAT |
| 8 | 1042 | 68.1 | 756 | 2 | Q6DDX0 |
| 9 | 966.5 | 63.1 | 818 | 2 | Q6NMV0 |
| 10 | 966.5 | 63.1 | 818 | 2 | AAH67375 |
| 11 | 736 | 48.1 | 877 | 2 | Q8MRJ3 |
| 12 | 736 | 48.1 | 877 | 2 | Q9VTE0 |
| 13 | 736 | 48.1 | 877 | 2 | AAFS0194 |
| 14 | 736 | 48.1 | 887 | 2 | Q7KUD4 |
| 15 | 736 | 48.1 | 887 | 2 | AAH11936 |
| 16 | 720 | 47.0 | 879 | 2 | Q7QZ01 |
| 17 | 456.5 | 29.8 | 1071 | 2 | Q20500 |
| 18 | 419 | 27.4 | 1021 | 2 | Q81006 |
| 19 | 419 | 27.4 | 1021 | 2 | Q62398 |
| 20 | 376 | 24.6 | 762 | 2 | Q95YD2 |
| 21 | 287 | 18.7 | 501 | 2 | Q9NSJ3 |
| 22 | 270.5 | 17.7 | 546 | 2 | Q9TYSO |
| 23 | 266 | 17.0 | 546 | 2 | Q8MKR3 |
| 24 | 260 | 17.0 | 433 | 2 | Q70158 |
| 25 | 255 | 16.7 | 1265 | 2 | Q80693 |
| 26 | 253.5 | 16.6 | 456 | 2 | Q22152 |
| 27 | 235.5 | 15.4 | 355 | 2 | Q9KVG8 |
| 28 | 222 | 14.5 | 361 | 2 | Q6XGD7 |
| 29 | 222 | 14.5 | 361 | 2 | AAH70299 |
| 30 | 213.5 | 13.9 | 679 | 2 | Q961T6 |
| 31 | 211.5 | 13.8 | 380 | 2 | Q95035 |

ALIGNMENTS

| | | | | | | |
|----|-------|------|------|---|----------|--------------------|
| 32 | 211.5 | 13.8 | 639 | 2 | Q9H7T5 | 09h7t5 homo sapien |
| 33 | 211.5 | 13.8 | 782 | 2 | Q9NP80 | 09np80 homo sapien |
| 34 | 210.5 | 13.7 | 776 | 2 | Q8K1N1 | 08k1n1 mus musculu |
| 35 | 210.5 | 13.7 | 803 | 2 | Q9DC20 | 09dc20 mus musculu |
| 36 | 204.5 | 13.4 | 577 | 2 | Q9KSM3 | 09ksm3 anabaena ci |
| 37 | 202.5 | 13.2 | 346 | 2 | Q6JBI3 | 06jbi3 dictyocaulu |
| 38 | 202.5 | 13.2 | 346 | 2 | AAH06310 | AAH06310 dictyocau |
| 39 | 202 | 13.2 | 253 | 2 | Q6JBI2 | 06jbi2 dictyocaulu |
| 40 | 202 | 13.2 | 253 | 2 | AAH06311 | AAH06311 dictyocau |
| 41 | 201 | 13.1 | 382 | 2 | Q9M1W9 | 09m1w9 arabidopsis |
| 42 | 201 | 13.1 | 382 | 2 | Q93KQ3 | 093kq3 arabidopsis |
| 43 | 199.5 | 13.0 | 671 | 2 | Q7RKE1 | 07rke1 plasmodium |
| 44 | 198 | 12.9 | 390 | 2 | Q8YUN7 | 08yun7 anabaena sp |
| 45 | 190.5 | 12.4 | 1294 | 2 | Q7SFE6 | 07sfe6 neurospora |

RESULT 1

| | | | |
|------------|--|------|---------|
| PA26_HUMAN | STANDARD; | PRT; | 806 AA. |
| AC | Q60733; Q75645; Q8N452; Q9UG29; Q9UI70; Q9Y671; | | |
| DT | 30-MAY-2000 (Rel. 39, Created) | | |
| DT | 30-MAY-2000 (Rel. 39, Last sequence update) | | |
| DT | 01-OCT-2004 (Rel. 45, Last annotation update) | | |
| DE | 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (IPLA2) (Cat-PLA2) (Group VI phospholipase A2) (GVI PLA2). | | |
| GN | Name=PLA2G6; Synonyms=IPLA2; | | |
| OS | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | |
| OX | NCBI_TaxID=9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND ANKYRIN-IPLA2-2). | | |
| RC | TISSUE=B-cell, and Testis; | | |
| RX | MEDLINE=98079046; PubMed=9417066; | | |
| RA | Larsson P.K.A., Claesson H.E., Kennedy B.P.; | | |
| RT | Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity." | | |
| RL | J. Biol. Chem. 273:207-214(1998). | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2). | | |
| RC | TISSUE=Pancratic Islets; | | |
| RX | MEDLINE=99194813; PubMed=10092647; | | |
| RA | Ma Z., Wang X., Nowatzke W., Ramanadham S., Turk J.; | | |
| RT | "Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (IPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the IPLA2 gene on chromosome 22q13.1."; | | |
| RL | J. Biol. Chem. 274:9607-9616(1999). | | |
| RN | [3] | | |
| RP | SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. | | |
| RX | MEDLINE=99269033; PubMed=10336645; | | |
| RA | Larsson Forell P.K.A., Kennedy B.P., Claesson H.-E.; | | |
| RT | "The human calcium-independent phospholipase A2 gene. Multiple enzymes with distinct properties from a single gene."; | | |
| RL | Eur. J. Biochem. 262:575-585(1999). | | |
| RN | [4] | | |
| RP | SEQUENCE FROM N.A. (ISOFORM LH-IPLA). | | |
| RC | TISSUE=Testis; | | |
| RA | Amstorge W., Winkner U., Mewes H.-W., Gassenhuber J., Wiemann S.; | | |
| RT | Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases. | | |
| RN | [5] | | |
| RP | SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND THR-343. | | |
| RA | Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.; | | |
| RA | Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.; | | |
| RA | Sherwood J.K., Sherwood A.M., Leitauer B.J., Nickerson D.A.; | | |
| RT | "NIHES-SNPs, environmental genome project, NIHES ES15478, Department of Genome Sciences, Seattle, WA (URL: http://esp.gs.washington.edu)."; | | |
| RL | Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases. | | |

[6]
 RA SEQUENCE FROM N.A.
 RA MEDLINE=20057265; PubMed=10591208; DOI=10.1038/990031;
 RA Dunham I., Hunt A.R., Collins J.E., Brunetewich R., Beare D.M.,
 RA Clamp M., Smit L.J., Alnecough R., Almeida J.P., Babbage A.K.,
 RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corry N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dham P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Levesha M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McEwan O.T.,
 RA McClellan J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.C.T.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sultson J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mituyama S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malat J.E., Nguyen T., Pan H.,
 RA Phan Q., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisose S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bems G., Bentley J., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hindle K., Kemp K., Latreille P., Layman D., Olesky P., Rottling T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salter S.,
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanek J.P.,
 RA Peyrard M., Kedra D., Seroussi E., Fransoni I., Tapia I., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tlathun Y., Wright H.,
 RA "The DNA sequence of human chromosome 22,"
 RA Nature 402:489-495(1999).
 RA [7]
 RA SEQUENCE FROM N.A. (ISOFORMS LH-1PLA2 AND SH-1PLA2).
 RA TISSUE=Brain;
 RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
 RA Dlatshenko L., Marutka K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lonellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzanski M.I., Skalska U., Smalley D.E.,
 RA Schenck A., Schein J.E., Jones S.J.M., Maier M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences,"
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RA -1- FUNCTION: Catalyzes the release of fatty acids from phospholipide.
 CC It has been implicated in normal phospholipid remodeling, nitric
 CC oxide-induced or vasopressin-induced arachidonic acid release and

CC in leukotriene and prostaglandin production. May participate in
 CC fas mediated apoptosis and in regulating transmembrane ion flux in
 CC glucose-stimulated B-cells.
 CC -1- FUNCTION: Isoform ankyrin-1PLA2-1 and isoform ankyrin-1PLA2-2,
 CC which lack the catalytic domain, are probably involved in the
 CC negative regulation of 1PLA2 activity.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a carboxylate.
 CC SUBUNIT: Forms large oligomeric 270-350 kDa structures.
 CC -1- SUBCELLULAR LOCATION: Isoform LH-1PLA2 was found to be membrane
 CC bound. Isoform SH-1PLA2 is cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=LH-1PLA2;
 CC IsoId=O60733-1; Sequence=VSP_000278;
 CC Name=SH-1PLA2;
 CC IsoId=O60733-2; Sequence=VSP_000281; VSP_000282;
 CC Name=Ankyrin-1PLA2-1;
 CC IsoId=O60733-3; Sequence=VSP_000281; VSP_000282;
 CC Name=Ankyrin-1PLA2-2;
 CC IsoId=O60733-4; Sequence=VSP_000277, VSP_000279, VSP_000280;
 CC TISSUE SPECIFICITY: Four different transcripts were found to be
 CC expressed in a distinct tissue distribution.
 CC -1- SIMILARITY: Contains 7 ANK repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF064594; AAC97486.1; -;
 DR EMBL: AF102988; AAD41722.1; -;
 DR EMBL: AF102989; AAD41723.1; -;
 DR EMBL: AF117692; AAD30424.1; -;
 DR EMBL: AF117677; AAD30424.1; JOINED.
 DR EMBL: AF117678; AAD30424.1; JOINED.
 DR EMBL: AF117679; AAD30424.1; JOINED.
 DR EMBL: AF117680; AAD30424.1; JOINED.
 DR EMBL: AF117681; AAD30424.1; JOINED.
 DR EMBL: AF117682; AAD30424.1; JOINED.
 DR EMBL: AF117683; AAD30424.1; JOINED.
 DR EMBL: AF117684; AAD30424.1; JOINED.
 DR EMBL: AF117685; AAD30424.1; JOINED.
 DR EMBL: AF117686; AAD30424.1; JOINED.
 DR EMBL: AF117687; AAD30424.1; JOINED.
 DR EMBL: AF117688; AAD30424.1; JOINED.
 DR EMBL: AF117689; AAD30424.1; JOINED.
 DR EMBL: AF117690; AAD30424.1; JOINED.
 DR EMBL: AF117691; AAD30424.1; JOINED.
 DR EMBL: AF116267; AAF34728.1; -;
 DR EMBL: AF116252; AAF34728.1; JOINED.
 DR EMBL: AF116253; AAF34728.1; JOINED.
 DR EMBL: AF116254; AAF34728.1; JOINED.
 DR EMBL: AF116255; AAF34728.1; JOINED.
 DR EMBL: AF116256; AAF34728.1; JOINED.
 DR EMBL: AF116257; AAF34728.1; JOINED.
 DR EMBL: AF116258; AAF34728.1; JOINED.
 DR EMBL: AF116259; AAF34728.1; JOINED.
 DR EMBL: AF116260; AAF34728.1; JOINED.
 DR EMBL: AF116261; AAF34728.1; JOINED.
 DR EMBL: AF116262; AAF34728.1; JOINED.
 DR EMBL: AF116263; AAF34728.1; JOINED.
 DR EMBL: AF116264; AAF34728.1; JOINED.
 DR EMBL: AF116265; AAF34728.1; JOINED.
 DR EMBL: AF116266; AAF34728.1; JOINED.
 DR EMBL: AF116267; AAF34728.1; JOINED.
 DR EMBL: AL080187; CAB45768.1; -;
 DR EMBL: AY522921; AAR92478.1; -;
 DR EMBL: AY522922; CAA18446.1; -;
 DR EMBL: BC036742; AAH36742.2; -;
 DR EMBL: BC036742; AAH36742.2; -;
 DR EMBL: BC031904; AAH51904.1; -;

DR HSSP; Q60778; 10Y3.
DR Genew; HGNC:9039; PLA2G6.

Query Match 99.5%; Score 1524; DB 1; Length 806;
Best Local Similarity 100.0%; Pred. No. 1.7e-128;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLMHSRARKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 60
DB 451 LODLMHSRARKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 510
QY 61 LFDWVAGTGTGILALAILHSKSMAYVRGYFRMKDEVPFSGSRPYESGPLEEFLKREFG 120
DB 511 LFDWVAGTGTGILALAILHSKSMAYVRGYFRMKDEVPFSGSRPYESGPLEEFLKREFG 570
QY 121 HTKMTDVRKRWMLTGLSDROPALHLFRNYDAPEVVRBPRFQNVNLRPPAPSPDQV 180
DB 571 HTKMTDVRKRWMLTGLSDROPALHLFRNYDAPEVVRBPRFQNVNLRPPAPSPDQV 630
QY 181 WRARSSGAAPTYFRPGRFLDGLANNPTLDAMTEIHENODLIRKQANVKKLSIV 240
DB 631 WRARSSGAAPTYFRPGRFLDGLANNPTLDAMTEIHENODLIRKQANVKKLSIV 690
QY 241 VSLGTGRSPQVPTCVDFRPSNPMELAKTVFGAKELGKRVVDDCTDPDGR 291
DB 691 VSLGTGRSPQVPTCVDFRPSNPMELAKTVFGAKELGKRVVDDCTDPDGR 741

RESULT 2

CAG30429 PRELIMINARY; PRT; 806 AA.
ID CAG30429
AC CAG30429
DT 01-JUN-2004 (TEMBLrel. 27, Created)
DT 01-JUN-2004 (TEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TEMBLrel. 27, Last annotation update)
DE PLA2G6 protein.
GN PLA2G6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A.,
RA Cole C.G., Goward M.E., Aguado B., Mallia M., Mokrab Y., Huckle E.J.,
RA Beare D.M., Dunham I.,
RL Submitted (May-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR456543; CAG30429.1; -
SQ SEQUENCE 806 AA; 89902 MW; 8E55CD4EB9ACAD8B CRC64;

Query Match 99.5%; Score 1524; DB 2; Length 806;
Best Local Similarity 100.0%; Pred. No. 1.7e-128;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLMHSRARKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 60
DB 451 LODLMHSRARKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 510
QY 61 LFDWVAGTGTGILALAILHSKSMAYVRGYFRMKDEVPFSGSRPYESGPLEEFLKREFG 120
DB 511 LFDWVAGTGTGILALAILHSKSMAYVRGYFRMKDEVPFSGSRPYESGPLEEFLKREFG 570
QY 121 HTKMTDVRKRWMLTGLSDROPALHLFRNYDAPEVVRBPRFQNVNLRPPAPSPDQV 180
DB 571 HTKMTDVRKRWMLTGLSDROPALHLFRNYDAPEVVRBPRFQNVNLRPPAPSPDQV 630
QY 181 WRARSSGAAPTYFRPGRFLDGLANNPTLDAMTEIHENODLIRKQANVKKLSIV 240
DB 631 WRARSSGAAPTYFRPGRFLDGLANNPTLDAMTEIHENODLIRKQANVKKLSIV 690
QY 241 VSLGTGRSPQVPTCVDFRPSNPMELAKTVFGAKELGKRVVDDCTDPDGR 291
DB 691 VSLGTGRSPQVPTCVDFRPSNPMELAKTVFGAKELGKRVVDDCTDPDGR 741

RESULT 3

PA26_MOUSE STANDARD; PRT; 752 AA.
ID PA26_MOUSE
AC P97819; Q99LA9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cat-
DE PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=iPLA2G6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=97236816; Pubmed=9079688;
RA Balboa M.A., Balsinde J., Jones S.S., Dennis E.A.,
RT "Identity between the Ca2+-independent phospholipase A2 enzymes from
RT p38801 macrophages and Chinese hamster ovary cells.";
RL J. Biol. Chem. 272:8576-8580(1997).
RN [2]
RP REVISIONS TO 2-3; 9; 11 AND 211.
RA Balboa M.A., Balsinde J., Jones S.S., Dennis E.A.,
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schlier G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Dapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedon T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Millaby S.J.,
RA Bosak S.A., McKean P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H2O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Contains 7 ANK repeats.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U88624; AAB48511.2; -
CC EMBL; BC003487; AAB03487.1; -
DR HSSP; Q60778; 10Y3.
DR MGD; MGI:1859152; PLA2G6.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ANK; 6.
DR PRINTS; PRO1415; ANKYRIN.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PSS0088; ANK_REPEAT; 4.

```

DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KM ANK repeat; Hydrolase; Lipid degradation; Repeat.
FT REPEAT 151 181 ANK 1.
FT REPEAT 185 215 ANK 2.
FT REPEAT 219 248 ANK 3.
FT REPEAT 251 281 ANK 4.
FT REPEAT 286 312 ANK 5.
FT REPEAT 316 345 ANK 6.
FT REPEAT 349 378 ANK 7.
FT ACT SITE 465 465 Potential.
SQ SEQUENCE 752 AA; 83702 MW; AAC3347B0E1292E9 CRC64;

Query Match 95.6%; Score 1463; DB 1; Length 752;
Best Local Similarity 94.8%; Pred. No. 5.1e-123;
Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODMHSRARRKRAFLTSGSRDEKRTDHLCLDGGGVKLLIQLLIAEKASGVATD 60
DB 397 LODMHSRARRKRAFLTSGSRDEKRTDHLCLDGGGVKLLIQLLIAEKASGVATD 456
QY 61 LFDWVAGTGTGILALAIHLSKSMAYRMGVFRMKDEVRGSRPYSGPLEEFLKEPGE 120
DB 457 LFDWVAGTGTGILALAIHLSKSMAYRMGVFRMKDEVRGSRPYSGPLEEFLKEPGE 516
QY 121 HTKMTDVRKPKWLTGTLSDRQPAELHFRNYDAPETVREPRNQVNLPPAQSPDQLV 180
DB 517 HTKMTDVRKPKWLTGTLSDRQPAELHFRNYDAPETVREPRNQVNLPPAQSPDQLV 576
QY 181 WRAARSSGAAPTYFRNGRFLDGGILLANPTLDAMTEIHEYNDLIRKQGANVKLSTV 240
DB 577 WRAARSSGAAPTYFRNGRFLDGGILLANPTLDAMTEIHEYNDLIRKQGANVKLSTV 636
QY 241 VSLGTGRSPQVPTCVDFRPSNPWEIAKTVFGAKELGKGVVDCCTDPDGR 291
DB 637 VSLGTGRSPQVPTCVDFRPSNPWEIAKTVFGAKELGKGVVDCCTDPDGR 687

RESULT 4
07PFX2 PRELIMINARY; PRT; 752 AA.
AC 07PFX2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phospholipase A2, group VI.
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshlyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Skowood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
```

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; TISSUE=Osteoblast;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052845; AAH52845.1; -
DR GO; GO:0003824; F:cathecolytic activity; IEA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002641; Patectin.
DR Pfam; PF00023; ANK; 6.
DR Pfam; PF01734; Patectin; 1.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KM ANK repeat.
SQ SEQUENCE 752 AA; 83717 MW; DAC3347B0E14AFC CRC64;

Query Match 95.6%; Score 1463; DB 2; Length 752;
Best Local Similarity 94.8%; Pred. No. 5.1e-123;
Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODMHSRARRKRAFLTSGSRDEKRTDHLCLDGGGVKLLIQLLIAEKASGVATD 60
DB 397 LODMHSRARRKRAFLTSGSRDEKRTDHLCLDGGGVKLLIQLLIAEKASGVATD 456
QY 61 LFDWVAGTGTGILALAIHLSKSMAYRMGVFRMKDEVRGSRPYSGPLEEFLKEPGE 120
DB 457 LFDWVAGTGTGILALAIHLSKSMAYRMGVFRMKDEVRGSRPYSGPLEEFLKEPGE 516
QY 121 HTKMTDVRKPKWLTGTLSDRQPAELHFRNYDAPETVREPRNQVNLPPAQSPDQLV 180
DB 517 HTKMTDVRKPKWLTGTLSDRQPAELHFRNYDAPETVREPRNQVNLPPAQSPDQLV 576
QY 181 WRAARSSGAAPTYFRNGRFLDGGILLANPTLDAMTEIHEYNDLIRKQGANVKLSTV 240
DB 577 WRAARSSGAAPTYFRNGRFLDGGILLANPTLDAMTEIHEYNDLIRKQGANVKLSTV 636
QY 241 VSLGTGRSPQVPTCVDFRPSNPWEIAKTVFGAKELGKGVVDCCTDPDGR 291
DB 637 VSLGTGRSPQVPTCVDFRPSNPWEIAKTVFGAKELGKGVVDCCTDPDGR 687

RESULT 5
09JK61 PRELIMINARY; PRT; 807 AA.
AC 09JK61;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ca2+-independent phospholipase A2 long form (Pla2g6 protein).
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH/Swiss;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshlyuk S., Carninci P., Prange C.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman A.C., Green E.D., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Krzywnski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences,"
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RA Strainsberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF259401; AAF72651.1; -;
 DR EMBL; BC057209; AAH57209.1; -;
 DR HSSP; Q60778; 10Y3.
 DR MGD; MG11859152; P1a2g6.
 DR GO; GO:0003824; P: catalytic activity; IEA.
 DR GO; GO:0045735; P: nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Pataatin.
 DR Pfam; PF000023; ANK_6.
 DR Pfam; PF01734; Pataatin; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat.
 SQ SEQUENCE 807 AA: 89559 MW: 3838889731100294 CRC64;

Query Match 95.6%; Score 1463; DB 2; Length 807;
 Best Local Similarity 94.8%; Pred. No. 5.6e-123;
 Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
 QY 1 LQDLMIISRRKRAFFILGSRDEKRTDHLCLDGGGVKGLIITQLIAIEKASGVATKD 60
 DB 452 LQDLMIISRRKRAFFILGSRDEKRTDHLCLDGGGVKGLIITQLIAIEKASGVATKD 511
 QY 61 LFPWVAGTSGTGGILALAILHKSMAVMRGVYFPMKDEVPFRSGPYSGPLEEFLKKEFGE 120
 DB 512 LFPWVAGTSGTGGILALAILHKSMAVMRGVYFPMKDEVPFRSGPYSGPLEEFLKKEFGE 571
 QY 121 HTMTDVRRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 180
 DB 572 HTMTDVRRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 631
 QY 181 WRAARSSGAAPTYFRPNRGRLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
 DB 632 WRAARSSGAAPTYFRPNRGRLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 691
 QY 241 VSLGTGRSPQVPTCYDVPFRSPNPMELAKTVFGAKELGKRVNDCCTDPDGR 291
 DB 692 VSLGTGRSPQVPTCYDVPFRSPNPMELAKTVFGAKELGKRVNDCCTDPDGR 742
 RESULT 6
 AAH57209 PRELIMINARY; PRT; 807 AA.
 AC AAH57209;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE P1a2g6 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strainsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Siemsen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.T.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman A.C., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gittwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences,"
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RA Strainsberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057209; AAH57209.1; -;
 DR HSSP; Q60778; 10Y3.
 DR MGD; MG11859152; P1a2g6.
 DR GO; GO:0003824; P: catalytic activity; IEA.
 DR GO; GO:0045735; P: nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Pataatin.
 DR Pfam; PF000023; ANK_6.
 DR Pfam; PF01734; Pataatin; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat.
 SQ SEQUENCE 807 AA: 89559 MW: 3838889731100294 CRC64;

Query Match 95.6%; Score 1463; DB 2; Length 807;
 Best Local Similarity 94.8%; Pred. No. 5.6e-123;
 Matches 276; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
 QY 1 LQDLMIISRRKRAFFILGSRDEKRTDHLCLDGGGVKGLIITQLIAIEKASGVATKD 60
 DB 452 LQDLMIISRRKRAFFILGSRDEKRTDHLCLDGGGVKGLIITQLIAIEKASGVATKD 511
 QY 61 LFPWVAGTSGTGGILALAILHKSMAVMRGVYFPMKDEVPFRSGPYSGPLEEFLKKEFGE 120
 DB 512 LFPWVAGTSGTGGILALAILHKSMAVMRGVYFPMKDEVPFRSGPYSGPLEEFLKKEFGE 571
 QY 121 HTMTDVRRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 180
 DB 572 HTMTDVRRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLPPAPQSPDQV 631
 QY 181 WRAARSSGAAPTYFRPNRGRLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
 DB 632 WRAARSSGAAPTYFRPNRGRLDGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 691
 QY 241 VSLGTGRSPQVPTCYDVPFRSPNPMELAKTVFGAKELGKRVNDCCTDPDGR 291
 DB 692 VSLGTGRSPQVPTCYDVPFRSPNPMELAKTVFGAKELGKRVNDCCTDPDGR 742
 RESULT 7
 PA26_RAT STANDARD; PRT; 751 AA.
 ID PA26_RAT;
 AC P97570;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE 85 kDa calcium-independent phospholipase A2 (BC 3.1.1.4) (iPLA2) (Cat-
 DE PLA2) (Group VI phospholipase A2) (GVI PLA2).
 GN Name=iPLA2g6;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=pancreatic islets;
 RX MEDLINE=97269008; PubMed=9111008;

RA Ma 2., Ramanadham S., Kempe K., Chi X.S., Ladenson J., Turk J.,
 RT "pancreatic islets express a Ca²⁺-independent phospholipase A2 enzyme
 RT that contains a repeated structural homologue to the integral
 RT membrane protein binding domain of ankyrin.",
 RL J. Biol. Chem. 272:11118-11127(1997).
 CC -1- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
 CC It has been implicated in normal phospholipid remodeling, nitric
 CC oxide-induced or vasopressin-induced arachidonic acid release and
 CC in leukotriene and prostaglandin production. May participate in
 CC fas mediated apoptosis and in regulating transmembrane ion flux in
 CC glucose-stimulated B-cells.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a carboxylate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver,
 CC heart and skeletal muscle.
 CC -1- SIMILARITY: Contains 7 ANK repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.embnet.org/announcements>
 CC or send an email to license@ebi-emb.ch).
 CC -----
 CC EMBL: U51898; AAC53136.1; -.
 CC HSSP: O60778; 10Y3.
 CC DR RGD; 628667; P1A295.
 CC DR InterPro: IPR002110; ANK.
 CC DR Pfam; PF00023; ANK; 6.
 CC DR PRINTS; PRO1415; ANKYRIN.
 CC DR SMART; SM00248; ANK; 6.
 CC DR PROSITE; PSS0088; ANK_REPEAT; 4.
 CC DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
 CC KM ANK repeat; Hydrolase; Lipid degradation; Repeat.
 CC FT REPEAT 150 180 ANK 1.
 CC FT REPEAT 184 214 ANK 2.
 CC FT REPEAT 218 247 ANK 3.
 CC FT REPEAT 250 280 ANK 4.
 CC FT REPEAT 285 311 ANK 5.
 CC FT REPEAT 315 344 ANK 6.
 CC FT REPEAT 348 377 ANK 7.
 CC FT ACT SITE 464 464 Potential.
 CC SQ SEQUENCE 751 AA; 83582 MW; 393BBADA7FCC99B CRC64;
 Query Match 95.0%; Score 1454; DB 1; Length 751;
 Best Local Similarity 94.2%; Pred. No. 3.3e-122;
 Matches 274; Conservative 9; Mismatches 8; Indels 0; Gaps 0;
 QY 1 LODLMHSRARKPAFILGSRDEKRTDHLCLDGGGVKGLIIQLIAIEKASGVATKD 60
 Db 396 LODLMPSRARKPAFILGSRDEKRTDHLCLDGGGVKGLIIQLIAIEKASGVATKD 455
 QY 61 LFPWVAGTSGGIIAIALILHSKSMAYNRGMVFRMKDEVFGSRPYESGPLEEFLKRE 120
 Db 456 LFPWVAGTSGGIIAIALILHSKSMAYNRGMVFRMKDEVFGSRPYESGPLEEFLKRE 515
 QY 121 HTKWTDVRKRWMLTGLSDRPAELHLFNNYDAPEVFRPRFNQNNLA PPAQPSD 180
 Db 516 HTKWTDVRKRWMLTGLSDRPAELHLFNNYDAPEVFRPRFNQNNLA PPAQPSD 575
 QY 181 WRARSSGAAPTYFRPNRGRFLDGLANPFLDAMTEIHENODLIRKGOANRYKSLIV 240
 Db 576 WRARSSGAAPTYFRPNRGRFLDGLANPFLDAMTEIHENODLIRKGOANRYKSLIV 635
 QY 241 VSLGTGSPQVPTCVDFRPSNFWELAKTVFGAKELGKRVVDCCTDPGR 291
 Db 636 VSLGTGSPQVPTCVDFRPSNFWELAKTVFGAKELGKRVVDCCTDPGR 686
 RESULT 8
 Q6DDKO

ID Q6DDKO PRELIMINARY; PRT; 756 AA.
 AC Q6DDKO;
 DT 01-OCT-2004 (TrEMBLrel. 28, Created)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Ciftton S.W.,
 RA Richardson P.,
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative",
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusik A., Farmer A.A., Rubin A.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomiyaki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulik S.W.,
 RA Vallion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hulton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywicki M.I., Skaleka U., Smallos D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Klein S., Strausberg R.,
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC077558; AA077558.1; -.
 KM Hypothetical protein.
 SQ SEQUENCE 756 AA; 84303 MW; C0278741CA52A71 CRC64;
 Query Match 68.1%; Score 1042; DB 2; Length 756;
 Best Local Similarity 67.9%; Pred. No. 5.5e-85;
 Matches 199; Conservative 34; Mismatches 56; Indels 4; Gaps 1;
 QY 2 QDLMHISRARKPAFILGSRDEKRTDHLCLDGGGVKGLIIQLIAIEKASGVA 57
 Db 398 RDEYVYSTALSGMLVRODTPREDGIRVYKDRLLCLDGGVIRGLVLMQLIAIEKASGR 457
 QY 58 TKDLFDWVAGTSGGIIAIALILHSKSMAYNRGMVFRMKDEVFGSRPYESGPLEEFLKRE 117
 Db 458 LRFWVAGTSGGIIAIALIVGMPEISVRCILYFRMKDEVFGSRPYESGPLEEFLKRE 517
 QY 118 FGEHTKTDVRKRWMLTGLSDRPAELHLFNNYDAPEVFRPRFNQNNLA PPAQPSD 177
 Db 518 FGEHTKTDVRKRWMLTGLSDRPAELHLFNNYDAPEVFRPRFNQNNLA PPAQPSD 577
 QY 178 QLVWRARSSGAAPTYFRPNRGRFLDGLANPFLDAMTEIHENODLIRKGOANRYKSL 237
 Db 578 QLVWRARSSGAAPTYFRPNRGRFLDGLANPFLDAMTEIHENODLIRKGOANRYKSL 637

QY 238 SIWLSIGTGRSPQVPTCVDFRPSNPWELAKTVGAKELGKGMVDDCTDPDG 290
 DB 638 GIVSLGTGRPQISVGSVDVFRPSNPWELAKTVGAKELGKGMVDDCTDSDG 690

RESULT 9
 06NMYO PRELIMINARY; PRT; 818 AA.
 ID 06NMYO
 AC 06NMYO
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE ZGC:77476.
 GN Name=zgc:77476;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 MDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnicki M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC067375; AA67375.1;
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR002641; Patacin.
 DR Pfam: PF00023; Ank_6.
 DR Pfam: PF01734; Patacin.1.
 DR PRINTS; PRO1415; ANKYRN.
 DR SMART; SM00248; ANK_6.
 DR PROSITE; PSS00297; ANK_REPEAT.4.
 DR PROSITE; PSS0297; ANK_REPEAT.1.
 KW ANK repeat.
 SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8EA9 CRC64;

Query Match 63.1%; Score 966.5; DB 2; Length 818;
 Best Local Similarity 63.9%; Pred. No. 4e-78;
 Matches 184; Conservative 31; Mismatches 48; Indels 25; Gaps 1;

QY 28 DHHLCDDGGGVKGLIIIIQLIIAIEKASGVATKDLFDWVAGTSGGILALAIHLSKSNAYM 87
 DB 465 DRLICDDGGGKIGLVIIQLIIAIEKAGRIPLRFLPWSVSTSGGILALAIHVGKSNAYL 524

QY 88 RGMVFMKDEVPFRSGRPSYSGPLSEFLKREFGHTTKTIDVRKPKMUTGTLSDROPALH 147
 DB 525 RCLYFRKKEGVFPKSGRPSYSGPLSEFLKREFGHTTKTIDVRKPKMUTGTLSDROPALH 584

QY 148 LFRNYDAPETVRBPRFQNVNLRPPAP-----SDQLVWR 182

DB 585 LFRNYDAPALQRDPYKSTATFQPLATVPGWMEDELLVGYTRPRKRKRVTDDEQLVWR 644

QY 183 AARSSGAAPTYFRPNRPFELDGLANPPLDANTEIHEYNQDILRKQANKVKKLSIVS 242
 DB 645 AARSSGAAPTYFRPNRPFELDGLANPPLDANTEIHEYNQDILRKQANKVKKLSIVS 704

QY 243 LGTGRSPQVPTCVDFRPSNPWELAKTVGAKELGKGMVDDCTDPDG 290
 DB 705 LGTGRSPQVAVNSVDVFRPSNPWELAKTVGAKELGKGMVDDCTDSDG 752

RESULT 10
 AAH67375 PRELIMINARY; PRT; 818 AA.
 ID AAH67375
 AC AAH67375
 DT 24-MAY-2004 (TREMBlrel. 27, Created)
 DT 24-MAY-2004 (TREMBlrel. 27, Last sequence update)
 DT 24-MAY-2004 (TREMBlrel. 27, Last annotation update)
 DE ZGC:77476.
 GN ZGC:77476.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_TaxID=7955;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 MDLINE=22388257; PubMed=12477932;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnicki M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC067375; AA67375.1;
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR002641; Patacin.
 DR Pfam: PF00023; Ank_6.
 DR Pfam: PF01734; Patacin.1.
 DR PRINTS; PRO1415; ANKYRN.
 DR SMART; SM00248; ANK_6.
 DR PROSITE; PSS00297; ANK_REPEAT.4.
 DR PROSITE; PSS0297; ANK_REPEAT.1.
 KW ANK repeat.
 SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8EA9 CRC64;

Query Match 63.1%; Score 966.5; DB 2; Length 818;
 Best Local Similarity 63.9%; Pred. No. 4e-78;
 Matches 184; Conservative 31; Mismatches 48; Indels 25; Gaps 1;

QY 28 DHHLCDDGGGVKGLIIIIQLIIAIEKASGVATKDLFDWVAGTSGGILALAIHLSKSNAYM 87
 DB 465 DRLICDDGGGKIGLVIIQLIIAIEKAGRIPLRFLPWSVSTSGGILALAIHVGKSNAYL 524

QY 88 RGMVFMKDEVPFRSGRPSYSGPLSEFLKREFGHTTKTIDVRKPKMUTGTLSDROPALH 147
 DB 525 RCLYFRKKEGVFPKSGRPSYSGPLSEFLKREFGHTTKTIDVRKPKMUTGTLSDROPALH 584

QY 148 LFRNYDAPETVRBPRFQNVNLRPPAP-----SDQLVWR 182
 DB 585 LFRNYDAPALQRDPYKSTATFQPLATVPGWMEDELLVGYTRPRKRKRVTDDEQLVWR 644

QY 183 AARSGAATYFPNPGFLDGLANNPTLDANTEIHEYNODLIRKQANKVKLSIVS 242
 DB 645 AARSGAATYFPNPGFLDGLANNPTLDANTEIHEYNODLIRKQANKVKLSIVS 704
 QY 243 LGTGRSPQVAVTVDVFRPSNPWEAKTVFGAKELGKVVDDCTDPDG 290
 DB 705 LGTGRSPQVAVTVDVFRPSNPWEAKTVFGAKELGKVVDDCTDPDG 752

RESULT 11
 Q8MR13 PRELIMINARY; PRT; 386 AA.
 ID Q8MR13;
 AC 08MR13;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE LD44515P.
 GN ORFNames=CG6718;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Chang M., Chavez C., Dorsett V., Dreanek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Munro J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY122192; AAM52704.1; -
 DR FlyBase; FBgn0036053; CG6718.
 DR GO; GO:0003824; F: catalytic activity; IEA.
 DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro; IPR002641; Patactin.
 DR Pfam; PF01734; Patactin; 1.
 DR SF; SF:01734; Patactin; 1.
 SQ SEQUENCE 386 AA; 42693 MW; B32B7BCFC38541DD CRC64;

Query Match 48.1%; Score 736; DB 2; Length 386;
 Best Local Similarity 50.3%; Pred. No. 9,7e-58;
 Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;

QY 16 ILGSMDEKRTNHLCTDGGGKGLIIQLLAIEKASGAVATKDLFDWVAGTSGGIIA 75
 DB 48 IAAEIDKPYGRRLCTDGGGIRGLVLMLEIEKLSRTPIIHMFMDIAGTSGGIIA 107
 QY 76 LAILHGSMAVMRGMYFRMKDEVFRGSRPYESGPLEEFLLRREGEHTKMTDVKPKVMTL 135
 DB 108 LALGCKRTKRCQKGVIRKMEQCFVSGRPYNSSEFESILNDNGEPFVMTDIGHPKIMVT 167
 QY 136 GTLSROPALHLFRNYDAPEYR---EPFNQNVNIRPPAOPSDDQVWRPARRSGAAPT 192
 DB 168 GWADBRKPVDLHFRNYTSASDILGITYTPINNRI---PPQPSSEQLVWMAAATGAAPS 224
 QY 193 YFPRNRPFLDGLANNPTLDANTEIHEYNODLIRKQANKVKLSIVS LGTGRSPQV 252
 DB 225 YFPAFGFPLDGLANNPTLDANTEIHEYNMALARSAERSEALPVSVVMSLGTHIIVTE 284

QY 253 VTCVDVFRPSNPWEAKTVFGAKELGKVVDDCTDPDG 291
 DB 285 LKQIDVFRPSNPWEAKTVFGAKELGKVVDDCTDPDG 323

RESULT 12
 Q9VT60 PRELIMINARY; PRT; 877 AA.
 ID Q9VT60;
 AC 09VT60;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)

DT 01-MAY-2004 (T-EMBLrel. 26, Last annotation update)
 DE CG6718-PA.
 GN ORFNames=CG6718;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gockyne J.D.,
 RA Amaniatis P.G., Scherle S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blaise R.G., Chame M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Adell J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolhakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Paulis B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibbegam C.,
 RA Uetani M., Kalish F., Karpen G.H., Ke Z., Kienison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mouton S.M., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Poul V., Reese M.G.,
 RA Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodagert, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RL "The genome sequence of Drosophila melanogaster.";
 Science 287:1215-2195(2000).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537573;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Chame M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherle S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Celniker S.E., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.,
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomic perspective.";
 Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN (4)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;

RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731332;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Georg R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.C., Champe M., Pfeiffer B.D.,
RA Abiri J.F., Agagyan A., An H.J., Andrews-Plambeck C., Baldwin D.,
RA Ballew R.M., Basu A.V., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Bocchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dourkin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Gang N.S., Gelbart W.M., Glasner K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Hough C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibeagwa C.,
RA Jatalai M., Kalish F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laekio P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Mishina N.V., Modyarty C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazzolo M., Piltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Schaefer F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spyer E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodgett M., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426055; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RL *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Mitera S., Crosby M.A., Kungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kramlinger J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.B.,
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RL systematic review";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kramlinger J.S., Begeman C.M., Krommiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RT "The transposable elements of the *Drosophila melanogaster* euchromatin

RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN (5)
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO03550; AAF50194.3; -
 DR FLYBASE; FBgn0036053; CG6718.
 SQ SEQUENCE 877 AA; 96863 MW; C9DC2C6C282869B CRC64;
 Query Match 48.1%; Score 736; DB 2; Length 877;
 Best Local Similarity 50.9%; Pred. No. 2,9e-57;
 Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;
 QY 16 IIGSMDEKRTDHLCLDGGGKGLIIQLIAIEKASVATKDFDVAAGTGTGILA 75
 DB 539 IAAEIGDKPYGRGLCLDGGGIRGLVQLVQLMEIKLSRTPIIHMDWIACTGTGILA 598
 QY 76 LALHSKSMAYMGVFRMDDEVFRGSRPESGPLEFLRREGHTKMTDVKKPKMLT 135
 DB 599 LALGCGKTMQCKGLYLRKEQCFVGSRPNSSEFSLKDNLGEFVMTDIGHPKIMWT 658
 QY 136 GTLSDRQPAELHFRNYDAPEYR---EPFRNQVNLPRPAPSQDLVWRARSSGAAPT 192
 DB 659 GWAADKRPVHLFRNTSASDLIGVTPINNRI---PPQPSQQLVWMAATGAAPS 715
 QY 193 YFRPNRFLDGLLANNPLDAMTEIHEYNQDLIRKQANKVKLSIVSLGTGRSPQV 252
 DB 716 YFRPFRFLDGLLANNPLDAMTEIHEYNMALSARESEALPVSVMSLGTGHPVTE 775
 QY 253 VTCVDVFRPNPWEAKTVGAKELGKMYVDCCTDPDRCR 291
 DB 776 LKQIDVFRPESIPWDTAKLAVIGTGTGLVLDQATCSGDR 814
 RESULT 14
 Q7KUD4 PRELIMINARY; PRT; 887 AA.
 AC Q7KUD4;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE CG6718-BB (CG6718-PC).
 GN ORFNames=CG6718;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
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 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
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RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
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 RA Jalali M., Kalush F., Karp G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
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 RA Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
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 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Murzy D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutten G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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 RX MEDLINE=22426059; PubMed=12537572;
 RA Miura S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO03550; AAN1936.2; -
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR002641; Patecin.
 DR Pfam: PF000023; Ank; 5.
 DR Pfam: PF017943; Patecin; 1.
 DR PRINTS; PRO1415; ANKYRIN.
 DR SMART; SM00248; ANK; 6.
 DR PROSITE; PS50088; ANK_REPEAT; 3.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KW ANK repeat.

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SQ SEQUENCE 887 AA; 97778 MW; 1387084E7265BEE5 CRC64;
Query Match 48.1%; Score 736; DB 2; Length 887;
Best Local Similarity 50.9%; Pred. No. 3e-57;
Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;

QY 16 ILGSMDEKRTDHLCLDGGGVKGLIIQLLAIEKASGVATKDLFDWVAGTSGGIIA 75
DB 549 IAAIEIDKPYGRRLCLDGGGIRGLVVMLEIEKLSRTPIIHMDWAGTSGGIIA 608
QY 76 LALHSKSNAYMGATFRMKDEVRFSRPSGPLEBFLKREGEHTKMTDVKKVMLT 135
DB 609 LALGCGKTRKQCGGLYLRKMEQCFVSRPNSEFFESILKDNIGEFNVMTDIXPKIMVT 668
QY 136 GTISDPOPAELHFRNYDAPEYR---EPRFNQVNLRPAPQSDOLVWRAAASGAAPT 192
DB 669 GWADKRPVDLHFRNYTASDLIGVTPINNRI---PPQSEBOLVWRAAATGAAPS 725
QY 193 YFRPNGRFLDGGGLANNPTLDAMTEIHEYNODLIRKQANKVKKLSIVSLGTRSPQV 252
DB 726 YFRAPGRFLDGGGLANNPTLDAMTEIHEYNMALKRSAGRESEALPVSVVMSLGTGHPYTE 785

QY 253 VTCVDVFRSPNPWELATVFEAKELGRVVDCTDPDGR 291
DB 786 LKQIDVFRPESIMDTAKLAVGISTIGLVDAQTCSDGR 824

RESULT 15
AAAN11936 PRELIMINARY; PRT; 887 AA.
AC AAAN1936;
DT 01-APR-2004 (TREMBlrel. 27, Created)
DT 01-APR-2004 (TREMBlrel. 27, Last sequence update)
DE CG6718-PB.
GN CG6718.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baau A.U., Bakken J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Eickler A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Klumel B.E., Kohira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson J.,
RA Merklov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M.,
RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupier M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Ye J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Zeng X.H., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Paclik J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernan B.P.,
RA Beutenkourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatic
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AEO03550; AAAN1936.2;
SQ SEQUENCE 887 AA; 97778 MW; 1387084E7265BEE5 CRC64;
Query Match 48.1%; Score 736; DB 2; Length 887;
Best Local Similarity 50.9%; Pred. No. 3e-57;
Matches 142; Conservative 47; Mismatches 84; Indels 6; Gaps 2;

QY 16 ILGSMDEKRTDHLCLDGGGVKGLIIQLLAIEKASGVATKDLFDWVAGTSGGIIA 75
DB 549 IAAIEIDKPYGRRLCLDGGGIRGLVVMLEIEKLSRTPIIHMDWAGTSGGIIA 608
QY 76 LALHSKSNAYMGATFRMKDEVRFSRPSGPLEBFLKREGEHTKMTDVKKVMLT 135
DB 609 LALGCGKTRKQCGGLYLRKMEQCFVSRPNSEFFESILKDNIGEFNVMTDIXPKIMVT 668
QY 136 GTISDPOPAELHFRNYDAPEYR---EPRFNQVNLRPAPQSDOLVWRAAASGAAPT 192
DB 669 GWADKRPVDLHFRNYTASDLIGVTPINNRI---PPQSEBOLVWRAAATGAAPS 725
QY 193 YFRPNGRFLDGGGLANNPTLDAMTEIHEYNODLIRKQANKVKKLSIVSLGTRSPQV 252
DB 726 YFRAPGRFLDGGGLANNPTLDAMTEIHEYNMALKRSAGRESEALPVSVVMSLGTGHPYTE 785

```

Thu Dec 16 19:13:28 2004

us-10-612-668-19.rup

Page 12

Qy 253 VTCTDVFPSPNPELAKTVFPAKELGKMYVDDCCDPGR 291
: : ||||| : : || : : || || ||
Db 786 LKQIDVFPRESIWDTKLAYGISTIGNLVLDQATCSGR 824

Search completed: December 15, 2004, 13:13:10
Job time : 66.5892 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:51:45 : Search time 59.1231 Seconds
(without alignments)
1771.710 Million cell updates/sec

Title: US-10-612-668-19
Perfect score: 1531
Sequence: 1 LQDLMHISARKKAPILSGM.....GAKELGKRVVDCCTDGR 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|----------------------|
| 1 | 1531 | 100.0 | 292 | AAW17846 | AAW17846 Cytochrome |
| 2 | 1531 | 100.0 | 292 | ABB82230 | Abb82230 Calcium i |
| 3 | 1531 | 100.0 | 687 | AAW17847 | AAW17847 Cytochrome |
| 4 | 1531 | 100.0 | 687 | ABB82231 | Abb82231 Human cpl |
| 5 | 1531 | 100.0 | 688 | AAW17848 | AAW17848 Cytochrome |
| 6 | 1531 | 100.0 | 688 | ABB82232 | Abb82232 Human cpl |
| 7 | 1524 | 99.5 | 667 | ADMO5093 | Admo5093 Human pro |
| 8 | 1524 | 99.5 | 784 | ADD93407 | Add93407 Human lip |
| 9 | 1524 | 99.5 | 806 | AAE25968 | AAE25968 Human PLA |
| 10 | 1524 | 99.5 | 806 | ADO19776 | ADO19776 Human PRO |
| 11 | 1471 | 96.1 | 752 | AAAR8018 | AAAR8018 Calcium-1 |
| 12 | 1471 | 96.1 | 752 | AAW01479 | AAW01479 Calcium-1 |
| 13 | 1471 | 96.1 | 752 | AAW13163 | AAW13163 Ca-indupe |
| 14 | 1471 | 96.1 | 752 | AAW17849 | AAW17849 Hamster c |
| 15 | 1471 | 96.1 | 752 | AAW81825 | AAW81825 Chinese h |
| 16 | 1471 | 96.1 | 752 | ABB82215 | Abb82215 Calcium i |
| 17 | 1454 | 95.0 | 751 | ADDA6244 | ADDA6244 Rat Prote |
| 18 | 1454 | 95.0 | 751 | ADBE6032 | ADBE6032 Rat Prote |
| 19 | 1454 | 95.0 | 751 | ADBE5230 | ADBE5230 Rat Prote |
| 20 | 1454 | 95.0 | 751 | ADBE6036 | ADBE6036 Rat Prote |
| 21 | 890 | 58.1 | 401 | AAAB92811 | AAAB92811 Human pro |
| 22 | 736 | 48.1 | 877 | ABBB62624 | ABBB62624 Drosophila |
| 23 | 234 | 15.3 | 387 | ADG76683 | ADG76683 Phospholip |
| 24 | 213.5 | 13.9 | 679 | AAAB18224 | AAAB18224 Plasmodiu |
| 25 | 211.5 | 13.8 | 370 | AAAB56905 | AAAB56905 Human pro |

| | | | | | |
|----|-------|------|-----|-----------|---------------------|
| 26 | 211.5 | 13.8 | 380 | AAAB2509 | AAAB2509 Human ORF |
| 27 | 211.5 | 13.8 | 445 | AAW41310 | AAW41310 Human pol |
| 28 | 211.5 | 13.8 | 562 | AAW39524 | AAW39524 Human pol |
| 29 | 211.5 | 13.8 | 639 | AAAB5818 | AAAB5818 Human pro |
| 30 | 211.5 | 13.8 | 682 | AAAB63224 | AAAB63224 Human act |
| 31 | 208.5 | 13.6 | 350 | ADG76717 | ADG76717 Phospholip |
| 32 | 204.5 | 13.4 | 577 | ADMA8198 | ADMA8198 Polypepti |
| 33 | 201 | 13.1 | 382 | ADMA8197 | ADMA8197 Polypepti |
| 34 | 190 | 12.4 | 378 | ADG76635 | ADG76635 Phospholip |
| 35 | 183.5 | 12.0 | 411 | AAAB52551 | AAAB52551 Nicotiana |
| 36 | 182.5 | 11.9 | 410 | AAE02387 | AAE02387 Wheat lip |
| 37 | 182 | 11.9 | 37 | ADD15928 | ADD15928 Peptide r |
| 38 | 182 | 11.9 | 404 | AAAG30647 | AAAG30647 Arabidops |
| 39 | 182 | 11.9 | 414 | AAAG30646 | AAAG30646 Arabidops |
| 40 | 179 | 11.7 | 428 | AAAG29735 | AAAG29735 Arabidops |
| 41 | 177 | 11.6 | 410 | AAAG99331 | AAAG99331 Maize pat |
| 42 | 177 | 11.6 | 410 | AAAG99329 | AAAG99329 Maize pat |
| 43 | 177 | 11.6 | 410 | AAAG93049 | AAAG93049 Corn pata |
| 44 | 177 | 11.6 | 410 | ADMG3051 | ADMG3051 Corn pata |
| 45 | 176 | 11.5 | 383 | AAAG50026 | AAAG50026 Arabidops |

ALIGNMENTS

RESULT 1
AAW17846
ID AAW17846 standard; protein; 292 AA.

| | | | | | |
|----|---|--|--|--|--|
| XX | AAW17846; | | | | |
| AC | 07-AUG-1997 (first entry) | | | | |
| DT | | | | | |
| XX | Cytochrome phospholipase A2/B (clone 19b product). | | | | |
| DE | | | | | |
| XX | Cytochrome phospholipase A2/B; sPLA2/B; arachidonic acid cascade; | | | | |
| KM | Inflammation; inhibitor; antiinflammatory. | | | | |
| XX | | | | | |
| OS | Homo sapiens. | | | | |
| XX | | | | | |
| PN | W09717448-A2. | | | | |
| XX | | | | | |
| PD | 15-MAY-1997. | | | | |
| XX | | | | | |
| PF | 07-NOV-1996; 96MO-US017794. | | | | |
| XX | | | | | |
| PR | 08-NOV-1995; 95US-00555568. | | | | |
| XX | | | | | |
| PA | (GENY) GENETICS INST INC. | | | | |
| XX | | | | | |
| XX | Jones S, Tang J; | | | | |
| XX | WPI; 1997-281037/25. | | | | |
| DR | N-PSDB; AAT68824. | | | | |
| XX | | | | | |
| PT | Calcium independent phospholipase A2/B - used to reduce inflammation in a | | | | |
| PT | mammalian subject. | | | | |
| XX | | | | | |
| PS | Claim 12; Page 46-47; 74pp; English. | | | | |
| XX | | | | | |
| CC | A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17845) is | | | | |
| CC | characterized by activity in the absence of calcium, by activity in a | | | | |
| CC | mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl | | | | |
| CC | phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a | | | | |
| CC | lack of stimulation by ATP, and by including in its sequence at least one | | | | |
| CC | of the amino acid sequences given in AAW17839- 44). It is encoded by | | | | |
| CC | partial cDNA clone 19b (AAT68824), derived from Burkitt's lymphoma Raji | | | | |
| CC | (ATCC CCR86) cells. Other PLA2/B enzymes (AAW17845, AAW17847-48) have | | | | |
| CC | also been identified. sPLA2/B enzymes are thought to be involved in the | | | | |
| CC | release of arachidonic acid in specific tissues. Recombinant sPLA2/B | | | | |
| CC | polypeptides produced in transformed host cells can be used to screen for | | | | |
| CC | sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the | | | | |
| CC | arachidonic acid cascade | | | | |

```

XX SQ Sequence 292 AA;
Query Match 100.0%; Score 1531; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.7e-163;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLMIISARKAPAFILGSRDEKRTDHLCLDGGVKGIIITQLLAIKASGVATKD 60
DB 1 LODLMIISARKAPAFILGSRDEKRTDHLCLDGGVKGIIITQLLAIKASGVATKD 60
QY 61 LFDWVAGTGTGILALAILHSKSMAYRMGMVFPMKDEVRGSRPYSGPLEEFLKKEFGE 120
DB 61 LFDWVAGTGTGILALAILHSKSMAYRMGMVFPMKDEVRGSRPYSGPLEEFLKKEFGE 120
QY 121 HTKMTDVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQVNLPPAPSPDQLV 180
DB 121 HTKMTDVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQVNLPPAPSPDQLV 180
QY 181 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
DB 181 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKVVNDCTDPDGRP 292
DB 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKVVNDCTDPDGRP 292

RESULT 2
ABB82230
ID ABB82230 standard; protein; 292 AA.
XX ABB82230;
XX
XX 08-JAN-2003 (first entry)
XX
XX Calcium independent phospholipase A2/B (cPLA2/B) (clone 19b).
XX
XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
XX antiinflammatory; antiarthritic; antipruritic; antirheumatic; cytosolic;
XX antiseptic; human.
XX
XX Homo sapiens.
XX
XX US2002106364-A1.
XX
XX 08-AUG-2002.
XX
XX 09-AUG-2001; 2001US-00927180.
XX
XX 27-JUL-1994; 94US-00281193.
XX 14-APR-1995; 95US-00422106.
XX 14-APR-1995; 95US-00422106.
XX 26-JUN-1995; 95WO-US008069.
XX 08-NOV-1995; 95US-00555568.
XX 09-SEP-1998; 98US-00149988.
XX 06-MAR-2000; 2000US-00519223.
XX
XX (GENY ) GENETICS INST INC.
XX
XX Jones S, Tang J;
XX
XX WPI; 2002-739923/80.
XX N-PSDB; ABV73009.
XX
XX Novel composition comprising purified mammalian calcium independent
XX phospholipase enzyme, useful for the screening of inhibitors of
XX phospholipase activity, is active in the absence of calcium.
XX
XX Claim 6; Page 21-22; 41pp; English.
XX
XX The invention relates to a purified mammalian calcium independent
XX cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is

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CC characterized by activity in the absence of calcium and has a molecular
CC weight of 86 kd on SDS-PAGE. A composition (I) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying an
CC inhibitor of phospholipase activity which involves combining (II),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC by increased levels of prostaglandins, leukotriene or platelet activating
CC factor. A composition comprising an antibody which binds to (I) is useful
CC as research and diagnostic tool, and is also useful in the study of
CC phospholipase A2 activity and inflammatory conditions. The present
CC sequence represents a human cPLA2/B enzyme (clone 19b)
XX
XX SQ Sequence 292 AA;
Query Match 100.0%; Score 1531; DB 5; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.7e-163;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLMIISARKAPAFILGSRDEKRTDHLCLDGGVKGIIITQLLAIKASGVATKD 60
DB 1 LODLMIISARKAPAFILGSRDEKRTDHLCLDGGVKGIIITQLLAIKASGVATKD 60
QY 61 LFDWVAGTGTGILALAILHSKSMAYRMGMVFPMKDEVRGSRPYSGPLEEFLKKEFGE 120
DB 61 LFDWVAGTGTGILALAILHSKSMAYRMGMVFPMKDEVRGSRPYSGPLEEFLKKEFGE 120
QY 121 HTKMTDVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQVNLPPAPSPDQLV 180
DB 121 HTKMTDVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQVNLPPAPSPDQLV 180
QY 181 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
DB 181 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
QY 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKVVNDCTDPDGRP 292
DB 241 VSLGTRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKVVNDCTDPDGRP 292

RESULT 3
AAW17847
ID AAW17847 standard; protein; 687 AA.
XX AAW17847;
XX
XX 07-AUG-1997 (first entry)
XX
XX Cytosolic phospholipase A2/B (alternatively spliced clone 19a).
XX
XX Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
XX inflammation; inhibitor; antiinflammatory.
XX
XX Homo sapiens.
XX
XX WO9717448-A2.
XX
XX 15-MAY-1997.
XX
XX 07-NOV-1996; 96WO-US017794.
XX
XX 08-NOV-1995; 95US-00555568.
XX
XX (GENY ) GENETICS INST INC.
XX
XX Jones S, Tang J;
XX
XX WPI, 1997-281037/25.
XX N-PSDB; AAT68825.
XX

```

PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
 PT mammalian subject.
 XX
 PS Claim 12; Page 49-51; 74pp; English.
 CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is
 CC characterized by activity in the absence of calcium, by activity in a
 CC mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-
 CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
 CC lack of stimulation by ATP, and by including in its sequence at least one
 CC of the amino acid sequences given in AAW17839-44). It is an
 CC alternatively spliced variant of another isolated polypeptide (AAW17845)
 CC and is encoded by an isolated cDNA (AAW68825). Other PLA2/B enzymes
 CC (AAW17846, AAW17848) have also been identified. sPLA2/B enzymes are
 CC thought to be involved in the release of arachidonic acid in specific
 CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
 CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
 CC drugs which inhibit the arachidonic acid cascade
 CC
 XX Sequence 687 AA:
 SQ
 Query Match 100.0%; Score 1531; DB 2; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1e-162;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LODLMIISRRKPAFLIGSRDEKRTDHLCLDGGGVKGLIIQLLIAEKSGVATKD 60
 DB 396 LODLMIISRRKPAFLIGSRDEKRTDHLCLDGGGVKGLIIQLLIAEKSGVATKD 455
 QY 61 LPDWVAGTGTGGLAALAIHLSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
 DB 456 LPDWVAGTGTGGLAALAIHLSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 515
 QY 121 HTKMTDVRKPKVWLNGTSLDROPAELHLFRNYDAPETVREPRNQNVLRPAPQSPDQV 180
 DB 516 HTKMTDVRKPKVWLNGTSLDROPAELHLFRNYDAPETVREPRNQNVLRPAPQSPDQV 575
 QY 181 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHYNDLIRKQANVKKLSIV 240
 DB 576 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHYNDLIRKQANVKKLSIV 635
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 292
 DB 636 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 687
 RESULT 4
 ABB82231
 ID ABB82231 standard; protein; 687 AA.
 XX
 AC ABB82231;
 XX
 DT 08-JAN-2003 (first entry)
 XX
 DE Human cPLA2/B splice variant (clone 19a).
 XX
 KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KM antiinflammatory; antiatheritic; antipneumatic; antirheumatic; cytosolic;
 KW antiasthmatic; human.
 XX
 OS Homo sapiens.
 XX
 PN US2002106364-A1.
 XX
 PD 08-AUG-2002.
 XX
 PF 09-AUG-2001; 2001US-00927180.
 XX
 PR 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-00422420.
 PR 26-JUN-1995; 95MO-US008069.
 PR 08-NOV-1995; 95US-00555568.

PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX
 PA (GENEY) GENETICS INST INC.
 XX
 PI Jones S, Tang J;
 XX
 XX WPI; 2002-739923/80.
 DR N-PSDB; ABV73010.
 DR
 XX Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 XX
 PS Claim 6; Page 23-25; 41pp; English.
 XX
 XX The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (I),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
 CC 19a)
 XX
 SQ Sequence 687 AA:
 Query Match 100.0%; Score 1531; DB 5; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1e-162;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LODLMIISRRKPAFLIGSRDEKRTDHLCLDGGGVKGLIIQLLIAEKSGVATKD 60
 DB 396 LODLMIISRRKPAFLIGSRDEKRTDHLCLDGGGVKGLIIQLLIAEKSGVATKD 455
 QY 61 LPDWVAGTGTGGLAALAIHLSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
 DB 456 LPDWVAGTGTGGLAALAIHLSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 515
 QY 121 HTKMTDVRKPKVWLNGTSLDROPAELHLFRNYDAPETVREPRNQNVLRPAPQSPDQV 180
 DB 516 HTKMTDVRKPKVWLNGTSLDROPAELHLFRNYDAPETVREPRNQNVLRPAPQSPDQV 575
 QY 181 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHYNDLIRKQANVKKLSIV 240
 DB 576 WRAARSSGAAPTYFRPNGRFLDGLANNPTLDAMTEIHYNDLIRKQANVKKLSIV 635
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 292
 DB 636 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 687
 RESULT 5
 AAW17848
 ID AAW17848 standard; protein; 688 AA.
 XX
 AC AAW17848;
 XX
 DT 07-AUG-1997 (first entry)
 XX
 DE Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
 XX
 KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;

KW Inflammation; inhibitor; antiinflammatory.
 XX Homo sapiens.
 OS
 XX MO9717448-A2.
 PN
 XX 15-MAY-1997.
 PD
 XX 07-NOV-1996; 96MO-US017794.
 PF
 XX 08-NOV-1995; 95US-00555568.
 PR
 XX (GENY) GENETICS INST INC.
 PA
 XX Jones S, Tang J;
 PI WPI; 1997-281037/25.
 DR N-PSDB; AAT68826.
 XX
 PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
 PT mammalian subject.
 XX
 PS Claim 12; Page 54-56; 74pp; English.
 XX
 CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17848) is
 CC characterized by activity in the absence of calcium, by activity in a
 CC mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-
 CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
 CC lack of stimulation by ATP, and by including in its sequence at least one
 CC of the amino acid sequences given in AAW17839-44). It is an
 CC alternatively spliced variant of another isolated polypeptide (AAW17846)
 CC and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes
 CC (AAW17845, AAW17847) have also been identified. sPLA2/B enzymes are
 CC thought to be involved in the release of arachidonic acid in specific
 CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
 CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
 CC drugs which inhibit the arachidonic acid cascade
 XX
 SQ Sequence 688 AA:
 Query Match 100.0%; Score 1531; DB 2; Length 688;
 Best Local Similarity 100.0%; Pred. No. 1e-162;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQDLMIISRAKRAFAFLGSRDEKRTDHLCLDGGVKGIIITQLLIAEKASGVATKD 60
 DB 397 LQDLMIISRAKRAFAFLGSRDEKRTDHLCLDGGVKGIIITQLLIAEKASGVATKD 456
 QY 61 LFDWVAGTSTGGILALAILHSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFKREFGE 120
 DB 457 LFDWVAGTSTGGILALAILHSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFKREFGE 516
 QY 121 HTKMTDVRKPKWMLTGLSDRQPAELHLFRNYDAPEVREPRNQVNLPRPAQPSDQLV 180
 DB 517 HTKMTDVRKPKWMLTGLSDRQPAELHLFRNYDAPEVREPRNQVNLPRPAQPSDQLV 576
 QY 181 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNODLIRKGOANRYKXLSIV 240
 DB 577 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNODLIRKGOANRYKXLSIV 636
 QY 241 VSLGTGRSPQVPTCVDFRPNPMEIAKTVFGAKELGKXNVVDCCTDPDGRP 292
 DB 637 VSLGTGRSPQVPTCVDFRPNPMEIAKTVFGAKELGKXNVVDCCTDPDGRP 688
 RESULT 6
 ID ABB82232 standard; protein; 688 AA.
 XX
 AC ABB82232;
 XX
 DT 08-JAN-2003 (first entry)
 XX

DE Human cPLA2/B splice variant (clone 19b).
 XX
 XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KW antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytosolic;
 KW antiaesthetic; human.
 XX
 XX Homo sapiens.
 OS
 XX US2002106364-A1.
 PN
 XX 08-AUG-2002.
 PD
 XX 09-AUG-2001; 2001US-00927180.
 PF
 XX 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-004223420.
 PR 26-JUN-1995; 95MO-US008069.
 PR 08-NOV-1995; 95US-00555568.
 PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX
 PA (GENY) GENETICS INST INC.
 XX
 PT Jones S, Tang J;
 PT WPI; 2002-739923/80.
 DR N-PSDB; ABV73011.
 XX
 PT Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 XX
 PS Claim 6; Page 28-30; 41pp; English.
 XX
 CC The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (I),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
 CC 19b)
 XX
 SQ Sequence 688 AA:
 Query Match 100.0%; Score 1531; DB 5; Length 688;
 Best Local Similarity 100.0%; Pred. No. 1e-162;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQDLMIISRAKRAFAFLGSRDEKRTDHLCLDGGVKGIIITQLLIAEKASGVATKD 60
 DB 397 LQDLMIISRAKRAFAFLGSRDEKRTDHLCLDGGVKGIIITQLLIAEKASGVATKD 456
 QY 61 LFDWVAGTSTGGILALAILHSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFKREFGE 120
 DB 457 LFDWVAGTSTGGILALAILHSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFKREFGE 516
 QY 121 HTKMTDVRKPKWMLTGLSDRQPAELHLFRNYDAPEVREPRNQVNLPRPAQPSDQLV 180
 DB 517 HTKMTDVRKPKWMLTGLSDRQPAELHLFRNYDAPEVREPRNQVNLPRPAQPSDQLV 576
 QY 181 WRAARSSGAAPTYFRPNRGFLDGLLANNPTLDAMTEIHEYNODLIRKGOANRYKXLSIV 240

Db 577 WRAASGGAFTYFRPNGRFLDGLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 636
 Qy 241 VSLGTGRSPQVPVTCYDVFRRSPNPMELAKTVFGAKELGKVVVDCCTDPDGR 292
 Db 637 VSLGTGRSPQVPVTCYDVFRRSPNPMELAKTVFGAKELGKVVVDCCTDPDGR 688

RESULT 7

ADM05093
 ID ADM05093 standard; protein; 667 AA.

AC ADM05093;

DT 20-MAY-2004 (first entry)

DE Human protein of the invention SEQ ID NO:3778.

KW human; gene therapy; diagnostic marker; pharmaceutical.

OS Homo sapiens.

PN EP1347046-A1.

PD 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S,
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I,
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;

XX MPI; 2003-723558/69.

DR N-PSDB; ADM02650.

XX New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.

XX Claim 1; SEQ ID NO 3778; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.

XX Sequence 667 AA;

Query Match 99.5%; Score 1524; DB 7; Length 667;
 Best Local Similarity 100.0%; Pred. No. 6.1e-162;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LODLMIISRRKRAFLIGSWRDEKRTDHLCLDGGVVKLLITOLLIAEKSGVATKD 60
 Db 312 LODLMIISRRKRAFLIGSWRDEKRTDHLCLDGGVVKLLITOLLIAEKSGVATKD 371
 Qy 61 LFDPMVAGTSTGGITALLAIIHKSMAVYRGMVFRPKDEVFRRSGRPYSGPLKEEFG 120
 Db 372 LFDPMVAGTSTGGITALLAIIHKSMAVYRGMVFRPKDEVFRRSGRPYSGPLKEEFG 431
 Qy 121 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRFNQVNLPPAQPSPQV 180
 Db 432 HTKMTDVRKPKVMTGLTSDRQPAELHLFRNYDAPETVREPRFNQVNLPPAQPSPQV 491

Qy 181 WRAASGGAFTYFRPNGRFLDGLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 240
 Db 492 WRAASGGAFTYFRPNGRFLDGLANNPTLDAMTEIHEYNODLIRKQANKVKLSIV 551

Qy 241 VSLGTGRSPQVPVTCYDVFRRSPNPMELAKTVFGAKELGKVVVDCCTDPDGR 291
 Db 552 VSLGTGRSPQVPVTCYDVFRRSPNPMELAKTVFGAKELGKVVVDCCTDPDGR 602

RESULT 8

ADD93407
 ID ADD93407 standard; protein; 784 AA.

AC ADD93407;

DT 29-JAN-2004 (first entry)

DE Human lipid-associated molecule LIPAM-14 polypeptide.

KW Human; lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;
 KW antichryoid; antidiabetic; cytosolic; dermatological; immunosuppressive;
 KW antiinflammatory; thyromimetic; antibacterial; cerebroprotective;
 KW gastrointestinal; hepatotropic; nephrotoxic; anticonvulsant;
 KW antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;
 KW virocidic; uteropathic; antirheumatic; cardiant; cardiovascular; anti-HIV;
 KW nootropic.

XX Homo sapiens.

PN WO2003083081-A2.

XX 09-OCT-2003.

XX 27-MAR-2003; 2003WO-UG009755.

XX 29-MAR-2002; 2002US-0368722P.

XX 03-MAY-2002; 2002US-0377576P.

XX 05-JUL-2002; 2002US-0393934P.

XX 27-SEP-2002; 2002US-0414269P.

XX (INCYTE) INCYTE CORP.

XX Emerling BM, Marquis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;
 PI Baughn MR, Lee EA, Griffin JA, Kabie AE, Elliott VS, Chang H;
 PI Lee S, Ramkumar J, Bulloch SA, Hafalia ADA, Khare R, Jiang X;
 PI Jackson AA;

XX MPI; 2003-788347/74.

DR N-PSDB; ADD93426.

XX New LIPAM polypeptides, useful for diagnosing, preventing, and treating
 PT disorders associated with abnormal expression or activity of LIPAM, e.g.
 PT neuromuscular, immunological, cardiovascular disorders, cancer and/or
 PT infections.

XX Claim 69; Page 206-207; 238pp; English.

XX The present sequence is the protein sequence of human lipid-associated
 CC molecule LIPAM-14 (Incyte polypeptide 7512662CD1), a protein that shows
 CC homology to human Ca2+-independent phospholipase A2 short isoform. This
 CC is one of 19 LIPAM polypeptides of the invention. The invention relates
 CC to these novel LIPAMs and the nucleic acids encoding them, and to the use
 CC of nucleic acids and proteins in the diagnosis, treatment and prevention
 CC of disorders associated with abnormal expression or activity of LIPAM
 CC such as neurodegenerative disorders (e.g. Parkinson's disease,
 CC Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy,
 CC catatonias), endocrine disorders (e.g. diabetes, Graves disease), cancers
 CC (e.g. leukemia, cervical or breast cancers), immunological disorders
 CC (e.g. scleroderma, systemic lupus erythematosus, allergies),
 CC gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g.
 CC Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal,
 CC parasitic, protozoal, helminthic), cardiovascular disorders (e.g.

CC atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention
 CC also relates to the assessment of the effects of exogenous compounds on
 CC the expression of nucleic acids and lipids. The invention provides
 CC expression vectors, host cells, antibodies, agonists and antagonists,
 CC transgenic organisms, and arrays and microarrays of the polynucleotides.

XX Sequence 784 AA;

Query Match 99.5%; Score 1524; DB 7; Length 784;
 Best Local Similarity 100.0%; Pred. No. 7, 9e-162;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLMIISRRKPAFLIGSMRDEKRTDHLCLDGGVGKLIITQLLIAIEKASGVATKD 60
 DB LODLMIISRRKPAFLIGSMRDEKRTDHLCLDGGVGKLIITQLLIAIEKASGVATKD 488
 QY 61 LFDWVAGTGTGGILALAIHLSKSMAYRMGMVFRMKDEVRGSRPYSGPLEEFLKREFGE 120
 DB LFDWVAGTGTGGILALAIHLSKSMAYRMGMVFRMKDEVRGSRPYSGPLEEFLKREFGE 548
 QY 121 HTKMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQNVLRRPAQPSDQV 180
 DB HTKMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQNVLRRPAQPSDQV 608
 QY 181 WRAARSSGAAPTYFRPNGRFLDGGILLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIV 240
 DB WRAARSSGAAPTYFRPNGRFLDGGILLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIV 668
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVGAKELGKRVVDCCTDPDGR 291
 DB VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVGAKELGKRVVDCCTDPDGR 719

RESULT 9

AAE25968
 ID AAE25968 standard; protein; 806 AA.

AC AAE25968;

DT 15-NOV-2002 (first entry)

XX Human PLA2 group VI (Ca2+-independent) protein.

KW Human; antisense; phospholipase A2; infection; inflammation; tumour;
 KM antisense therapy; PLA2 protein.

OS Homo sapiens..

PN US6410325-B1.

XX 25-JUN-2002.

XX 09-MAY-2001; 2001US-00651896.

XX 09-MAY-2001; 2001US-00851896.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Freier SM, Watt AT;

XX WPI; 2002-616513/66.

XX N-PSDB; AAD42941.

PT Novel antisense compounds useful for inhibiting gene expression of human
 PT phospholipase A2, group VI and for treating diseases associated with
 PT expression of phospholipase A2, group VI.

XX Disclosure; Col 109-116; 72pp; English.

XX The present invention relates to novel antisense compounds which inhibit
 CC the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
 CC The invention is useful for inhibiting the expression of PLA2, group VI
 CC (Ca2+-independent) in human cells or tissues and for treating an animal,

CC particularly a human suspected of having or being prone to a disease or
 CC condition associated with expression of human PLA2, group VI (Ca2+-
 CC independent). It is useful for diagnostics, therapeutics and as research
 CC reagent, e.g. prophylactically to prevent or delay infection, tumour
 CC formation or inflammation. The present sequence is human PLA2 group VI
 CC (Ca2+-independent) protein

XX Sequence 806 AA;

Query Match 99.5%; Score 1524; DB 5; Length 806;
 Best Local Similarity 100.0%; Pred. No. 8, 2e-162;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLMIISRRKPAFLIGSMRDEKRTDHLCLDGGVGKLIITQLLIAIEKASGVATKD 60
 DB LODLMIISRRKPAFLIGSMRDEKRTDHLCLDGGVGKLIITQLLIAIEKASGVATKD 510
 QY 61 LFDWVAGTGTGGILALAIHLSKSMAYRMGMVFRMKDEVRGSRPYSGPLEEFLKREFGE 120
 DB LFDWVAGTGTGGILALAIHLSKSMAYRMGMVFRMKDEVRGSRPYSGPLEEFLKREFGE 570
 QY 121 HTKMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQNVLRRPAQPSDQV 180
 DB HTKMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQNVLRRPAQPSDQV 630
 QY 181 WRAARSSGAAPTYFRPNGRFLDGGILLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIV 240
 DB WRAARSSGAAPTYFRPNGRFLDGGILLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIV 690
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVGAKELGKRVVDCCTDPDGR 291
 DB VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVGAKELGKRVVDCCTDPDGR 741

RESULT 10

ADO19776
 ID ADO19776 standard; protein; 806 AA.

AC ADO19776;

DT 12-AUG-2004 (first entry)

XX Human PRO polypeptide #350.

XX Human; PRO; immune related disorder; systemic lupus erythematosus;
 KM rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KM systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KM autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KM diabetes mellitus; renal disease; demyelinating disease;
 KM central nervous system; peripheral nervous system;
 KM demyelinating polyneuropathy; Guillain-Barre syndrome;
 KM chronic inflammatory demyelinating polyneuropathy.

XX Homo sapiens.

XX WO2004043361-A2.

XX 27-MAY-2004.

XX 06-NOV-2003; 2003WO-US035268.

XX 08-NOV-2002; 2002US-0425235P.

XX (GETH) GENENTECH INC.

XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PW;
 PI Wood WI, Wu TD;

XX WPI; 2004-42067/39.

XX N-PSDB; ADO19775.

PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO6838 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,

PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthritis.

XX Claim 7, SEQ ID NO 700, 1731pp, English.

XX The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polypeptide of the
CC invention.

XX Sequence 806 AA;

Query Match 99.5%; Score 1524; DB 8; Length 806;

Best Local Similarity 100.0%; Pred. No. 8, 2e-162;

Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMIISRRKPAFLIGSMRDEKRTDHLCLDGGGVGLIITQLIAIEKASGVATKD 60
DB 451 LQDLMIISRRKPAFLIGSMRDEKRTDHLCLDGGGVGLIITQLIAIEKASGVATKD 510
QY 61 LFDWVAGTGTGILALAIHLSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFLKEEFG 120
DB 511 LFDWVAGTGTGILALAIHLSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFLKEEFG 570
QY 121 HTMTDVRKPKVWLTGTLSDROPABELHFRNYDAPEVIREPRFNQVNLKPPAPSDQIV 180
DB 571 HTMTDVRKPKVWLTGTLSDROPABELHFRNYDAPEVIREPRFNQVNLKPPAPSDQIV 630
QY 181 WRARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 240
DB 631 WRARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 690
QY 241 VSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKGVVDCCTDPDGR 291
DB 691 VSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKGVVDCCTDPDGR 741

RESULT 11

AAR83018
ID AAR83018 standard; protein; 752 AA.

XX AAR83018;

XX 15-JUN-1996 (first entry)

XX Calcium-independent cytosolic phospholipase-A2/B enzyme.

XX CMO; calcium-independent cytosolic phospholipase-A2/B; enzyme;
KW phospholipase-A2; phospholipase-B; drug screening; anti-inflammatory;
XX antibody.

XX Criceetus griseus.

XX US5466595-A.

XX 14-NOV-1995.

XX 27-JUL-1994; 94US-00281193.

XX 27-JUL-1994; 94US-00281193.

XX (GEMV) GENETICS INST INC.

XX Tang J, Jones S;

XX

DR WPI; 1996-009526/01.

DR N-PSDB; AAT05842.

XX Isolated polynucleotide encoding cytosolic phospholipase A2/8 - for
PT producing enzyme for use in screening anti-inflammatory agents and prodn.
PT of antibodies.

XX

XX Claim 5; Col 15-22; 24pp; English.

XX The enzyme may be produced recombinantly in host cells such as animal
CC cells, insect cells, eukaryotes, prokaryotes, etc. The protein may also
CC be expressed in transgenic animals (e.g. milk of transgenic cow). The
CC protein is used to screen for agents which inhibit phospholipase activity
CC for use as anti-inflammatory agents. These agents can be used to treat
CC e.g. rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease
CC and other disease mediated by increased levels of prostaglandins,
CC leukotriene or platelet activating factor. The enzyme can also be used
CC for the production of antibodies for use as research or diagnostic tools

XX Sequence 752 AA;

Query Match 96.1%; Score 1471; DB 2; Length 752;

Best Local Similarity 95.2%; Pred. No. 7e-156;

Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LQDLMIISRRKPAFLIGSMRDEKRTDHLCLDGGGVGLIITQLIAIEKASGVATKD 60
DB 397 LQDLMIISRRKPAFLIGSMRDEKRTDHLCLDGGGVGLIITQLIAIEKASGVATKD 456
QY 61 LFDWVAGTGTGILALAIHLSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFLKEEFG 120
DB 457 LFDWVAGTGTGILALAIHLSKSMAYVRGMYFRMKDEVFRGSRPYESGPLEEFLKEEFG 516
QY 121 HTMTDVRKPKVWLTGTLSDROPABELHFRNYDAPEVIREPRFNQVNLKPPAPSDQIV 180
DB 517 HTMTDVRKPKVWLTGTLSDROPABELHFRNYDAPEVIREPRFNQVNLKPPAPSDQIV 576
QY 181 WRARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 240
DB 577 WRARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 636
QY 241 VSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKGVVDCCTDPDGR 291
DB 637 VSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKGVVDCCTDPDGR 687

RESULT 12

AAW01479
ID AAW01479 standard; protein; 752 AA.

XX AAW01479;

XX 25-MAR-2003 (revised)

XX 12-FEB-1997 (first entry)

XX Calcium-independent cytosolic phospholipase A2/B.

XX cPLA2/B; calcium-independent cytosolic phospholipase A2/B;
KW arachidonic acid; 1-palmitoyl-2-[14C]-arachidonyl-phosphatidylcholine;
XX anti-inflammatory; screen; rheumatoid arthritis.

XX Synthetic.

XX US5554511-A.

XX 10-SEP-1996.

XX 14-APR-1995; 95US-00422420.

XX 27-JUL-1994; 94US-00281193.

XX (GEMV) GENETICS INST INC.

XX

PI Tang J, Jones S;
 XX WPI: 1996-424653/42.
 DR N-PSDB; AAT4578.
 XX
 XX Prodn. of a Ca-independent cytosolic phospholipase A(2)/B - by culturing
 PT host cells contg. the phospholipase gene, useful for screening anti-
 PT inflammatory agents for treating e.g. rheumatoid arthritis.
 XX
 PS Claim 1; Col 15-22; 24pp; English.
 CC The present sequence is that of a calcium-independent cytosolic
 CC phospholipase A2/B (cPLA2/B) enzyme. cPLA2/B is important in the release
 CC of arachidonic acid in specific tissues characterised by unique membrane
 CC phospholipids. The invention provides a process for producing such an
 CC enzyme. The enzyme has a mol. wt. of 86 kD on SDS-PAGE and the presence
 CC of one or more amino acid sequences selected from AAM01480-92. cPLA2/B
 CC has activity in a mixed micelle assay with 1-palmitoyl-2-(14C)-
 CC arachidonyl- phosphatidylcholine. The enzyme is useful for screening anti-
 CC -inflammatory agents mediated by the arachidonic acid cascade, for
 CC treating, e.g. rheumatoid arthritis (Updated on 25-MAR-2003 to correct PF
 CC field.)
 CC
 XX Sequence 752 AA:
 SQ
 Query Match 96.1%; Score 1471; DB 2; Length 752;
 Best Local Similarity 95.2%; Pred. No. 7e-156;
 Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
 QY "1 LODLMHSRRKPAFLIGSNRDEKRTDHLCLDGGVGKLIITQLLIAEKSGVATKD 60
 DB 397 LODLMHSRRKPAFLIGSNRDEKRTDHLCLDGGVGKLIITQLLIAEKSGVATKD 456
 QY 61 LFDWVAGTSGGILALAILHSKSMAYMRGVFRMKDEVFRSGSPYSGLEEFKKEFGE 120
 DB 457 LFDWVAGTSGGILALAILHSKSMAYMRGVFRMKDEVFRSGSPYSGLEEFKKEFGE 516
 QY 121 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRPNQVNLPRPAQSPDQV 180
 DB 517 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRPNQVNLPRPAQSPDQV 576
 QY 181 WRAARSSGAAPTYFRPNRFLDGLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 240
 DB 577 WRAARSSGAAPTYFRPNRFLDGLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 636
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVGAKELGKXVVDCCDTPDGR 291
 DB 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVGAKELGKXVVDCCDTPDGR 687

RESULT 13

AAW13163
 ID AAW13163 standard; protein; 752 AA.
 XX
 AC AAW13163;
 XX
 DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 20-MAY-1997 (first entry)

Ca-independent phospholipase A2/B protein.
 XX
 XX Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;
 KM chromatography; DEAE anion exchange; hydrophobic interaction; lambda;
 KM heparin Toyopearl; chromatofocusing; eukaryotic expression vector; COS;
 KM CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade.
 XX
 OS Cricetus griseus; ovary cells.
 XX
 PN US5589170-A.
 PD 31-DEC-1996.
 XX

PF 14-APR-1995; 95US-00422106.
 XX
 XX 27-JUL-1994; 94US-00281193.
 XX
 XX (GEMV) GENETICS INST INC.
 XX
 XX Tang J, Jones S;
 XX WPI: 1997-076789/07.
 DR N-PSDB; AAT59199.
 XX
 XX Compen. comprising calcium-independent phospholipase enzyme - for
 PT screening for anti-inflammatory agents.
 PS Claim 5; Col 15-22; 24pp; English.
 CC This is the amino acid sequence of the Ca-independent phospholipase A2/B
 CC from Chinese hamster ovary cells. The protein was isolated from these
 CC cells by conventional chromatographic methods e.g. DEAE anion exchange,
 CC hydrophobic interaction, heparin Toyopearl and Mono P 5/20
 CC chromatofocusing chromatography. The purified protein has mol. wt. of 86
 CC kD and an optimum pH 6. The protein was used for amino acid sequencing
 CC from which pools of degenerate probes were synthesised. The probes were
 CC used to screen a CHO cell cDNA library in lambda ZAPIT vector. Of 40000
 CC recombinant phages screened, 12 positive plaques were isolated. One of
 CC these, designated clone 9, contained this sequence. The phospholipase
 CC gene can be inserted into eukaryotic vectors for expression in COS or CHO
 CC cells. The protein, or peptides derived from it e.g. AAW13164-76, can be
 CC used to identify phospholipase inhibitors that can be used as anti-
 CC inflammatory agents, esp. against components of the arachidonic acid
 CC cascade. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT
 CC -2003 to standardise OS field)
 CC
 XX Sequence 752 AA:
 SQ
 Query Match 96.1%; Score 1471; DB 2; Length 752;
 Best Local Similarity 95.2%; Pred. No. 7e-156;
 Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;
 QY "1 LODLMHSRRKPAFLIGSNRDEKRTDHLCLDGGVGKLIITQLLIAEKSGVATKD 60
 DB 397 LODLMHSRRKPAFLIGSNRDEKRTDHLCLDGGVGKLIITQLLIAEKSGVATKD 456
 QY 61 LFDWVAGTSGGILALAILHSKSMAYMRGVFRMKDEVFRSGSPYSGLEEFKKEFGE 120
 DB 457 LFDWVAGTSGGILALAILHSKSMAYMRGVFRMKDEVFRSGSPYSGLEEFKKEFGE 516
 QY 121 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRPNQVNLPRPAQSPDQV 180
 DB 517 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRPNQVNLPRPAQSPDQV 576
 QY 181 WRAARSSGAAPTYFRPNRFLDGLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 240
 DB 577 WRAARSSGAAPTYFRPNRFLDGLANNPTLDAMTEIHEYNDLIRKGOANKVKLSIV 636
 QY 241 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVGAKELGKXVVDCCDTPDGR 291
 DB 637 VSLGTGRSPQVPVTCVDVFRPSNPWELAKTVGAKELGKXVVDCCDTPDGR 687

RESULT 14

AAW17849
 ID AAW17849 standard; protein; 752 AA.
 XX
 AC AAW17849;
 XX
 DT 27-AUG-2003 (revised)
 DT 07-AUG-1997 (first entry)

Hamster cytosolic phospholipase A2/B.
 XX
 XX Cytosolic phospholipase A2/B; arachidonic acid cascade;
 KM inflammation; inhibitor; antiinflammatory; CHO.
 XX

| | |
|-----------|---|
| XX | Cricetus. |
| OS | |
| XX | |
| FX | Key |
| FT | Active-site |
| FT | Location/Qualifiers 465 |
| PT | /note= "mutagenesis of Ser-465 results in loss of activity" |
| XX | |
| XX | M09717448-A2. |
| PN | |
| XX | |
| PD | 15-MAY-1997. |
| XX | |
| PF | 07-NOV-1996; 96WO-US017794. |
| XX | |
| PR | 08-NOV-1995; 95US-00555568. |
| XX | |
| PA | (GENY) GENETICS INST INC. |
| PI | Jones S, Tang J; |
| DR | WPI, 1997-281037/25. |
| DR | N-PSDB; AAT68827. |
| XX | |
| PT | Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject. |
| PS | |
| XX | Example 4, Page 33-36; 74pp; English. |
| XX | |
| CC | A novel hamster cytosolic phospholipase A2/B (gPLA2/B) (AAW17849) is thought to be involved in the arachidonic acid cascade. Its amino acid sequence was deduced from a cDNA clone (AAT68827) obt'd. from a CHO-DUX CC cDNA library. The recombinant enzyme has been expressed in CHO and COS host cells. Human gPLA2/B polypeptides (see also AAU17845-48) have also been isolated. These can be used to screen for inhibitors useful as antiinflammatory agents that block the arachidonic acid cascade in mammals. (Updated on 27-AUG-2003 to correct OS field.) |
| CC | |
| XX | |
| SQ | Sequence 752 AA: |
| | |
| | Query Match 96.1%; Score 1471; DB 2; Length 752; |
| | Best Local Similarity 95.2%; Pred. No. 76-156; |
| | Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0 |
| QY | 1 LODLHHSRARKKPAFILLGSMRDERTDHLCLDGGVKGLIITOLLIAIEKSGVATKD 60 |
| DB | LQDLMPISRRARPPAFILSSMRDEKRTHLLCLDGGGVGIVTIIOLLAIEKSGVATKD 456 |
| QY | 61 LFDWAGSTGGIILALAILHKSMAVMRGVFRMDDEVGRSGRPYESGPLERFLKEBGE 120 |
| DB | 457 LFDWAGSTGGIILALAILHKSMAVMRGVFRMDDEVGRSGRPYESGPLERFLKEBGE 516 |
| QY | 121 HTKMTDVKKPKMVLGTSLSDROPAELHLFRNYDAPETVAREPFPNQNVLNRPAPSPDQLV 180 |
| DB | 517 HTKMTDVKKPKMVLGTSLSDROPAELHLFRNYDAPETVAREPFPNQNINLKRPYQPADQLV 576 |
| QY | 181 WRARRSSGAAPTFFRNPRFLDGLGIANNPTLDAMTEIHEYNODLIRKQANKVKKLSTIV 240 |
| DB | 577 WRARRSSGAAPTFFRNPRFLDGLGIANNPTLDAMTEIHEYNQDMIRKQGKNVKKLSTIV 636 |
| QY | 241 VSLGTGRBPQPVVTCVDVFRPBNPEMLAKTVVGAAGELGMVVDDCCTDPDGR 291 |
| DB | 637 VSLGTGRBPQPVVTCVDVFRPBNPEMLAKTVVGAAGELGMVVDDCCTDPDGR 687 |
| RESULT 15 | |
| AAW81825 | |
| ID | AAW81825 standard; protein; 752 AA. |
| XX | |
| AC | AAW81825; |
| XX | |
| DT | 02-FEB-1999 (first entry) |
| DE | Chinese hamster calcium independent cPLA2/B protein. |

| | |
|----|---|
| XX | Calcium independent; cytosolic phospholipase A2/B; screening; |
| XX | anti-inflammatory; arachidonic acid cascade; chinese hamster. |
| XX | |
| OS | Cricetulus griseus. |
| XX | |
| PN | US5840511-A. |
| XX | |
| PD | 24-NOV-1998. |
| XX | |
| PP | 23-OCT-1996; 96US-00735716. |
| XX | |
| PR | 27-JUL-1994; 94US-00281193. |
| PR | 14-APR-1995; 95US-00422106. |
| XX | |
| PA | (GEMY) GENETICS INST INC. |
| XX | |
| PI | Tang J, Jones S; |
| XX | |
| DR | WPI; 1999-034032/03. |
| DR | N-PSDB; AAV64840. |
| XX | |
| PT | Screening assay for phospholipase inhibitors - using specified |
| PT | phospholipase polypeptide. |
| XX | |
| PS | Claim 1b; Col 21-24; 24pp; English. |
| XX | |
| CC | This sequence represents a novel calcium independent cytosolic |
| CC | phospholipase A2/B enzyme isolated from chinese hamster ovary cells. This |
| CC | protein can be used for screening unknown compounds for anti-inflammatory |
| CC | activity mediated by the arachidonic acid cascade |
| XX | |
| QQ | Sequence 752 AA; |

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Query Match      96.1%; Score 1471; DB 2; Length 752;
Best Local Similarity 95.2%; Pred. No. 7e-156;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY      1 LODIMHISRRKRPAPFIIIGSWDEKRRTHDHLCLDGGGVKGLIITQLLIAIKASGAVATKD 60
Db      397 LODIMPIISRRKRPAPFIIISWMDERGRIDHLLCLDGGGVKGLIITQLLIAIKASGAVATKD 456

QY      61 LFDVVAATSTSGGILALAIISKSAVMRWGMYFRMKDEVFPGSRPYESGPLEEPLKBERGE 120
Db      457 LFDVVAATSTSGGILALAIISKSAVMRWGMYFRMKDEVFPGSRPYESGPLEEPLKBERGE 516

QY      121 HTKKTIVRKPKVMLTGTLSDROPNELHLFRYDAPEPTREERFQNVNLARPAOSDQVL 180
Db      517 HTKKTIVRKPKVMLTGTLSDROPNELHLFRYDAPEPTREERFQNVNLARPPTPAQDVL 576

QY      181 WRAARSSGAAPTYERFPRNGRFLDGGILANNPTLIDAMTEIHEYNOOLIRKQGANVKKLSIV 240
Db      577 WRAARSSGAAPTYERFPRNGRFLDGGILANNPTLIDAMTEIHEYNOQMIIRKQGANVKKLSIV 636

QY      241 VSLGTGSPQVPTVCVDFPRPSNWEMLAKTYFGAKELGKRVVDDCTPBDGR 291
Db      637 VSLGTGSPQVPTVCVDFPRPSNWEMLAKTYFGAKELGKRVVDDCTPBDGR 687

Search completed: December 15, 2004, 13:08:05
Job time : 61.1231 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 15, 2004, 13:01:00 ; Search time 14.8871 Seconds
(without alignments)
1300.780 Million cell updates/sec

Title: US-10-612-668-19

Perfect score: 1531

Sequence: 1 LQDLMHSRARKAPFLIGSM.....GAKELGMVVDCTDPDGRP 292

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCITUS COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | DB ID | Description |
|------------|-------|--------------|-------|---------------------------------------|
| 1 | 1531 | 100.0 | 292 2 | US-08-555-568B-19 Sequence 19, Appl |
| 2 | 1531 | 100.0 | 292 3 | US-09-519-223-19 Sequence 19, Appl |
| 3 | 1531 | 100.0 | 292 4 | US-09-927-180-19 Sequence 19, Appl |
| 4 | 1531 | 100.0 | 687 2 | US-08-555-568B-21 Sequence 21, Appl |
| 5 | 1531 | 100.0 | 687 3 | US-09-519-223-21 Sequence 21, Appl |
| 6 | 1531 | 100.0 | 687 4 | US-09-927-180-21 Sequence 21, Appl |
| 7 | 1531 | 100.0 | 688 2 | US-08-555-568B-23 Sequence 23, Appl |
| 8 | 1531 | 100.0 | 688 3 | US-09-519-223-23 Sequence 23, Appl |
| 9 | 1531 | 100.0 | 688 4 | US-09-927-180-23 Sequence 23, Appl |
| 10 | 1471 | 96.1 | 752 1 | US-08-281-193-2 Sequence 2, Appl |
| 11 | 1471 | 96.1 | 752 2 | US-08-422-106-2 Sequence 2, Appl |
| 12 | 1471 | 96.1 | 752 3 | US-08-735-716-2 Sequence 2, Appl |
| 13 | 1471 | 96.1 | 752 4 | US-08-555-568B-2 Sequence 2, Appl |
| 14 | 1471 | 96.1 | 752 5 | US-09-519-223-2 Sequence 2, Appl |
| 15 | 1471 | 96.1 | 752 6 | US-09-927-180-2 Sequence 2, Appl |
| 16 | 1471 | 96.1 | 752 7 | PCT-US95-08069-2 Sequence 2, Appl |
| 17 | 736 | 48.1 | 896 4 | US-09-270-767-46130 Sequence 46130, A |
| 18 | 610 | 39.8 | 545 4 | US-09-270-767-61684 Sequence 61684, A |
| 19 | 371 | 24.2 | 143 4 | US-09-755-630B-290 Sequence 33298, A |
| 20 | 177 | 11.6 | 410 4 | US-09-755-630B-292 Sequence 292, App |
| 21 | 177 | 11.6 | 410 4 | US-09-755-274-10 Sequence 10, Appl |
| 22 | 177 | 11.6 | 410 4 | US-09-755-274-12 Sequence 12, Appl |
| 23 | 177 | 11.4 | 337 4 | US-09-755-630B-293 Sequence 293, App |
| 24 | 175 | 11.4 | 410 2 | US-08-449-986-2 Sequence 2, Appl |
| 25 | 175 | 11.4 | 410 2 | US-08-449-986-2 Sequence 2, Appl |
| 26 | 175 | 11.4 | 410 2 | US-08-449-986-2 Sequence 2, Appl |
| 27 | 175 | 11.4 | 410 2 | US-08-449-986-2 Sequence 2, Appl |

| | | | | |
|----|-------|------|-------|--------------------------------------|
| 28 | 175 | 11.4 | 410 4 | US-09-755-630B-288 Sequence 288, App |
| 29 | 175 | 11.4 | 410 4 | US-09-755-630B-291 Sequence 291, App |
| 30 | 175 | 11.4 | 410 4 | US-09-755-274-8 Sequence 8, Appl |
| 31 | 175 | 11.4 | 410 4 | US-09-755-274-11 Sequence 11, Appl |
| 32 | 175 | 11.4 | 508 4 | US-09-755-630B-289 Sequence 289, App |
| 33 | 175 | 11.4 | 508 4 | US-09-755-630B-289 Sequence 289, App |
| 34 | 142.5 | 9.3 | 383 1 | US-07-936-163-4 Sequence 4, Appl |
| 35 | 140 | 9.1 | 381 1 | US-07-936-163-3 Sequence 3, Appl |
| 36 | 140 | 9.1 | 386 4 | US-09-755-630B-278 Sequence 278, App |
| 37 | 140 | 9.1 | 386 4 | US-09-755-274-5 Sequence 5, Appl |
| 38 | 139 | 9.1 | 366 4 | US-09-755-274-263 Sequence 263, App |
| 39 | 139 | 9.1 | 366 4 | US-09-755-274-29 Sequence 29, Appl |
| 40 | 138 | 9.0 | 367 4 | US-09-755-630B-7 Sequence 7, Appl |
| 41 | 138 | 9.0 | 367 4 | US-09-755-274-41 Sequence 41, Appl |
| 42 | 138 | 9.0 | 386 4 | US-09-755-630B-2 Sequence 2, Appl |
| 43 | 138 | 9.0 | 386 4 | US-09-755-630B-265 Sequence 265, App |
| 44 | 138 | 9.0 | 386 4 | US-09-755-630B-286 Sequence 286, App |
| 45 | 138 | 9.0 | 386 4 | US-09-755-274-1 Sequence 1, Appl |

ALIGNMENTS

```
RESULT 1
US-08-555-568B-19
Sequence 19, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-555-568B-19
Query Match 100.0%; Score 1531; DB 2; Length 292;
Best Local Similarity 100.0%; Pred. No. 8.5e-168;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 LQDLMHSRARKAPFLIGSMRDEKRTDHLCLDGGVKGKLIITQLIAIEKSGVATKD 60
Db 1 LQDLMHSRARKAPFLIGSMRDEKRTDHLCLDGGVKGKLIITQLIAIEKSGVATKD 60
Cy 61 LFDVVAAGTSGTGLALALILHSKSMAYVRGMYFRMKDEVFRGSRPYSGPLEEFLKREFGE 120
Db 61 LFDVVAAGTSGTGLALALILHSKSMAYVRGMYFRMKDEVFRGSRPYSGPLEEFLKREFGE 120
```

| | | | |
|----|-----|--|-----|
| QY | 12 | HTKMTDYKKPKMVLGTSLSDROPAELHLEPRNDAPEYVPEPRNQVNLRPPAQSDOLY | 180 |
| Db | 121 | HTKMTDYKKPKMVLGTSLSDROPAELHLEPRNDAPEYVPEPRNQVNLRPPAQSDOLY | 180 |
| QY | 181 | WPAARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMEIHEYNDLLRRKQOANKYKLSIV | 240 |
| Db | 181 | WPAARSSGAAPTYFRPNGRFLDGGLLANNPTLDAMEIHEYNDLLRRKQOANKYKLSIV | 240 |
| QY | 241 | VSIGTGRSPQVPEVTCVDVFRPSNPMEIATVFGAKELGKVVNDCCDTPDGRP | 292 |
| Db | 241 | VSIGTGRSPQVPEVTCVDVFRPSNPMEIATVFGAKELGKVVNDCCDTPDGRP | 292 |

Db 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 292

RESULT 4

US-08-555-568B-21
 ; Sequence 21, Application US/08555568B
 ; Patent No. 5976854
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 Cambridgepark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 21:
 ; LENGTH: 687 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-555-568B-21

Query Match 100.0%; Score 1531; DB 2; Length 687;

Best Local Similarity 100.0%; Pred. No. 3.3e-167; Mismatches 0; Indels 0; Gaps 0;

Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMIISRAKPAFLIGSRDEKRTDHLCLDGGVKGIIIIQLLIAIEKASGVATKD 60
 Db 396 LQDLMIISRAKPAFLIGSRDEKRTDHLCLDGGVKGIIIIQLLIAIEKASGVATKD 455
 QY 61 LFPWVAGTSGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
 Db 456 LFPWVAGTSGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 515
 QY 121 HTKMTVVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPRPAQPSDOLV 180
 Db 516 HTKMTVVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPRPAQPSDOLV 575
 QY 181 WRAARSSGAAPTYFRPNRGRFLDGLLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 240
 Db 576 WRAARSSGAAPTYFRPNRGRFLDGLLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 635
 QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 292
 Db 636 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 687

RESULT 5

US-09-519-223-21
 ; Sequence 21, Application US/09519223
 ; Patent No. 6274140
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon

APPLICANT: Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/519,223

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/555,568

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 687 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-519-223-21

Query Match 100.0%; Score 1531; DB 3; Length 687;

Best Local Similarity 100.0%; Pred. No. 3.3e-167; Mismatches 0; Indels 0; Gaps 0;

Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDLMIISRAKPAFLIGSRDEKRTDHLCLDGGVKGIIIIQLLIAIEKASGVATKD 60
 Db 396 LQDLMIISRAKPAFLIGSRDEKRTDHLCLDGGVKGIIIIQLLIAIEKASGVATKD 455
 QY 61 LFPWVAGTSGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
 Db 456 LFPWVAGTSGGILALAILHSKSMAYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGE 515
 QY 121 HTKMTVVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPRPAQPSDOLV 180
 Db 516 HTKMTVVRKPKWMLTGLSDROPALHLFRNYDAPETVREPRNQNVLPRPAQPSDOLV 575
 QY 181 WRAARSSGAAPTYFRPNRGRFLDGLLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 240
 Db 576 WRAARSSGAAPTYFRPNRGRFLDGLLANNPTLDAMTEIHEYNODLIRKQANVKKLSIV 635
 QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 292
 Db 636 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGR 687

RESULT 6

US-09-927-180-21
 ; Sequence 21, Application US/09927180
 ; Patent No. 6645736
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 Cambridgepark Drive

CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 1531; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 3.3e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LODMHISRAKRAFLIGSRDEKRTDHLCLDGGVGLIIQLLIAEKASGVATKD 60
DB 396 LODMHISRAKRAFLIGSRDEKRTDHLCLDGGVGLIIQLLIAEKASGVATKD 456
QY 61 LFPWVAGTGTGGLALAILHSKSMAYRMGYFRMKDEVFRSGRPYSGPLEEFLKEFGE 120
DB 456 LFPWVAGTGTGGLALAILHSKSMAYRMGYFRMKDEVFRSGRPYSGPLEEFLKEFGE 516
QY 121 HTKMTVRRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLRPAPQSPDQV 180
DB 516 HTKMTVRRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLRPAPQSPDQV 576
QY 181 WRAARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
DB 576 WRAARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 636
QY 241 VSLGTRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKVVVDCCTDPDGRP 292
DB 636 VSLGTRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKVVVDCCTDPDGRP 687

RESULT 7
US-08-555-568B-23
Sequence 23, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-555-568B-23

Query Match 100.0%; Score 1531; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.3e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LODMHISRAKRAFLIGSRDEKRTDHLCLDGGVGLIIQLLIAEKASGVATKD 60
DB 397 LODMHISRAKRAFLIGSRDEKRTDHLCLDGGVGLIIQLLIAEKASGVATKD 456
QY 61 LFPWVAGTGTGGLALAILHSKSMAYRMGYFRMKDEVFRSGRPYSGPLEEFLKEFGE 120
DB 457 LFPWVAGTGTGGLALAILHSKSMAYRMGYFRMKDEVFRSGRPYSGPLEEFLKEFGE 516
QY 121 HTKMTVRRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLRPAPQSPDQV 180
DB 517 HTKMTVRRKPKWLTGTLSDROPALHLFRNYDAPETVREPRFNQVNLRPAPQSPDQV 576
QY 181 WRAARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 240
DB 577 WRAARSSGAAPTYFRNGRFLDGLANNPTLDAMTEIHEYNDLIRKQANVKKLSIV 636
QY 241 VSLGTRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKVVVDCCTDPDGRP 292
DB 637 VSLGTRSPQVPYTCVDVFRPSNPWELAKTVFGAKELGKVVVDCCTDPDGRP 688

RESULT 8
US-09-519-223-23
Sequence 23, Application US/09519223
Patent No. 6274140
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/519,223
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/555,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-519-223-23

Query Match 100.0%; Score 1531; DB 3; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.3e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIIIQLLIAEKASGVATKD 60
DB 397 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIIIQLLIAEKASGVATKD 456
QY 61 LFDWVAGTSTGGILALAILHSKSMAYVRGMYPRMKDEVFRGSRPYESGPLEEFKKEFGE 120
DB 457 LFDWVAGTSTGGILALAILHSKSMAYVRGMYPRMKDEVFRGSRPYESGPLEEFKKEFGE 516
QY 121 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQV 180
DB 517 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQV 576
QY 181 WRAASSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIV 240
DB 577 WRAASSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIV 636
QY 241 VSLGTGRSPQVPTCVDFRPSNPWEIAKTVEGAKELGKMWVDCCTDPDGR 292
DB 637 VSLGTGRSPQVPTCVDFRPSNPWEIAKTVEGAKELGKMWVDCCTDPDGR 688

RESULT 9
US-09-927-180-23
Sequence 23, Application US/09927180
Patent No. 6645736
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 100.0%; Score 1531; DB 4; Length 688;
Best Local Similarity 100.0%; Pred. No. 3.3e-167;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIIIQLLIAEKASGVATKD 60
DB 397 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIIIQLLIAEKASGVATKD 456
QY 61 LFDWVAGTSTGGILALAILHSKSMAYVRGMYPRMKDEVFRGSRPYESGPLEEFKKEFGE 120
DB 457 LFDWVAGTSTGGILALAILHSKSMAYVRGMYPRMKDEVFRGSRPYESGPLEEFKKEFGE 516
QY 121 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQV 180
DB 517 HTMTDVRKPKWLTGTLSDROPALHLFRNYDAPETVREPRNQVNLPRPAQPSDQV 576
QY 181 WRAASSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIV 240
DB 577 WRAASSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNDLIRKQANKVKKLSIV 636
QY 241 VSLGTGRSPQVPTCVDFRPSNPWEIAKTVEGAKELGKMWVDCCTDPDGR 292
DB 637 VSLGTGRSPQVPTCVDFRPSNPWEIAKTVEGAKELGKMWVDCCTDPDGR 688

RESULT 10
US-08-281-193-2
Sequence 2, Application US/08281193
Patent No. 546595
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-281-193-2

Query Match 96.1%; Score 1471; DB 1; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.1e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIIIQLLIAEKASGVATKD 60
DB 397 LODMHSRARKPAFLIGSRDEKRTDHLCLDGGVKGIIIIQLLIAEKASGVATKD 456
QY 61 LFDWVAGTSTGGILALAILHSKSMAYVRGMYPRMKDEVFRGSRPYESGPLEEFKKEFGE 120
DB 457 LFDWVAGTSTGGILALAILHSKSMAYVRGMYPRMKDEVFRGSRPYESGPLEEFKKEFGE 516

QY 121 HTMTDVRKPKWLTGTLSDROPALHLPFNYPDAPETVREPRFNQVNLPPAPQSDQV 180
 DB 517 HTMTDVRKPKWLTGTLSDROPALHLPFNYPDAPETVREPRFNQVNLPPAPQSDQV 576
 QY 181 WRAARSSGAAPTYFRPNRGRFLDGLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 240
 DB 577 WRAARSSGAAPTYFRPNRGRFLDGLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 636
 QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKKNVDDCTDPDGR 291
 DB 637 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKKNVDDCTDPDGR 687

RESULT 11

US-08-422-106-2
 ; Sequence 2, Application US/08422106
 ; Patent No. 5583170
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 15
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/422,106
 ; FILING DATE: 14-APR-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/281,193
 ; FILING DATE: 27-JUL-1994
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-422-106-2

Query Match 96.1%; Score 1471; DB 1; Length 752;
 Best Local Similarity 95.2%; Pred. No. 3.1e-160;
 Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODLMHISRARKRAFLTGSNRDEKRTDHLCLDGGGVKGLIITQLLIAIEKASGVATKD 60
 DB 397 LODLMHISRARKRAFLTGSNRDEKRTDHLCLDGGGVKGLIITQLLIAIEKASGVATKD 456
 QY 61 LFDWVAGSTGTGILALAILHSKSMAYRMGYFRMKDEVRFSRPRYSGPLEEFKKEFG 120
 DB 457 LFDWVAGSTGTGILALAILHSKSMAYRMGYFRMKDEVRFSRPRYSGPLEEFKKEFG 516
 QY 121 HTMTDVRKPKWLTGTLSDROPALHLPFNYPDAPETVREPRFNQVNLPPAPQSDQV 180
 DB 517 HTMTDVRKPKWLTGTLSDROPALHLPFNYPDAPETVREPRFNQVNLPPAPQSDQV 576
 QY 181 WRAARSSGAAPTYFRPNRGRFLDGLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 240
 DB 577 WRAARSSGAAPTYFRPNRGRFLDGLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 636
 QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKKNVDDCTDPDGR 291
 DB 637 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKKNVDDCTDPDGR 687

RESULT 12
 ; US-08-735-716-2
 ; Sequence 2, Application US/08735716
 ; Patent No. 5840511
 ; GENERAL INFORMATION:

APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 15
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/735,716
 ; FILING DATE: 23-OCT-1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/281,193
 ; FILING DATE: 27-JUL-1994
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-735-716-2

Query Match 96.1%; Score 1471; DB 2; Length 752;
 Best Local Similarity 95.2%; Pred. No. 3.1e-160;
 Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODLMHISRARKRAFLTGSNRDEKRTDHLCLDGGGVKGLIITQLLIAIEKASGVATKD 60
 DB 397 LODLMHISRARKRAFLTGSNRDEKRTDHLCLDGGGVKGLIITQLLIAIEKASGVATKD 456
 QY 61 LFDWVAGSTGTGILALAILHSKSMAYRMGYFRMKDEVRFSRPRYSGPLEEFKKEFG 120
 DB 457 LFDWVAGSTGTGILALAILHSKSMAYRMGYFRMKDEVRFSRPRYSGPLEEFKKEFG 516
 QY 121 HTMTDVRKPKWLTGTLSDROPALHLPFNYPDAPETVREPRFNQVNLPPAPQSDQV 180
 DB 517 HTMTDVRKPKWLTGTLSDROPALHLPFNYPDAPETVREPRFNQVNLPPAPQSDQV 576
 QY 181 WRAARSSGAAPTYFRPNRGRFLDGLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 240
 DB 577 WRAARSSGAAPTYFRPNRGRFLDGLANNPTLDAMTEIHEYNODLIRKGOANVKKLSIV 636
 QY 241 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKKNVDDCTDPDGR 291
 DB 637 VSLGTGRSPQVPTCVDFRPSNPWELAKTVFGAKELGKKNVDDCTDPDGR 687

RESULT 13
 ; US-08-555-568B-2
 ; Sequence 2, Application US/08555568B
 ; Patent No. 5976854
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Genetics Institute, Inc.
 ; STREET: 87 Cambridgepark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568B
 ; FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-555-568B-2

Query Match 96.1%; Score 1471; DB 2; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.1e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODLMIISARKAPAFILGSMRDEKRTDHLCLDGGGVGLIIQLLIIEKASGVATKD 60
DB 397 LODLMIISARKAPAFILGSMRDEKRTDHLCLDGGGVGLIIQLLIIEKASGVATKD 456
QY 61 LFDWVAGSTGGILALAIHLSKSMAYMRGVFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
DB 457 LFDWVAGSTGGILALAIHLSKSMAYMRGVFRMKDEVFRGSRPYESGPLEEFLKREFGE 516
QY 121 HRTMTDVRKPKWMLTGLSDROPALHLFRNYDAPEVTAREPRNQVNLRRPAPQSDQLY 180
DB 517 HRTMTDVRKPKWMLTGLSDROPALHLFRNYDAPEVTAREPRNQVNLRRPAPQSDQLY 576
QY 181 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANKVKLSIV 240
DB 577 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANKVKLSIV 636
QY 241 VSLGTRSPQVPTCVDFRPSNPWEIATVFGAKELGKRVVDCCTDPDGR 291
DB 637 VSLGTRSPQVPTCVDFRPSNPWEIATVFGAKELGKRVVDCCTDPDGR 687

RESULT 14
US-09-519-223-2
Sequence 2, Application US/09519223
Patent No. 6274140
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/519,223
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-519-223-2

Query Match 96.1%; Score 1471; DB 3; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.1e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 LODLMIISARKAPAFILGSMRDEKRTDHLCLDGGGVGLIIQLLIIEKASGVATKD 60
DB 397 LODLMIISARKAPAFILGSMRDEKRTDHLCLDGGGVGLIIQLLIIEKASGVATKD 456
QY 61 LFDWVAGSTGGILALAIHLSKSMAYMRGVFRMKDEVFRGSRPYESGPLEEFLKREFGE 120
DB 457 LFDWVAGSTGGILALAIHLSKSMAYMRGVFRMKDEVFRGSRPYESGPLEEFLKREFGE 516
QY 121 HRTMTDVRKPKWMLTGLSDROPALHLFRNYDAPEVTAREPRNQVNLRRPAPQSDQLY 180
DB 517 HRTMTDVRKPKWMLTGLSDROPALHLFRNYDAPEVTAREPRNQVNLRRPAPQSDQLY 576
QY 181 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANKVKLSIV 240
DB 577 WRAARSSGAAPTYFRNGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANKVKLSIV 636
QY 241 VSLGTRSPQVPTCVDFRPSNPWEIATVFGAKELGKRVVDCCTDPDGR 291
DB 637 VSLGTRSPQVPTCVDFRPSNPWEIATVFGAKELGKRVVDCCTDPDGR 687

RESULT 15
US-09-927-180-2
Sequence 2, Application US/09927180
Patent No. 6645736
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2

Query Match 96.1%; Score 1471; DB 4; Length 752;
Best Local Similarity 95.2%; Pred. No. 3.1e-160;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | LODLMHISRRKPAFILGSRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD | 60 |
| DB | 397 | LODLMPISRRKPAFILSSMRDEKRIHDHLLCLDGGGVKGLVITQLLIAIEKASGVATKD | 456 |
| QY | 61 | LFDWVAGTSTGGILALAIHSKSMAYMRCMYFRMKDEVFRGSRPYESGPLEEFKREFGE | 120 |
| DB | 457 | LFDWVAGTSTGGILALAIHSKSMAYMRCMYFRMKDEVFRGSRPYESGPLEEFKREFGE | 516 |
| QY | 121 | HTKMTVVRKPKWLTGTLSDROPALHLPNNYDAPETVRPPFNQVNLRPAPQPSDQLV | 180 |
| DB | 517 | HTKMTVVRKPKWLTGTLSDROPALHLPNNYDAPEVIREPPFNQVNLRPAPQPSDQLV | 576 |
| QY | 181 | WRPAASSGAAPTVERPNGRFLDGLLANNPTLDAMTEIHEYNODLIRKGOANKVKLSIV | 240 |
| DB | 577 | WRPAASSGAAPTVERPNGRFLDGLLANNPTLDAMTEIHEYNODMIRKGOANKVKLSIV | 636 |
| QY | 241 | VSLGTGRSPQVPVTCVDFRPSNPWEIAKTVFGAKELGKXNVVDCCTDPDGR | 291 |
| DB | 637 | VSLGTGRSPQVPVTCVDFRPSNPWEIAKTVFGAKELGKXNVVDCCTDPDGR | 687 |

Search completed: December 15, 2004, 13:15:33
Job time : 16.8871 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 13:13:21 : Search time 51.2542 Seconds
(Without alignments)
2034.879 Million cell updates/sec

Title: US-10-612-668-19
Perfect score: 1531
Sequence: 1 LODMHISARKRAFLGSM.....GATELGKVVDCCTDDGR 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues
Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing filter 45 summaries

Database :

- 1: /cgn2_6/prodata/2/pubppa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubppa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubppa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubppa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubppa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubppa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubppa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubppa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubppa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubppa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubppa/US09C_PUBCOMB.pep.*
- 13: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubppa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/2/pubppa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/prodata/2/pubppa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/2/pubppa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/prodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------------------|-------------------|
| 1 | 1531 | 100.0 | 292 | 9 US-09-927-180-19 | Sequence 19, Appl |
| 2 | 1531 | 100.0 | 687 | 9 US-09-927-180-21 | Sequence 21, Appl |
| 3 | 1531 | 100.0 | 688 | 9 US-09-927-180-23 | Sequence 23, Appl |
| 4 | 1524 | 99.5 | 667 | 15 US-10-108-260A-3778 | Sequence 3778, Ap |
| 5 | 1471 | 96.1 | 752 | 9 US-09-927-180-2 | Sequence 2, Appl |
| 6 | 456.5 | 29.8 | 1071 | 14 US-10-369-493-6865 | Sequence 6865, Ap |
| 7 | 419 | 27.4 | 1023 | 14 US-10-369-493-6689 | Sequence 6689, Ap |
| 8 | 419 | 27.4 | 1023 | 14 US-10-369-493-6680 | Sequence 6680, Ap |
| 9 | 261 | 17.0 | 468 | 14 US-10-425-115-196524 | Sequence 4998, Ap |
| 10 | 245 | 16.0 | 1053 | 17 US-10-425-115-196524 | Sequence 196524, |
| 11 | 235 | 15.3 | 1254 | 16 US-10-437-963-169583 | Sequence 169583, |
| 12 | 234 | 15.3 | 387 | 15 US-10-421-654-66 | Sequence 66, Appl |
| 13 | 211.5 | 13.8 | 370 | 9 US-09-925-300-1483 | Sequence 1483, Ap |

| | | | | | |
|----|-------|------|-----|-------------------------|-------------------|
| 14 | 208.5 | 13.6 | 350 | 15 US-10-421-654-100 | Sequence 100, App |
| 15 | 204.5 | 13.4 | 577 | 14 US-10-310-154-616 | Sequence 616, App |
| 16 | 201 | 13.1 | 325 | 15 US-10-424-599-259117 | Sequence 259117, |
| 17 | 201 | 13.1 | 382 | 14 US-10-310-154-615 | Sequence 615, App |
| 18 | 195.5 | 12.8 | 382 | 15 US-10-424-599-258423 | Sequence 258423, |
| 19 | 193.5 | 12.6 | 387 | 16 US-10-437-963-177823 | Sequence 177823, |
| 20 | 190 | 12.4 | 378 | 15 US-10-421-654-18 | Sequence 18, Appl |
| 21 | 178 | 11.6 | 435 | 17 US-10-425-115-343159 | Sequence 343159, |
| 22 | 177 | 11.6 | 410 | 10 US-09-755-630A-290 | Sequence 290, App |
| 23 | 177 | 11.6 | 410 | 10 US-09-755-630A-292 | Sequence 292, App |
| 24 | 177 | 11.6 | 410 | 17 US-10-658-180-230 | Sequence 290, App |
| 25 | 177 | 11.6 | 410 | 17 US-10-658-180-292 | Sequence 292, App |
| 26 | 177 | 11.6 | 434 | 15 US-10-425-114-33447 | Sequence 33447, A |
| 27 | 177 | 11.6 | 437 | 15 US-10-425-114-39376 | Sequence 39376, A |
| 28 | 177 | 11.6 | 439 | 15 US-10-425-114-47375 | Sequence 47375, A |
| 29 | 177 | 11.6 | 441 | 15 US-10-425-114-57061 | Sequence 57061, A |
| 30 | 177 | 11.6 | 442 | 16 US-10-437-963-138254 | Sequence 138254, |
| 31 | 176 | 11.5 | 423 | 15 US-10-425-115-282153 | Sequence 282153, |
| 32 | 176 | 11.5 | 438 | 15 US-10-425-114-72032 | Sequence 72032, A |
| 33 | 176 | 11.5 | 438 | 15 US-10-425-114-72035 | Sequence 72035, A |
| 34 | 176 | 11.5 | 448 | 15 US-10-425-114-65072 | Sequence 65072, A |
| 35 | 175 | 11.4 | 337 | 10 US-09-755-630A-293 | Sequence 293, App |
| 36 | 175 | 11.4 | 337 | 17 US-10-658-180-293 | Sequence 293, App |
| 37 | 175 | 11.4 | 410 | 10 US-09-755-630A-288 | Sequence 288, App |
| 38 | 175 | 11.4 | 410 | 10 US-09-755-630A-291 | Sequence 288, App |
| 39 | 175 | 11.4 | 410 | 17 US-10-658-180-288 | Sequence 288, App |
| 40 | 175 | 11.4 | 410 | 17 US-10-658-180-291 | Sequence 291, App |
| 41 | 175 | 11.4 | 436 | 15 US-10-425-114-39450 | Sequence 39450, A |
| 42 | 175 | 11.4 | 436 | 15 US-10-425-114-47374 | Sequence 47374, A |
| 43 | 175 | 11.4 | 508 | 10 US-09-755-630A-289 | Sequence 289, App |
| 44 | 175 | 11.4 | 508 | 17 US-10-658-180-289 | Sequence 289, App |
| 45 | 174.5 | 11.4 | 405 | 16 US-10-437-963-129647 | Sequence 129647, |

ALIGNMENTS

RESULT 1
US-09-927-180-19
Sequence 19, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESSES:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:

LENGTH: 292 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-927-180-19

Query Match 100.0%; Score 1531; DB 9; Length 292;
Best Local Similarity 100.0%; Pred. No. 4,2e-152;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLMIISRRKPAFLIGSMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 1 LODLMIISRRKPAFLIGSMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
QY 61 LFDPMVAGTSTGGILALAIHLSKSMAYRMGMVFPMKDEVRGSRPYSGPLEEFLKKEPGE 120
DB 61 LFDPMVAGTSTGGILALAIHLSKSMAYRMGMVFPMKDEVRGSRPYSGPLEEFLKKEPGE 120
QY 121 HTKMTVRKPKWLTGTLSDROPALHLFRNYDAPETVAREPRNQVNLRPPAQSPDOLV 180
DB 121 HTKMTVRKPKWLTGTLSDROPALHLFRNYDAPETVAREPRNQVNLRPPAQSPDOLV 180
QY 181 WRAARSSGAAPTYFRNGRFLDGLIANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 181 WRAARSSGAAPTYFRNGRFLDGLIANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
QY 241 VSLGTRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 292
DB 241 VSLGTRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 292

RESULT 2
US-09-927-180-21

Sequence 21, Application US/09927180
Patent No. US20020106364A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 687 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-927-180-21

Query Match 100.0%; Score 1531; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODLMIISRRKPAFLIGSMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60
DB 396 LODLMIISRRKPAFLIGSMRDEKRTDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 455
QY 61 LFDPMVAGTSTGGILALAIHLSKSMAYRMGMVFPMKDEVRGSRPYSGPLEEFLKKEPGE 120
DB 456 LFDPMVAGTSTGGILALAIHLSKSMAYRMGMVFPMKDEVRGSRPYSGPLEEFLKKEPGE 515
QY 121 HTKMTVRKPKWLTGTLSDROPALHLFRNYDAPETVAREPRNQVNLRPPAQSPDOLV 180
DB 516 HTKMTVRKPKWLTGTLSDROPALHLFRNYDAPETVAREPRNQVNLRPPAQSPDOLV 575
QY 181 WRAARSSGAAPTYFRNGRFLDGLIANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 240
DB 576 WRAARSSGAAPTYFRNGRFLDGLIANNPTLDAMTEIHEYNDLIRKQANKVKLSIV 635
QY 241 VSLGTRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 292
DB 636 VSLGTRSPQVPVTCVDFRPSNPWELAKTVFGAKELGKRVVDCCTDPDGRP 687

RESULT 3

US-09-927-180-23

Sequence 23, Application US/09927180
Patent No. US20020106364A1

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (ERO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 688 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Query Match 100.0%; Score 1531; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.5e-151;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LQDLMIISRRKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 60
      397 LQDLMIISRRKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 456
      61 LFDWVAGTSTGGILALAILHSKSMAYVRGMYFRMKDEVFRGSRPYESGPLBEFLKREFG 120
      457 LFDWVAGTSTGGILALAILHSKSMAYVRGMYFRMKDEVFRGSRPYESGPLBEFLKREFG 516
      121 HTKMTDVRRKRWLTGTLSDROPALHLFRNYDAPEVTRPREFRNQNVLPRPAQPSQDLV 180
      517 HTKMTDVRRKRWLTGTLSDROPALHLFRNYDAPEVTRPREFRNQNVLPRPAQPSQDLV 576
      181 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
      577 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 636
      241 VSLGTGRSPQVPVTCVDVFRPSNPMELAKTVFGAKELGKNVVDCTDPDGR 292
      637 VSLGTGRSPQVPVTCVDVFRPSNPMELAKTVFGAKELGKNVVDCTDPDGR 688

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RESULT 4
US-10-108-260A-3778
; Sequence 3778, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108, 260A
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3778
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3778

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Query Match          99.5%; Score 1524; DB 15; Length 667;
Best Local Similarity 100.0%; Pred. No. 7,7e-151;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LQDLMIISRRKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 60
      312 LQDLMIISRRKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 371
      61 LFDWVAGTSTGGILALAILHSKSMAYVRGMYFRMKDEVFRGSRPYESGPLBEFLKREFG 120
      372 LFDWVAGTSTGGILALAILHSKSMAYVRGMYFRMKDEVFRGSRPYESGPLBEFLKREFG 431
      121 HTKMTDVRRKRWLTGTLSDROPALHLFRNYDAPEVTRPREFRNQNVLPRPAQPSQDLV 180
      432 HTKMTDVRRKRWLTGTLSDROPALHLFRNYDAPEVTRPREFRNQNVLPRPAQPSQDLV 491
      181 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
      492 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 551
      241 VSLGTGRSPQVPVTCVDVFRPSNPMELAKTVFGAKELGKNVVDCTDPDGR 291
      552 VSLGTGRSPQVPVTCVDVFRPSNPMELAKTVFGAKELGKNVVDCTDPDGR 602

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RESULT 5
US-09-927-180-2
; Sequence 2, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

```

```

; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2

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Query Match          96.1%; Score 1471; DB 9; Length 752;
Best Local Similarity 95.2%; Pred. No. 3,5e-145;
Matches 277; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

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QY      1 LQDLMIISRRKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 60
      397 LQDLMIISRRKPAFLIGSRDEKRTDHLCLDGGVGKGLIIQLIAIEKASGVATKD 456
      61 LFDWVAGTSTGGILALAILHSKSMAYVRGMYFRMKDEVFRGSRPYESGPLBEFLKREFG 120
      457 LFDWVAGTSTGGILALAILHSKSMAYVRGMYFRMKDEVFRGSRPYESGPLBEFLKREFG 516
      121 HTKMTDVRRKRWLTGTLSDROPALHLFRNYDAPEVTRPREFRNQNVLPRPAQPSQDLV 180
      517 HTKMTDVRRKRWLTGTLSDROPALHLFRNYDAPEVTRPREFRNQNVLPRPAQPSQDLV 576
      181 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 240
      577 WRAARSSGAAPTYFRPNRGRLDGGLLANNPTLDAMTEIHEYNDLIRKQGANVKKLSIV 636
      241 VSLGTGRSPQVPVTCVDVFRPSNPMELAKTVFGAKELGKNVVDCTDPDGR 291
      637 VSLGTGRSPQVPVTCVDVFRPSNPMELAKTVFGAKELGKNVVDCTDPDGR 687

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RESULT 6
US-10-369-493-6865
; Sequence 6865, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xiandeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B

```



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; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6865
; LENGTH: 1071
; TYPE: PRF
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6665
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Query Match      29.8%; Score 456.5; DB 14; Length 1071;
Best Local Similarity 34.5%; Pred. No. 3.2e-38;
Matches 102; Conservative 62; Mismatches 97; Indels 35; Gaps 8;
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QY 1 LQDLNHSIRKRAFLGSRDEKTHDHLCLDGGVSKLIIITLIATEKSGVATKX 60
DB 730 IQDTLDSGRKAKY-----NLSMDGGIRGLVITLIATEKSLDIDIFK 777
QY 61 LFDVAGTSGILALAIHSKSMAYRWGYFPMKDEVEFRG-SRPYSGPLEFKREFG 119
DB 778 YFDWAGTSGILMAGLATGKSLREMQOTYLLKQRFVGMIPYDTVQLEKFIQDFG 837
QY 120 EHTKMTDVKKPKMLTGTSRQPAELHFRNTDAETVAREPRFNQVNLPPAQSDDL 179
DB 838 TGT-VWEIPRMLIAVNVSEKLPVRLKARVYKPAKV-----ABETREKMP 884
QY 180 VWRPAASGSAAPYFPRN-GRFLDGLLANNPTLDANTEIHEYNODLIRKQANKYKLS 238
DB 885 LWMALRRSTRAPVLFEPSEKRYIDGIIISNPALDMSSEHAYNRELQSLGRSDAVQNM 944
QY 239 IVVSLGTGRSPQVPTCVDFR--PSNPWELAKTVFGAKELGKMYVDCCTDPDGRP 292
DB 945 VLVSEFTG--QIPSTVIEFTLSIDNSPLQSIKTI---KVLAMFIDQATASEGAP 994
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```

RESULT 7
US-10-369-493-6689
; Sequence 6689, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6689
; LENGTH: 1023
; TYPE: PRF
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6689
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Query Match      27.4%; Score 419; DB 14; Length 1023;
Best Local Similarity 33.9%; Pred. No. 2.6e-34;
Matches 95; Conservative 61; Mismatches 110; Indels 14; Gaps 7;
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DB 798 CTVRADTFPPVDELRLNRLPISEKE---NNDLGE--TDPELTIWATRTRSSAAPT 851
QY 194 FRN-GRFLDGLLANNPTLDANTEIHEYNODLIRKQANKYKLSIVSLGTRSPQV 252
DB 852 FSASEKFTIDGMSISNPVLDMSDIGFYNTTCQKRIREKQVDMQCVLSVGTGIRP 911
QY 253 VTCVDVFRPSNPWELAKTVFGAKELGKMYVDCCTDPDGRP 292
DB 912 VD-PSVFEWMDLFGMLR---GKKNLSLVVIDQATATEGAP 947
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RESULT 8
US-10-369-493-6690
; Sequence 6690, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6690
; LENGTH: 1023
; TYPE: PRF
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6690
```

```

Query Match      27.4%; Score 419; DB 14; Length 1023;
Best Local Similarity 33.9%; Pred. No. 2.6e-34;
Matches 95; Conservative 61; Mismatches 110; Indels 14; Gaps 7;
```

```

RESULT 9
US-10-369-493-4998
; Sequence 4998, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4998
; LENGTH: 1023
; TYPE: PRF
; ORGANISM: Caenorhabditis elegans
US-10-369-493-4998
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FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 4998
 LENGTH: 468
 TYPE: PRF
 ORGANISM: Caenorhabditis elegans
 US-10-369-493-4998

Query Match 17.0%; Score 261; DB 14; Length 468;
 Best Local Similarity 29.8%; Pred. No. 3.5e-18;
 Matches 78; Conservative 54; Mismatches 100; Indels 30; Gaps 10;

16 ILGSMDEKRTDHD-LLCLDGGVKGGLIIQLLIAEKASGVATKDLFDWVAGTSGGL 74
 180 VLASEKKQWPEBEVILLADGGIRAVITQMLIHIDYLLGKLVKELDDIAGTSCGVI 239
 75 ALAI-LHKSMAVMRGVPRMKDVF-RGSR--PYESGLEEFLEKREF--GEHTKTTDV 127
 240 TLLSTNNRIETRTKLLDMRDVRVTRGDAKVPKYSNGMEYIAHVTTWEDSKKSS1 299
 128 RKPWMLTGLSDROPALHLFRNY--DABETVREP-RFQNVNLRPPAPSDQLVRAA 184
 300 KRRRAVTVADTMVPRQLLFRSYRPEMBEACEHYKF-----LDPTVYELMKTL 350
 185 RSSGAAPYFRPGRFLDGLANPTLDAMTEIHEYNODLIRKQANKVK-----K 236
 351 RCTTAPYFESFNGSLDGLINNPFLALISDFLTNK--LKSFKSSSERENGNWK 408
 237 LSTVSLGTGRSPQVPTCYDV 258
 409 IGCVISLGTGVPTFKIDGL 430

RESULT 10

US-10-425-115-196524
 Sequence 196524, Application US/10425115
 Publication No. US20040214272A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 FILE REFERENCE: 38-21(53222)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO 196524
 LENGTH: 1053
 TYPE: PRF
 ORGANISM: Zea mays
 NAME/KEY: unsure
 LOCATION: (1)..(1053)
 OTHER INFORMATION: unsure at all Xaa locations
 FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_110814C.1.pep
 US-10-425-115-196524

Query Match 16.0%; Score 245; DB 17; Length 1053;
 Best Local Similarity 25.7%; Pred. No. 5.5e-16;
 Matches 86; Conservative 46; Mismatches 98; Indels 104; Gaps 12;

1 LODLM-----HISRAKPAFIIIGSMDEKRTHD-----HLCLDGGVKGGL 42
 220 LRDLRLRLTISQRRVSAARALAILGENENLRRAIRGRPVAKKGIIRILSMGGKMGGLA 279
 43 IIOILLIAEKASGVATKDLFDWVAGTSGILALAI-LHKSMAVMRGVPRM----- 94

280 TVQMLKQIGQSGKRIHEMFIDICGTSSTGMLAMALGIQWTLDOCEBIYTKGLVPAR 339
 95 ---KDR-----VPRGSRPIYSSGLEELTKR-----EPGEHTKMTD 126
 340 PIPKDEAATWKEKIDQLFKSSSQSFVVVHSGK-HSADQFERLLKMKCADEDDLLIESA 398
 127 VRK-PRVMLTGLSDROPALHLFRNYDAPEYREPRFQNVNLRPPAPSDQL----- 179
 399 VKGIRVFAVSTLVSWMPAQPIFRNYQYPPGTLE-----VSGMAESPSISALGTA 450
 180 -----VWRARSSGAAPTYFR-----PNGRFLDGGILANPTLDAM 215
 451 VSGAPVIGIRGAFWMSCKIRWEALIASGAAPYLLDDFSDVADRWDGAIIVANNPTIPAI 510
 216 TEIHEYNODLIRKQANKVKLSIVSLGTGNSP 249
 511 RBAQLLMPD-----TRIDCLVSIQGSVP 534

RESULT 11

US-10-437-963-169583
 Sequence 169583, Application US/10437963
 Publication No. US20040123343A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbazuk, Brad
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 169583
 LENGTH: 1254
 TYPE: PRF
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_67990C.1.pep
 US-10-437-963-169583

Query Match 15.3%; Score 235; DB 16; Length 1254;
 Best Local Similarity 25.9%; Pred. No. 8.1e-15;
 Matches 89; Conservative 48; Mismatches 101; Indels 106; Gaps 15;

1 LODLM-----HISRAKPAF-IIGSMDEKRTHD-----HLCLDGGVKGGL 41
 487 LRDLRLRLTISQRRVSKAAARALAILGENENLRRAIRGRPVAKKGIIRILSMGGKMGGL 546
 42 IIOILLIAEKASGVATKDLFDWVAGTSGILALAI-LHKSMAVMRGVPRM----- 94
 547 ATVOILKQIBQGGKRIHEMFIDICGTSSTGMLAMALGIQWTLDOCEBIYTKGLVFA 606
 95 ---KDE-----VPRGSRPIYSSGLEELTKR-----EPGEHTKMTD 125
 607 EPAKDEAATWKEKIDQLFKSSSQSFVVVHSGK-HSADQFERLLKMKCADEDDLLIES 665
 126 DVAK-PRVMLTGLSDROPALHLFRNYDAPEYFR-----PRQNVN 168
 666 AVGIRKPVAVSTLVSWMPAQPIFRNYQYPPGTVSSVMTESPSISAGTIPVSGAPVG 725
 169 LRP-----PAQP-----SDQLVWRARSSGAAPTY-----FRPN-GRFLDGGI 205
 726 IKPINTVGAVSAGAPVIGIRGAFWMSCKIRWEALIASGAAPYLLDDFSDVADRWDGAI 785
 206 LANNPTLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGNSP 249

DB 786 VANNPTFAIREAQLMMP-----TRIDCLVIGCGSVP 819

RESULT 12

US-10-421-654-66

/ Sequence 66, Application US/10421654
/ Publication No. US20040005604A1

/ GENERAL INFORMATION:

/ APPLICANT: Gramatikova, Svetlana

/ APPLICANT: Hazlewood, Geoff

/ APPLICANT: Lam, David E.

/ APPLICANT: Barton, Nelson R.

/ TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND

/ FILE REFERENCE: 09010-094001

/ CURRENT APPLICATION NUMBER: US/10/421,654

/ PRIOR FILING DATE: 2003-04-21

/ PRIOR FILING DATE: 2002-04-19

/ NUMBER OF SEQ ID NOS: 106

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 66

/ LENGTH: 387

/ TYPE: PRT

/ ORGANISM: Unknown

/ FEATURE:

/ OTHER INFORMATION: Obtained from an environmental sample

US-10-421-654-66

Query Match 15.3%; Score 234; DB 15; Length 387;
Best Local Similarity 27.8%; Pred. No. 1,8e-15;

Matches 89; Conservative 39; Mismatches 112; Indels 80; Gaps 13;

QY 30 LCLDGGGVKGLIIQLLAIE-----KASGAVTKLDFVAVAGTSGGIALILHS 81

DB 17 ILACDGGGILGLSVILAKIEADLTETKLGKDONFLADYDFVCGTSTGAILAACISSG 76

QY 82 KSNVAVKGMVFRMKDEV-----GSRPYESGPLEEFLKREGEHTTKTDVRRKVM 134

DB 77 MSMAKTRQFLDGGKMFDAVSLKRLQVSYDDEPLARQLRAAFDQLKETDAKLSAHL 136

QY 135 TGLSLRQPAELHLFENY--DAETVRE--PRFN---QNVNLRPPAGSDQLVRRAR 185

DB 137 KTL-----MVMNHNSTDSPPVSNPYAKYNNIARDCNLNPF-----LWQLVR 182

QY 186 SSGAATPYRP-----NGRFLDGGLLA--NNPTLDAMTEIHEYNODLIRKQGA 231

DB 183 ASIAATYTPPEYITRADGTPREYNIPIVDGVTYNNPAYLAFLAATAKPYALNPTGS 242

QY 232 NKVKLSIVSLGTGRSPQV--PVTQVD-----VFRPSNPELAKTVFGA- 274

DB 243 NQL-----LIVSVGTGSAANVRPLDVDNMLIHFAKNIPALMNAASAGDMTCRVLGEC 298

QY 275 -----KELGKAVVDCCTD 287

DB 299 RHGMLDRSFGDMVMPASRD 318

RESULT 13

US-09-925-300-1483

/ Sequence 1483, Application US/09925300

/ Patent No. US20020151681A1

/ GENERAL INFORMATION:

/ APPLICANT: Craig Rozen,

/ APPLICANT: Steve Ruben

/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

/ FILE REFERENCE: PA101

/ CURRENT APPLICATION NUMBER: US/09/925,300

/ PRIOR FILING DATE: 2001-08-10

/ PRIOR APPLICATION NUMBER: PCT/US00/05988

/ PRIOR FILING DATE: 2000-03-08

/ PRIOR APPLICATION NUMBER: 60/124,270

/ PRIOR FILING DATE: 1999-03-12

/ NUMBER OF SEQ ID NOS: 1890
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1483
/ LENGTH: 370
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-925-300-1483

Query Match 13.8%; Score 211.5; DB 9; Length 370;
Best Local Similarity 28.5%; Pred. No. 3.9e-13;
Matches 72; Conservative 33; Mismatches 107; Indels 41; Gaps 8;

QY 16 ILGSMDEKRTDHLCLDGGGVKGLIIQLLAIEKASGAVTKLDFVAVAGTSGGIAL 75

DB 18 LIGYVDPVKGRIIRISIDGGGTRGVVALQTLRKVELTQKVHQLFDYICVSTGAILA 77

QY 76 LAI-LHSKSMAYKGMVFRMKDEVFR-----GSRPYESGPLEEFLKREGEHT 122

DB 78 FMGLFHPMLDECEELYRKLGSQVPSQNYIVGTVMKSMASHAFYDSQTWENILKDRKGSAL 137

QY 123 KMTDVK--PKVMTGLTSDRQ-PAELHLFENYDAPETVREPRFNQNVNLRPPAQPSDQ 178

DB 138 METANPTCPKVAANSTIVNIGITPKAFVFNNG-----HPPGINSY-----LGGCY 187

QY 179 LVWRAARSSGAAPTYRP---NGRFLDGGLLANNPTLDAMTEIHEYNODLIRKQANV 234

DB 188 KMWQAIRASSAAPGYAEYALGNDLHQDGLLNNPSALAMHECKCLMPDV----- 238

QY 235 KKLIVSVSLGTGR 247

DB 239 -PLECTIVSLGTGR 250

RESULT 14

US-10-421-654-100

/ Sequence 100, Application US/10421654

/ Publication No. US20040005604A1

/ GENERAL INFORMATION:

/ APPLICANT: Gramatikova, Svetlana

/ APPLICANT: Hazlewood, Geoff

/ APPLICANT: Lam, David E.

/ APPLICANT: Barton, Nelson R.

/ TITLE OF INVENTION: PHOSPHOLIPASES, NUCLEIC ACIDS ENCODING THEM AND

/ FILE REFERENCE: 09010-094001

/ CURRENT APPLICATION NUMBER: US/10/421,654

/ PRIOR FILING DATE: 2003-04-21

/ PRIOR APPLICATION NUMBER: US 60/374,313

/ PRIOR FILING DATE: 2002-04-19

/ NUMBER OF SEQ ID NOS: 106

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 100

/ LENGTH: 350

/ TYPE: PRT

/ ORGANISM: Unknown

/ FEATURE:

/ OTHER INFORMATION: Obtained from an environmental sample

US-10-421-654-100

Query Match 13.6%; Score 208.5; DB 15; Length 350;
Best Local Similarity 28.0%; Pred. No. 7.5e-13;
Matches 76; Conservative 29; Mismatches 65; Indels 101; Gaps 13;

QY 30 LCLDGGGVKGLIIQLLAIEK-ASGAVTKLDFVAVAGTSGGIAL--LAILHSKSMAY 86

DB 6 ILISIDGGGIRGIIIPAILVELAKRLEGDLHKAFLMIACTSGIAGLTCRHP----- 60

QY 87 MEGWVFRMKDE-----VFRSGRPYESGP-----LEEF 113

DB 61 -----DDEETAACTPTDLKLYVDHGKILFEKKPIGLINPGLANDPRYQPBLENR 112

QY 114 LKREGEHTKMTDVRKPKMLTGTSLDRQPAELHLFRNDAETVREPRFNQNVNLRPPA 173

Db 113 LKAQGL-LTATLBDKGLTKVLITA--YDIQOQALFMANTD-----NENSNFR--- 156
 QY 174 QPSDQLVWRARSSGAAPTYFRP-----NGRF---LGGGLANNPTLDAMTEIH 219
 Db 157 -----YMEARARATSAAPTYFRPPALIERVGEKNXDKRFVLIDGVFANDPILAAAYEAR 210
 QY 220 EX---NODLIRKGQANKVKLSIVSLGTGR 247
 Db 211 KQKRGDEL-----VFLSLGTGO 228

RESULT 15

US-10-310-154-616
 ; Sequence 616, Application US/10310154
 ; Publication No. US20030233670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; APPLICANT: Chomet, Paul S.
 ; APPLICANT: Adams, Thomas H
 ; APPLICANT: Ruff, Thomas G.
 ; APPLICANT: Agarwal, Ameeta K.
 ; APPLICANT: Ahrens, Jeffrey E.
 ; APPLICANT: Ball, James A.
 ; APPLICANT: Banu, G.
 ; APPLICANT: Bell, Erin
 ; APPLICANT: Boddupalli, Raghava
 ; APPLICANT: Deikman, Jill
 ; APPLICANT: Deng, Molian
 ; APPLICANT: Dong, Jinhao
 ; APPLICANT: Duff, Stephen M.
 ; APPLICANT: Galligan, Meghan M.
 ; APPLICANT: Hinchey, Brenda S.
 ; APPLICANT: Huang, Shihshien
 ; APPLICANT: Johnson, G. Richard
 ; APPLICANT: Jung, Vincent
 ; APPLICANT: Kretzmer, Keith A.
 ; APPLICANT: Laccetti, Lucille B.
 ; APPLICANT: Lai, Chao-Qiang
 ; APPLICANT: Lee, Gary
 ; APPLICANT: Lin, Jie-Yi
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Lu, Bin
 ; APPLICANT: Luethy, Michael M.
 ; APPLICANT: Lund, Adrian
 ; APPLICANT: Madson, Linda L.
 ; APPLICANT: Malloy, Kathleen A.
 ; APPLICANT: McKiel, Christine L.
 ; APPLICANT: Miller, Philip W.
 ; APPLICANT: Padmavathi, Manohikanti
 ; APPLICANT: Parnell, Laurence D.
 ; APPLICANT: Scart, William G.
 ; APPLICANT: Tennessee, Dan
 ; APPLICANT: Vidya, K.R.
 ; APPLICANT: Wang, Haiyun
 ; APPLICANT: Xin, Zhanqiao
 ; APPLICANT: Xu, Nanfei
 ; APPLICANT: Yang, Chunzhi
 ; APPLICANT: Zeng, Xiaoping
 ; APPLICANT: Zhang, Qiang
 ; APPLICANT: Zhao, Yajuan
 ; APPLICANT: Zhou, Li
 ; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
 ; FILE REFERENCE: 38-15(52796)B
 ; CURRENT APPLICATION NUMBER: US/10/310,154
 ; CURRENT FILING DATE: 2002-12-04
 ; PRIOR APPLICATION NUMBER: 60/337,358
 ; PRIOR FILING DATE: 2001-12-04
 ; NUMBER OF SEQ ID NOS: 736
 ; SEQ ID NO 616
 ; LENGTH: 577
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis
 ; US-10-310-154-616

Query Match 13.4%; Score 204.5; DB 14; Length 577;
 Best Local Similarity 26.7%; Pred. No. 4.1e-12;
 Matches 86; Conservative 47; Mismatches 98; Indels 91; Gaps 14;
 QY 19 SMDKRTYDH-----LLCLDGGGVKGLIITQLLALAEKASGVATKOLFVWAGTSTG 71
 Db 216 SDESQOTNNTNTPKPKKLALIDGGIRGILPAILITEIEKTRQKQIFSLFDLJAGSSSG 275
 QY 72 GILALAILSK-----SMAYRGMYFFMKDEVFRG-----S 102
 Db 276 GILALGTYKPRDLAGSDSPVVAQYSAEELQIYLEYGAEIFEYEPWEOILGOLBEDIFVQ 335
 QY 103 RPYESGPLEEFLKREGEHTKMTDVAKPKYMLTGITSDQPAELHIFRYVDAEYREPR 162
 Db 336 PKYSSGREGRIIKQYFDSPLNNLK--EVFVY-----SIDLEQ--RIP 376
 QY 163 FNQNVMLRPPAOPSDQLVWR-----AARSSGAAPTYFRP-----NGRF--L 201
 Db 377 FFTN---KLEKQOTKSKKPKKLCGLGFTLIDALATATPTYPAPRVSSSHNTNGFTLV 433
 QY 202 DGGLLANNPTLDAMTEIHEYNODLIRKGQANKVKLSIVSLGTGRSPQVPTCVDFRFP 261
 Db 434 DGGLVANNPAMALALILBAQISRQE---NQOALNMEDI-LVSLGTG-----SLTSVYPTDQ 484
 QY 262 SNPMELAKTVFGAKKELGRVVD 283
 Db 485 VKXWGLIQ---WTKPILNNVLD 503

Search completed: December 15, 2004, 13:34:54
 Job time : 53.2542 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:52:55 ; Search time 31.0226 seconds
(without alignments)
2130.736 Million cell updates/sec

Title: US-10-612-668-21
Perfect score: 3620
Sequence: 1 MOPFGRLVNTEFSVNTLFSN.....GAKELGKMYVDCTDPR 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------|--------------------|
| 1 | 3566.5 | 98.5 | 851 | T12503 | hypothetical prote |
| 2 | 647.5 | 17.9 | 1071 | T22327 | hypothetical prote |
| 3 | 634.5 | 17.5 | 1023 | T26261 | hypothetical prote |
| 4 | 332 | 9.2 | 3924 | S37431 | ankyrin 2, neuona |
| 5 | 324.5 | 9.0 | 468 | T33857 | hypothetical prote |
| 6 | 324.5 | 9.0 | 2039 | T15347 | ankyrin-related un |
| 7 | 320 | 8.8 | 1549 | T13940 | ankyrin - fruit fl |
| 8 | 296 | 8.2 | 4377 | A55575 | ankyrin 3, long sp |
| 9 | 294.5 | 8.1 | 1765 | T42714 | ankyrin 3, splice |
| 10 | 294.5 | 8.1 | 1940 | T42715 | ankyrin 3, splice |
| 11 | 294.5 | 8.1 | 1943 | T42713 | ankyrin 3, splice |
| 12 | 294.5 | 8.1 | 1961 | T42716 | ankyrin 3, splice |
| 13 | 294 | 8.1 | 1856 | B35049 | ankyrin 1, erythro |
| 14 | 294 | 8.1 | 1880 | A35049 | ankyrin 1, erythro |
| 15 | 294 | 8.1 | 1881 | SJHUK | ankyrin 1, erythro |
| 16 | 285 | 7.9 | 1848 | S37771 | ankyrin, erythrocy |
| 17 | 285 | 7.9 | 1862 | T49502 | ankyrin - mouse |
| 18 | 282.5 | 7.8 | 397 | T46445 | hypothetical prote |
| 19 | 278.5 | 7.7 | 1411 | S30355 | alpha-latroinsecto |
| 20 | 269.5 | 7.4 | 1265 | T10211 | hypothetical prote |
| 21 | 268 | 7.4 | 456 | T24442 | hypothetical prote |
| 22 | 264 | 7.3 | 1423 | T37275 | death-associated p |
| 23 | 250.5 | 6.9 | 1435 | T32930 | hypothetical prote |
| 24 | 249 | 6.9 | 791 | T42691 | hypothetical prote |
| 25 | 244 | 6.7 | 247 | D84448 | probable ankyrin l |
| 26 | 242.5 | 6.7 | 1401 | S11527 | alpha-latrotoxin p |
| 27 | 242 | 6.6 | 2437 | S42612 | transmembrane prot |
| 28 | 239.5 | 6.6 | 426 | A82149 | hypothetical prote |
| 29 | 235.5 | 6.5 | 355 | B82354 | patatin-related pr |

| | | | | | | |
|----|-------|-----|------|---|--------|--------------------|
| 30 | 234.5 | 6.5 | 633 | 2 | T27499 | hypothetical prote |
| 31 | 231 | 6.4 | 934 | 1 | H71274 | probable ankyrin - |
| 32 | 229.5 | 6.3 | 368 | 2 | T18184 | ankyrin repeat pro |
| 33 | 225 | 6.2 | 254 | 2 | A35844 | notch protein - Af |
| 34 | 221.5 | 6.1 | 907 | 2 | I50404 | p50B/p97 (Lyt-10) |
| 35 | 221.5 | 6.1 | 1062 | 2 | T14151 | inv protein - mous |
| 36 | 220.5 | 6.1 | 1062 | 2 | T30255 | inversin - mouse |
| 37 | 220 | 6.1 | 1184 | 2 | T00253 | gene Ankhzn protel |
| 38 | 219 | 6.0 | 2531 | 2 | A46019 | notch-1 protein - |
| 39 | 215 | 5.9 | 2531 | 2 | A40043 | notch protein homo |
| 40 | 214.5 | 5.9 | 2531 | 2 | S18188 | notch protein homo |
| 41 | 213.5 | 5.9 | 679 | 2 | G71615 | phospholipase A2-1 |
| 42 | 213.5 | 5.9 | 782 | 2 | JC7284 | phospholipase A2 (|
| 43 | 213.5 | 5.9 | 933 | 2 | S17233 | transcription fact |
| 44 | 208.5 | 5.8 | 606 | 2 | AC2508 | hypothetical prote |
| 45 | 207 | 5.7 | 2352 | 2 | T30201 | Notch homolog prot |

ALIGNMENTS

RESULT 1

T12503
hypothetical protein DKFZp434A102.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C/Accession: T12503

R/Ansoerge, W.; Whitner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z17527

A:Accession: T12503

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <AMS>

A/Cross-references: EMBL:AL080187

A/Experimental source: adult testis; clone DKFZp434A102

C/Genetics:

A>Note: DKFZp434A102.1

Query Match 98.5%; Score 3566.5; DB 2; Length 851;
Best Local Similarity 92.3%; Pred. No. 1.5e-273;
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;

| | | | |
|----|-----|---|-----|
| Qy | 1 | MOPFGRLVNTEFSVNTLFSNPRFVKEVAVADYSSDRVREEGQLIFONTPNTMDCVLV | 60 |
| Db | 46 | MOPFGRLVNTEFSVNTLFSNPRFVKEVAVADYSSDRVREEGQLIFONTPNTMDCVLV | 105 |
| Qy | 61 | NPNRSQGFRLPOLLEADALVNPHOYSSQLPFYESSPQVLTTEVLQHLTDLIRNPSW | 120 |
| Db | 106 | NPNRSQGFRLPOLLEADALVNPHOYSSQLPFYESSPQVLTTEVLQHLTDLIRNPSW | 165 |
| Qy | 121 | SVHLAVELGIRBCFHSRIISCANCAENEGCTPLHLACKDGEIIVELYOYCHTOMD | 180 |
| Db | 166 | SVHLAVELGIRBCFHSRIISCANCAENEGCTPLHLACKDGEIIVELYOYCHTOMD | 225 |
| Qy | 181 | VTPYKGETVHYAVQGDNSQVLLGLGRNAVAGNONNGSLPLHLACOLGKEMRVLL | 240 |
| Db | 226 | VTPYKGETVHYAVQGDNSQVLLGLGRNAVAGNONNGSLPLHLACOLGKEMRVLL | 285 |
| Qy | 241 | LCNARCINMGPNVPIHSANKFSQKCAEWIISMSQSIIHSDPKRYGASPLHAKNAEMA | 300 |
| Db | 286 | LCNARCINMGPNVPIHSANKFSQKCAEWIISMSQSIIHSDPKRYGASPLHAKNAEMA | 345 |
| Qy | 301 | RMILKRCNVNSTSSAGNTALHVGVMRNPDCAILVLTGANDARGHGNTPLHLAMSK | 360 |
| Db | 346 | RMILKRCNVNSTSSAGNTALHVGVMRNPDCAILVLTGANDARGHGNTPLHLAMSK | 405 |
| Qy | 361 | DNVEMLKALVFGAEVDTPNDPGETPLFLASKIGK----- | 395 |
| Db | 406 | DNVEMLKALVFGAEVDTPNDPGETPLFLASKIGRLVTRKAILTLRTVGAEVCPPIHG | 465 |
| Qy | 396 | -----LQDLMIHSPARKDAFLGSRNDEKRTDHL | 425 |

Db 466 VPAQGSAAHPHPSLERAQPPISLNNLEIOLMIHSRARKPAFLIGSNRDEKRTDHL 525
 Qy 426 LCGDGGVKGKLIITQLIAIEKASGVATKDLFPMVAGTSTGGILALAILHKSMAVYRM 485
 Db 526 LCGDGGVKGKLIITQLIAIEKASGVATKDLFPMVAGTSTGGILALAILHKSMAVYRM 585
 Qy 486 YFRMKDEVFRSGSPYSEGLPEFLKREFGHTKMTDVRKPKVMTGTLSDROPALHLFR 545
 Db 586 YFRMKDEVFRSGSPYSEGLPEFLKREFGHTKMTDVRKPKVMTGTLSDROPALHLFR 645
 Qy 546 NYAPAEVFRPRPNQNNLAPPAOPSPQIYWRAPARSSGAAPTYFRPRGRFLDGLANP 605
 Db 646 NYAPAEVFRPRPNQNNLAPPAOPSPQIYWRAPARSSGAAPTYFRPRGRFLDGLANP 705
 Qy 606 TLDAITEHEYNODLIRKGOANKVKLSIVSLGTGSPQVPTCVDFPRSPNWEIAKT 665
 Db 706 TLDAITEHEYNODLIRKGOANKVKLSIVSLGTGSPQVPTCVDFPRSPNWEIAKT 765
 Qy 666 VFQAKELGKVVDCCTDPDGR 686
 Db 766 VFQAKELGKVVDCCTDPDGR 786

RESULT 2

T22327

hypothetical protein F47A4.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T22327

R/Mortimore, B.

submitted to the EMBL Data Library, June 1995

A/Reference number: Z19549

A/Accession: T22327

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1071 <M1>

A/Cross-references: UNIPROT:Q20500; EMBL:Z49888; PIDs:CAA90061.1; GSPDB:GN00028; CESP:F4

A/Experimental source: clone F47A4

C/Genetics:

A/Map position: X

A/Intons: 27/1, 59/2, 134/1, 199/2, 402/2, 460/3, 591/3, 634/3, 665/2, 1018/3

Query Match 17.9%; Score 647.5; DB 2; Length 1071;
 Best Local Similarity 27.0%; Pred. No. 1.5e-42;

Matches 194; Conservative 126; Mismatches 260; Indels 139; Gaps 20;

Qy 69 FRLEFLELDALVNFHQYSSQLPFYESSPOVLHTEVL---OHLTDLIRNHPMSVAH 124
 Db 315 FSLFRATDKDMDLHLCDKESFLFTSLDMSTMRADILRSKIEELVQIRLKPXYIMIH 374
 Qy 125 LAVELGIRECFHHSRI-----ISCANCAENEGCTPLHLACKGDEILVELVOY 174
 Db 375 VALATRLDLFFSOGMITKMTMETLEPPFSQRLCHITENCYPVHALTMDROKIVERLLEL 434
 Qy 175 CHTOMDVTYKGEVFHYAVQGDSQVTLQIGRNAVAG---LNVQNNQGLTPLHLACOLG 231
 Db 435 DPLFLCETDAGANNVWHV---NSSFCAQIIMDRCPASQHFIDERNNDGSPLENAVSTA 491
 Qy 232 KQEMNRYLLCNARCNIMGNGYPIHSAMKFSQKCAEMTISM-----DSS 277
 Db 492 KPLVATFPL-----IGKAKFTDRDRNELFVAMTSKNAQSVVEVAVLTDKP 535
 Qy 278 QIHSKDPYRGASPLHMAKNAMAMLLK---GCNNVSTSSAGNTALHYGVNRNRDCA 333
 Db 536 EIANERDALNSAIVHLYESLNALNRRKVEGLDIDVKNAGETLILPITTRKPDLL 595
 Qy 334 IYLLT---HGANDARGEHNTPLHLAMS-----KDVNEMI KALIVGAEVDTPNDGET 385
 Db 596 PLAVTLVYAHGANNATDPHNTALHKSAAVLDAKKISLSECVKPLISAGSNPNKINLARGS 655
 Qy 386 PTLVASTKGLQDLMIHSRA---RKPAFLIG-----SMRDE----- 418

Db 656 PRHLAASL-ONQEMALILKAAATRCPKYKGRSNCRRHDCSSADEYEETLOKIRIGNE 714
 Qy 419 -----KRTDHLICDGGVKGKLIITQLIAIEKASGVA 452
 Db 715 SDYEKTEFTASEKNTQDPLDGRSRGKAKVNNISMDGGIRLVIITQLIAIEEELGDD 774
 Qy 453 TKDLFPMVAGTSTGGILALAILHKSMAVYRMGYFRMKDEVFRG-SRPSGPLEEFLK 511
 Db 775 IFKYPFMSAGTSTGSLIMAGLAKSLREMOQYTLILKRVDFGIMPPYDVQLKRFID 834
 Qy 512 EFGHNTKMTDVRKPKVMTGTLSDROPALHLFRNDADETVFRPRPNQNNLAPPAOS 571
 Db 835 QFGTGI-VWEIPIYRMLIAVNSEKLPVLEMKRANKPANDV-----ABETPK 881
 Qy 572 DQVWRAASSGAAPTYFRPN-GRFLDGLANPPTLDAMTEIHEYNODLIRKGOANKVK 630
 Db 882 EMPLMALKRSTAPLFRFSEDRYIDGILSNPPLDMSVHAHNRLEQLSGRSNAV 941
 Qy 631 KLSIVSLGTGSPQVPTCVDFR--PSNWEIAKTVFQAKELGKVVDCCTDPDGRP 687
 Db 942 QMNVLSFGTG--QIPSTVIEITLSIDNSPLQSIKTI---KLLAMFIDQATASEGAP 994

RESULT 3

T26261

hypothetical protein W07A8.2 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T26261; T26892

R/Basham, V.

submitted to the EMBL Data Library, November 1996

A/Reference number: Z20184

A/Accession: T26261

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1023 <M1>

A/Cross-references: UNIPROT:O62338; EMBL:Z82075; PIDs:CAE04932.1; GSPDB:GN00023; CESP:W0

A/Experimental source: clone W07A8

R/Ainscough, R.

submitted to the EMBL Data Library, January 1998

A/Reference number: Z20281

A/Accession: T26892

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1023 <M1>

A/Cross-references: EMBL:AL021489; PIDs:CAA16371.1; GSPDB:GN00023; CESP:W07A8.2

A/Experimental source: clone Y44A6C

C/Genetics:

A/Map position: 5

A/Intons: 32/1, 83/2, 155/3, 202/2, 240/3, 264/1, 331/2, 411/1, 479/3, 534/3, 571/2, 706

Query Match 17.5%; Score 634.5; DB 2; Length 1023;
 Best Local Similarity 24.2%; Pred. No. 1.5e-41;

Matches 187; Conservative 148; Mismatches 287; Indels 151; Gaps 21;

Qy 37 RVEEGQLILFQNTPRTDVCVLNPRNSQSGRLFQLELEAD--ALVNFHQYSSQLPFG 94
 Db 204 RAKEEBEL---KKPLYLHALITLYNENKXYVNSLFRSHKLDVVALCERCRENPELFVY 260
 Qy 95 YESSPOV---LHTEVLQHLTDLIRNHPMSVAHLAVELGIRECFHH---SRISCANCAE 148
 Db 261 FRGNVNIKQVLT---IFHELRDMNTWSVHISKIGLIEFFENMKSHKLYLNTLV 315
 Qy 149 NEEGCTPLHLACKGDEILVELVOYCHTOMDVTYKGEVFHYAVQGDSQVTLQDL--G 206
 Db 316 QPGLSPPLMIAVQNTQIEVSWMLDH-GADINILSSEGVVHVAATAASGDILKILMET 374
 Qy 207 RNIVAGLQVNNQGLTPLHLACQLQKQEMNRYLLCNARCNIMGPNG-----Y 254
 Db 375 KKEETMINQDSNGYTPAYVA-----LINALSNQTLRGCGGIGSSDSTOMAN 424
 Qy 255 PIHSAMKFSQ--KCAEMTISMDSQIHSKDPYRGASPLHMAKNAMAMLLK---GCN 309


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Db 425 PIGAMKRGGLDVSRLKMLEKQDGLTERPTTGTVHICANKKGLILMEKFRQDT 484
Qy 310 VNSTSSAGNTALHVGVRNRPDCAIVLLTHGANADARGHGTPLHLAMSKDNVEMIKAL 369
Db 485 PEARNAIQOPLHTFVTKDELGLVMTLSAYGVMDADQINDINGTPLHCAVTRGTEIRML 544
Qy 370 IYGAEDVTNDGERTFPLASKIGKQDLMHSRAE-----KRAFI----- 411
Db 545 LCGAEPDINRKRKESPRHIAARLTERKAMQDILRALIICGAGACDDGFIGACFGCMHKT 604
Qy 412 -----LGSN----- 421
Db 605 GLTSCKTQGLSSSDDEQSMEDRVKDHSVSNAAAPYEPVLDPDTOLVEBAVNERETRA 664
Qy 422 HDH----- 456
Db 665 FPHBEALKRVKMLKELVEKKTSNVINVLGLDGGGIRGLVTVQMLCLRAFLDRPLIDY 724
Qy 457 FDMVAGTGTGGLALALILHKSMAVYMGVFRMKDEVFRG-SRPRYSGPLEEFLKREGE 515
Db 725 FDMVAGTGTGGLALALILHKSMAVYMGVFRMKDEVFRG-SRPRYSGPLEEFLKREGE 515
Qy 516 HTGQTVRKPKVMTGLSDROPALHLPYNDAPETVREPRFQNVNLRPPAQPSDOLV 575
Db 785 DRLMGDIKYRFECTYTRADTFPVQLELNNYRLPISEKE---NNDLGF---TDPNELTI 838
Qy 576 WRARSSGAAPYFRPN-GRFLDGLIANNPTLDAMTEIHEYNODLIRKQANKVKKLSI 634
Db 839 WKATRRSSAAPTFFSASEGKFDGCMISNPVLDLMSDIFGYWTCQKMRIPKRMVDMGC 898
Qy 635 VVSLGCRSPQVPTCDVFRSPNPWELAKTVGAKELGCMVNDCCDPPGRP 687
Db 899 VLSVGTITPTCPVD-PSVEBMNDLFQMLR---GMKRLSLVLDQATVATGAP 947

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RESULT 4

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S37431
Ankyrin 2, neuronal long splice form - human
N/Alternate names: ankyrin B, 440K splice form; ankyrin-B, brain ankyrin; non-erythroid
N/Contains: ankyrin 2, short form
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
C/Accession: S37431; A39643; B39643; A40334; A49462; S14553; S14569
R/Chan, W.
Submitted to the EMBL Data Library, September 1993
A/Reference number: S37431
A/Accession: S37431
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-3924 <CHA>
A/Cross-references: UNIPROT:Q01484; EMBL:Z26634; NID:G406287; PIDN:CAA81387.1; PID:G4062
R/Octo, E.; Kunitz, M.; McLaughlin, T.; Bennett, V.
J. Cell Biol. 114, 241-253, 1991
A/Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a
A/Reference number: A39643; MUID:91302466; PMID:1830053
A/Accession: A39643
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1443, 3585-3924 <OTT>
A/Cross-references: EMBL:X56958
R/Tee, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,
Genomics 10, 858-866, 1991
A/Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
A/Reference number: A40334; MUID:92009921; PMID:1833308
A/Accession: A40334
A/Molecule type: DNA
A/Residues: 463-474, 'PB', 477-495 <TSE>

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A/Cross-references: GB:M37123; NID:G178647; PIDN:AA62828.1; PID:G178648
R/Chan, W.; Kordeli, E.; Bennett, V.
J. Cell Biol. 123, 1463-1473, 1993
A/Title: 440-KD ankyrinB: structure of the major developmentally regulated domain and se
A/Reference number: A49462; MUID:94075409; PMID:8253844
A/Accession: A49462
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-3924 <RES>
A/Cross-references: EMBL:Z26634; NID:G406287; PIDN:CAA81387.1; PID:G406288
C/Genetics:
A/Gene: GDB:ANK2
A/Cross-references: GDB:127607; OMIM:106410
A/Map position: 4q25-4q27
C/Superfamily: ankyrin; ankyrin repeat homology
C/Keywords: alternative splicing
F/2-3924/Product: ankyrin 2, long form #status predicted <MAT>
F/2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>
F/63-95/Domain: ankyrin repeat homology <AN01>
F/96-128/Domain: ankyrin repeat homology <AN02>
F/129-161/Domain: ankyrin repeat homology <AN03>
F/162-190/Domain: ankyrin repeat homology <AN04>
F/191-223/Domain: ankyrin repeat homology <AN05>
F/232-264/Domain: ankyrin repeat homology <AN06>
F/265-297/Domain: ankyrin repeat homology <AN07>
F/298-330/Domain: ankyrin repeat homology <AN08>
F/331-363/Domain: ankyrin repeat homology <AN09>
F/364-396/Domain: ankyrin repeat homology <AN10>
F/397-429/Domain: ankyrin repeat homology <AN11>
F/430-462/Domain: ankyrin repeat homology <AN12>
F/463-495/Domain: ankyrin repeat homology <AN13>
F/496-528/Domain: ankyrin repeat homology <AN14>
F/529-561/Domain: ankyrin repeat homology <AN15>
F/562-594/Domain: ankyrin repeat homology <AN16>
F/595-627/Domain: ankyrin repeat homology <AN17>
F/628-660/Domain: ankyrin repeat homology <AN18>
F/661-693/Domain: ankyrin repeat homology <AN19>
F/694-726/Domain: ankyrin repeat homology <AN20>
F/727-759/Domain: ankyrin repeat homology <AN21>
F/760-792/Domain: ankyrin repeat homology <AN22>
F/793-825/Domain: ankyrin repeat homology <AN23>
Query Match 9.2%; Score 332; DB 2; Length 3924;
Best Local Similarity 27.3%; Pred. No. 9.7e-17;
Matches 100; Conservative 62; Mismatches 127; Indels 77; Gaps 9;
Qy 103 HTEVLQHTD-----LIRNHPWSVNLAVELGIRECFNH-----SRIL 141
Db 311 HDQVELLERGAPPLAFTNGSLPLHMAAQGDHVCVGHLLQHKAPVDDVLTLYLTALH 370
Qy 142 SCANC-----ANEBCGTPHLAKRGDDELIVLYOY----- 174
Db 371 VAAHCGHYRVTLLDKRANPNBALNGTTPHLIAKKRIKMWELLYRGASIOATTS 430
Qy 175 -----CH-----TQMDYDYGVTFVYAVAGDSOVLQLIGRAVAG 212
Db 431 GLTPHYAAMPGLINLVLLNLONGASPDVTNRIGETALLMAARAQGVYVRCILRRIG-AL 489
Qy 213 LNOVNOGLTPHLIACQLQKQEMVRVLLCNACNIMGNGY-PIHSANKFSQGAEMT 271
Db 490 VDARABEOTPLHIASTRIGTEIVQLLOHMAHPDAATNGYPLHISAREGQDVASVYL 549
Qy 272 ISMDSQHSKDPYRGASPLHMAK---NEMAMMLKRGCVNSTSAGNTALHVGVMN 328
Db 550 --LEAGAAHSLATKKFTPLHVAKYSDVAQLLQRRAAADSAGKNGLTPLHVAHYD 607
Qy 329 RPDCAIVLLTHGANADARGHGTPLHLAMSKDNVEMIKALIVFGAEDVTPNDFGSETPTF 388
Db 608 NQVVALLEKSGASPHATKNGTTPHLIAKKQWQIASTLANYGAETNIIVTKQVTPHLH 667
Qy 389 LASKIG 394
Db 668 LNSQEG 673

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RESULT 5

hypothetical protein D1037.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999C/Accession: T33857
Riedelwith, J.; Biewald, T.
submitted to the EMBL Data Library, November 1998A/Description: The sequence of C. elegans cosmid D1037.
A/Reference number: Z21424A/Accession: T33857
A/Status: preliminary; translated from GB/EMBL/DBJA/Molecule type: DNA
A/Residues: 1-468 <LED>A/Cross-references: EMBL:AA106592; PIDN:AACT8490.1; GSPDB:GN00019; CESP:D1037.5
A/Experimental source: strain Bristol N2; clone D1037C/Genetic(s):
A/Map position: 1

A/Introns: 66/3; 89/3; 113/3; 151/2; 247/1; 354/2

Query Match 9.0%; Score 324.5; DB 2; Length 468;
Best Local Similarity 27.0%; Pred. No. 1.4e-17;
Matches 110; Conservative 74; Mismatches 164; Indels 59; Gaps 16;286 YGASPLHMAKMAEMRLKRGCVNNTSGAGTALHVGWRN---RFPCAIVLLTHG 340
44 YDLSVITWLN---LRFILIRYCR-----SEVNCNHELEMANARAGNTDLKLYIH 94341 ANADAGEHENTPLHAMSNDVEMIKALIVGAEVD---TPNDFGETPFLASKIGLQ 397
95 IDLRMTDETGTAMHVAVMNQKIVMLVLCAPCQIKWIKNNNGTSTELCTDKKISE 154398 DLMHISRAKRP---AF-----ILGSRDEKRTIHD-LTCLDGGGVKGLIITQLLA 444
155 DFPSLNPSPSPGAFVDVSEYNNVLASEKQWKPEERVLALDGGGIRAVITIQMLH 214445 IEKASGVAATKDLFDWVAGTSGILALAI-LHSCNAYMGMYFRMKDEVF-RGSR---P 499
215 IDVLGKLVKEDDLAGTSCGGVITLLSTNNRIETKLLIDMRDRFIFGADKAVP 274500 YESGPLEEPKREF--GEHTKMTDVKRPKMYLTGSLSDROPALHLFRNY--DAPETVRE 555
275 KYSSNGMEVYARAVTTWEDSKMSIKHRAIVTVADTRWVPPLQLFRSYRPEWBEACE 334556 P-RPNQNVNLRPPAQSDQLVMPAARSSGAAPTFPRNGRFLDGLIANNPTIDAMTEIH 614
335 HYKF-----LDPTKVELMKTLCRTTAAAPFFESFNGLSGGGLIANNPTLALISDFP 365615 EYNODLIRKQANKVK-----KLSIVSLGTGRSPQVPTCVDP 653
386 LTMK--LEKSFASKSSSERENRGNMKICVISLGTGVPTFKIGIDIL 430

RESULT 6

ankyrin-related unc-44 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004C/Accession: T15347; T15346; T15344; T15345; A57282; B57282; C57282
Riedelwith, S.
submitted to the EMBL Data Library, February 1996A/Description: The sequence of C. elegans cosmid B0350.
A/Reference number: Z18332A/Accession: T15347
A/Status: preliminary; translated from GB/EMBL/DBJA/Molecule type: DNA
A/Residues: 1-2039 <GAT>A/Cross-references: UNIPROT:Q17489; EMBL:U50071; NID:g1208871; PID:g1208873; PIDN:AAA934
A/Accession: T15346
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-1000, 'SKLQHRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVAI
32, 'S', 2034-2035, 'GSPTRSVPEERHRSCHDEHSGT' <GA2>

A/Cross-references: EMBL:U50071; NID:g1208871; PID:g1208875; PIDN:AAA93445.1

A/Accession: T15344
A/Status: preliminary; translated from GB/EMBL/DBJA/Molecule type: DNA
A/Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSPS', 1916-1917, 'ORSTVASTSEQVE', 1934-1935, 'EK
<GA3>

A/Cross-references: EMBL:U50071; NID:g1208871; PID:g1208874; PIDN:AAA93444.1

A/Accession: T15345
A/Status: preliminary; translated from GB/EMBL/DBJA/Molecule type: DNA
A/Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSPAQRS', 1950, 'IVABS', 1956-1957, 'EQVE'
PTRSVPEERHRSCHDEHSGT' <GA4>A/Cross-references: EMBL:U50071; NID:g1208871; PID:g1208876; PIDN:AAA93446.1
R.Oenka, A.J., Franco, R., Yang, B., Shih, K.H., Tang, L.Z., Zhang, Y.Y., Boontarakulpoor
U. Cell Biol. 129, 1081-1092, 1995A/Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in Caer
A/Reference number: A57282; NID:95263663; PMID:7744957A/Accession: A57282
A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1852, 'GGC', 856-1000, 'SKLQHRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEEL
'SHRED', 2007-2008, 'TI', 2011, 2017, 'TI', 2020-2022, 'SHIS', <OTS>

A/Cross-references: GB:U21734; NID:g790607; PIDN:AAA5854.1; PID:g790608

A/Accession: B57282
A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E'
V', 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPTRSVPEERHRS', 1984-1985, 'EDHGS', 1
A/Cross-references: GB:U21731A/Accession: C57282
A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 194, 'F', 196, 'I', 198, 'DC', 201, 'G', 409, 'AV', 412, 'Q', 414, 824, 'S', 826, 'ER', 829, 'E'
4, 'TIV', 1828, 'ESTS', 1833, 'QV', 1836, 'E', 1934-1935, 'EQS', 1939, 'SEES', 1944, 'REDDGITVTT', 194;
A/Cross-references: GB:U21732; NID:g790603; PIDN:AAA5853.1; PID:g790604C/Genetic(s):
A/Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1879/C/Superfamily: ankyrin; ankyrin repeat homology
F/164-192/Domain: ankyrin repeat homology <AN04>
F/358-390/Domain: ankyrin repeat homology <AN1>
F/391-423/Domain: ankyrin repeat homology <AN11>Query Match 9.0%; Score 324.5; DB 2; Length 2039;
Best Local Similarity 24.1%; Pred. No. 1.4e-16;
Matches 129; Conservative 77; Mismatches 207; Indels 123; Gaps 16;147 AENEGCTPLHACRKGDEILVELVQYCHTQWDVTDYGEVTFHYAVQGDNSQVLLQ 206
420 ATTESGLTPLHVAFAFGALINIVYLLQ-GANPDVETVGEFPLHAAANQDVRVLI 478207 RNAVAGLNQVNNQGLTPHILACOLGQEMVRVLLCNACNIMGRNGY-PHISAMKFSQK 265
479 RRG-ARVDAQARLQTPHILASRLGNTDIVILLQAGANSNATTRNYSPLHAAEGGE 537266 GCAEMIISDSSQIHSKD---PRYGASPLHMAK---NAEMARMLDKRCNVNSTSSAGN 318
538 EVAGIILD-----KNADTLTLTKGFTPLHILASKNGNEVRLLEKRTPTVDIEGKNV 591319 TALHVGWENRDFCAIVLLTHGANADARGEHNTPLHAMSNDVEMIKALIVFGAEVDT 378
592 TPLHVAAHNNNDKVAIVLLLENGASAKAANKGTPLPHIAAKQWHEIASTLLQFKADPVA 651379 PNDGFTPLPLASKIGKLDLMLHISRAKRPAPILSGMRDEKTHHLCLDGGGVKGLI 438
652 KSRAGFTPLHLSQEGHKE-----ISGLL- 675439 IQLLILIEKASGVAATKDLFDWVAGTSGILALAILHSCNAYMGMYFRMKDEVFRGSR 498
676 -----LENGSDVGAK-----ANNGLTAMHLC-----AQEDHV----- 702

QY 499 PYESGPLEBEFLKREBGEHTWTIDVRKPKMLTGTLSRQPAEHLFRNYDAPETVREPRF 558
 DB 703 -----PVAQILYNNKNGEINKNTAGTTPPLVACHFGGLNANKPLVENGADVGKTR- 754
 QY 559 NONVNLPRPAQPSDQVLRRAARSSGAFTYFRPNRGLDGLLANNPTLDAMTEIHEYNQ 618
 DB 755 -SYTPLHQAQOQHNNCVRYLLENGASP-----NEGATGQTP- 792
 QY 619 DLIRKQANVKKLSTIVSLGTRSPV--PVTCDV-FRPSNPMLAKVFGAKE 671
 DB 793 -----SIAQLGYVSVVETLRTVETTVITETTVDERKRPORPEANETMFSSE 843
 RESULT 7
 T13940
 ankyrin - fruit fly (Drosophila melanogaster)
 C/Species: Drosophila melanogaster
 C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C/Accession: T13940
 R/Dubreuil, R.R.; Yu, J.
 Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994
 A/Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in Drosophila
 A/Reference number: Z17820; MUID:95024098; PMID:7937942
 A/Accession: T13940
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-1549 <DUB>
 A/Cross-references: UNIPROT:Q24241; EMBL:L35601; NID:9557083; PID:9557084; PIDN:AA037208
 C/Genetics:
 A/Cross-references: FlyBase:FBgn0011747

Query Match 8.8%; Score 320; DB 2; Length 1549;
 Best Local Similarity 22.7%; Pred. No. 2, 1e-16;
 Matches 141; Conservative 79; Mismatches 179; Indels 222; Gaps 23;
 QY 45 ILFQNTNRTWDCVLVNPNSQSGFRLEADLVNPHQSSQL-----PFYESSP 99
 DB 319 LLOQNP-----ILTKTKGLSALM-----AAGCHDEAHLNLDKAPVDEVTY 364
 QY 100 QVL-----HTEVLQHLTDLIRNHP-----NSVAHLA-----VELGIRECFH 136
 DB 365 DYTALVAAHCGHVAKLLDYKANPARNALNGFTPLHIACKKRIKMWELLIK---H 421
 QY 137 HSNILISGANCABEBCGTPHLACRKGDSILVELVOYCHTQMDVDTYKSETVPHVAVOG 136
 DB 422 GANI-----GATTESGLTPLHVASFWGCINIVLYLQH-BASADLPTRIGETPLHLARA 475
 QY 197 DNGQVQLQLGRNAV----- 210
 DB 476 NQADIRILRSKAVDAIVEGQTPHVASRLGNINIMLLQHGAINAQSDKYSALH 535
 QY 211 -----AGLNVNNGELTPLHACQLGQKQEMVRVILLNCARNINGPN 252
 DB 536 IAAKEGENTIVQYLENGAENNAVTKKGTPLHLCYKQNVYQILLQNGASIDFGKN 595
 QY 253 GY-PIISAMFSGQKCAEMTISDSS-----QT--HKD- 283
 DB 596 DVTPLHVAATYNNPSTIVELLKNGSSPNLCARNGQCAIHIACKKQVLEIMQQLQHDADV 655
 QY 284 ---PRYGASPLHMAK---NAEMARMLKRGCVNSTSAGNTALHVGEMRPFDCALVLL 337
 DB 656 NIISKSGFSLHLLAOGGANVDMQVLLLEYGV-ISAANKGLTPLHVAAGSHVAVSILL 714
 QY 338 THGANDARGEHNTPLHLMASKONVEMIKALIVFGAEVDTPNDFGETPTPLASKIGKIQ 397
 DB 715 EHGANISERTNGTTPHMAAHYGHLDLVKFIENDADIEMSNIGYTPHQAQOQ--- 771
 QY 398 DLWHISARPRAPFLSGMRDEKRTHDMLCLDGGVGVGLIIQILLIAEKASGATKDLF 457
 DB 772 ---HI-----MILNLHKKANPNALTD- 792
 QY 458 DWVAGTSGCILAALILHKSMAV---MRGVYFRMKDEVFRGSRPYESGPLEBEFLKREFG 514

DB 793 -----GNVALHI--ASNLCGYVTWMSLKIVTSTVNSN-----IGAIBEKLK- 833
 QY 515 EHTKMTDVRKPKMLTGTLSLD 535
 DB 834 -----VMTPELMQETLLSD 847

RESULT 8
 A55575
 ankyrin 3, long splice form - human
 N/Alternate names: ankyrin G
 C/Species: Homo sapiens (man)
 C/Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
 C/Accession: A55575
 R/Kordeli, E.; Lambert, S.; Bennett, V.
 J. Biol. Chem. 270, 2352-2359, 1995
 A/Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the axon
 A/Reference number: A55575; MUID:95138209; PMID:7836469
 A/Accession: A55575
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-4377 <KOR>
 A/Cross-references: UNIPROT:Q12955; GB:U13616; NID:9608024; PIDN:AAA64834.1; PID:9608025
 C/Genetics:
 A/Genes: GDB:ANK3
 A/Cross-references: GDB:424503; OMIM:600465
 A/Map position: 10q21-10q21
 C/Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
 C/Keywords: alternative splicing; peripheral membrane protein
 F/106-138/Domain: ankyrin repeat homology <AN01>
 F/139-171/Domain: ankyrin repeat homology <AN02>
 F/172-200/Domain: ankyrin repeat homology <AN03>
 F/201-233/Domain: ankyrin repeat homology <AN04>
 F/234-266/Domain: ankyrin repeat homology <AN05>
 F/267-299/Domain: ankyrin repeat homology <AN06>
 F/300-332/Domain: ankyrin repeat homology <AN07>
 F/333-365/Domain: ankyrin repeat homology <AN08>
 F/366-398/Domain: ankyrin repeat homology <AN09>
 F/399-431/Domain: ankyrin repeat homology <AN10>
 F/432-464/Domain: ankyrin repeat homology <AN11>
 F/465-497/Domain: ankyrin repeat homology <AN12>
 F/498-530/Domain: ankyrin repeat homology <AN13>
 F/531-563/Domain: ankyrin repeat homology <AN14>
 F/564-596/Domain: ankyrin repeat homology <AN15>
 F/597-629/Domain: ankyrin repeat homology <AN16>
 F/630-662/Domain: ankyrin repeat homology <AN17>
 F/663-695/Domain: ankyrin repeat homology <AN18>
 F/696-728/Domain: ankyrin repeat homology <AN19>
 F/729-761/Domain: ankyrin repeat homology <AN20>
 F/762-794/Domain: ankyrin repeat homology <AN21>
 F/795-827/Domain: ankyrin repeat homology <AN22>
 F/828-860/Domain: ankyrin repeat homology <AN23>
 Query Match 8.2%; Score 296; DB 2; Length 4377;
 Best Local Similarity 29.2%; Pred. No. 8, 1e-14;
 Matches 81; Conservative 54; Mismatches 130; Indels 12; Gaps 6;
 QY 124 HLAVELGIRECFHRSIRISGANCABEBCGTPHLACRKGDSILVELVOYCHTQMDVTD 183
 DB 504 HISARLGKADIVQQLAQGASPAATTSQYTPHLHARSHEHDVAFLDHL--GASISIT 562
 QY 184 YKSEYTPHVAVQDNGQVQLQLGRNAVAGLQVNNNGELTPLHACQLGQKQEMVRVILLCN 243
 DB 563 KKEFTPLHVAAKYKGLVAVNLLQKS-ASPDAGKSGTLPHVAHAHYDNQKVALLLDQ 621
 QY 244 ARGNINGPNY-PIISAMFSGQKCAEMTISDSSQIHSKDPYRGASPLHMAK---NA 297
 DB 622 ASPHAAAKQYTPHLHIAAKKQMDINTTILEYADANAV-----TRGSIASVHLAAQEGHY 677
 QY 298 EMARMLKRGCVNSTSAGNTALHVGEMRPFDCALVLLTHGANDARGEHNTPLHLA 357
 DB 678 DWVAGTSGCILAALILHKSMAV---MRGVYFRMKDEVFRGSRPYESGPLEBEFLKREFG 737

QY 358 MSKDNVEMIKALIVFGAEVDPNDPGETPFLASKIG 394
 Db 738 CHYGNIKIVFLQHSKKNVAKKNQGTPLHQAAGS 774

RESULT 9

T42714
 ankyrin 3, splice form 2 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T42714
 R/Peters, L.L.; John, K.M.; Lu, F.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
 J. Cell Biol. 130, 313-330, 1995
 A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A:Reference number: Z22237; NCID:95340633; PMID:7615634
 A/Accession: T42714
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1765 <PEP>
 A/Cross-references: UNIPROT:O61307; EMBL:LA0632; NID:9710548; PID:9710551; PIDN:AA01605
 A/Experimental source: strain C57BL/6J; kidney
 C/Genetics:
 A:Gene: Ank3
 A:Map position: 10
 A:Intons: 1587/1
 C:Superfamily: ankyrin; ankyrin repeat homology
 C/Keywords: alternative splicing

Query Match 8.1%; Score 294.5; DB 2; Length 1765;
 Best Local Similarity 24.7%; Pred. No. 2.6e-14;
 Matches 112; Conservative 81; Mismatches 191; Indels 69; Gaps 18;

QY 124 HLAVELG---IRECFHSRIISCANCAENBEGCTPLHACRGDDELIVELYOCHTOM 179
 Db 421 HVAEFMGNVIVISQLMNH---GASPTTVNRGETALHMAASGQAEVVRVLQ-DGAQV 475
 QY 180 DVDYKGETVFHFAVQGDNSQVQLQLGRNAVAGLVNNOGLTPHLACQLGKQEMRVYL 239
 Db 476 EAKAKDDQTPRLHISALRGKADIVQQLQOG-ASPNAATTSQYTPRLHAAEGHEVDVAFL 534
 QY 240 LLCNARCNITGPNQY-PIHSAMKFSQKCAEMTISDSSQIHSKDPKRYGASPLHMA--K 295
 Db 535 LDHGASLSTTTKKGFPPLHVAAYKGLVVASLLQKASAP--DAAGSGTLPLHVAHYD 592
 QY 296 NAEAMMLKRGONVSTASGNTALHVGMRNRPDCAVLTLHGANAADRGHNTPLH 355
 Db 593 NQVALLLLDQGSPPAAAKNGTTPHLIAAKKQMDIATSLLEYGADANAATROGLASVH 652
 QY 356 LMSKDNVEMIKALIVFGAEVDPNDPGETPFLAS---KIGKLDLM---HISRAKP 408
 Db 653 LAAQEGHVDVSVLLSRNANVNLSNKSGLTPHLAAQEDRVNVAEVLVNGAHVDAQTKM 712
 QY 409 AFLTGSMDKERTHDLCLDGGGVKGLIITQLLIAEKASGVATYDLFDWVAGSTGGI 468
 Db 713 GY-----TPRHVGC-HYGNIK---IVNELLQHSKVNKATKN-----GY 747
 QY 469 LALAILHSKSMAYMRGMVFRMKDEVRGSRPYE---SGPLEBFKPEFGHNTKMTDVRK- 524
 Db 748 TNL-----HQAQOQGHTHIINVLLONNASPNELTVNGTALAIARRLG-YISVVDTLKV 800
 QY 525 --PKVMLTGLSDRQPAELHLPFNYPADPTVRE 555
 Db 801 VTEIMTTTTITTEK-----HKMNVPEPTMNE 825

RESULT 10
 T42715
 ankyrin 3, splice form 3 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T42715

R/Peters, L.L.; John, K.M.; Lu, F.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
 J. Cell Biol. 130, 313-330, 1995
 A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A:Reference number: Z22237; NCID:95340633; PMID:7615634

A/Accession: T42715
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1940 <PEP>
 A/Cross-references: UNIPROT:O61307; EMBL:LA0632; NID:9710548; PID:9710549; PIDN:AA01604.
 A/Experimental source: strain C57BL/6J; kidney
 C/Genetics:
 A:Gene: Ank3
 A:Map position: 10
 A:Intons: 834/1
 C:Superfamily: ankyrin; ankyrin repeat homology
 C/Keywords: alternative splicing

Query Match 8.1%; Score 294.5; DB 2; Length 1940;
 Best Local Similarity 24.7%; Pred. No. 3e-14;
 Matches 112; Conservative 81; Mismatches 191; Indels 69; Gaps 18;

QY 124 HLAVELG---IRECFHSRIISCANCAENBEGCTPLHACRGDDELIVELYOCHTOM 179
 Db 421 HVAEFMGNVIVISQLMNH---GASPTTVNRGETALHMAASGQAEVVRVLQ-DGAQV 475
 QY 180 DVDYKGETVFHFAVQGDNSQVQLQLGRNAVAGLVNNOGLTPHLACQLGKQEMRVYL 239
 Db 476 EAKAKDDQTPRLHISALRGKADIVQQLQOG-ASPNAATTSQYTPRLHAAEGHEVDVAFL 534
 QY 240 LLCNARCNITGPNQY-PIHSAMKFSQKCAEMTISDSSQIHSKDPKRYGASPLHMA--K 295
 Db 535 LDHGASLSTTTKKGFPPLHVAAYKGLVVASLLQKASAP--DAAGSGTLPLHVAHYD 592
 QY 296 NAEAMMLKRGONVSTASGNTALHVGMRNRPDCAVLTLHGANAADRGHNTPLH 355
 Db 593 NQVALLLLDQGSPPAAAKNGTTPHLIAAKKQMDIATSLLEYGADANAATROGLASVH 652
 QY 356 LMSKDNVEMIKALIVFGAEVDPNDPGETPFLAS---KIGKLDLM---HISRAKP 408
 Db 653 LAAQEGHVDVSVLLSRNANVNLSNKSGLTPHLAAQEDRVNVAEVLVNGAHVDAQTKM 712
 QY 409 AFLTGSMDKERTHDLCLDGGGVKGLIITQLLIAEKASGVATYDLFDWVAGSTGGI 468
 Db 713 GY-----TPRHVGC-HYGNIK---IVNELLQHSKVNKATKN-----GY 747
 QY 469 LALAILHSKSMAYMRGMVFRMKDEVRGSRPYE---SGPLEBFKPEFGHNTKMTDVRK- 524
 Db 748 TNL-----HQAQOQGHTHIINVLLONNASPNELTVNGTALAIARRLG-YISVVDTLKV 800
 QY 525 --PKVMLTGLSDRQPAELHLPFNYPADPTVRE 555
 Db 801 VTEIMTTTTITTEK-----HKMNVPEPTMNE 825

RESULT 11
 T42713
 ankyrin 3, splice form 1 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T42713
 R/Peters, L.L.; John, K.M.; Lu, F.M.; Elcher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L.
 J. Cell Biol. 130, 313-330, 1995
 A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A:Reference number: Z22237; NCID:95340633; PMID:7615634
 A/Accession: T42713
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1943 <PEP>
 A/Cross-references: UNIPROT:O61307; EMBL:LA0632; NID:9710548; PID:9710550; PIDN:AA01606.
 A/Experimental source: strain C57BL/6J; kidney
 C/Genetics:

F:568-600/Domain: ankryn repeat homology <AN17>
 F:601-633/Domain: ankryn repeat homology <AN18>
 F:634-666/Domain: ankryn repeat homology <AN19>
 F:667-699/Domain: ankryn repeat homology <AN20>
 F:700-732/Domain: ankryn repeat homology <AN21>
 F:733-765/Domain: ankryn repeat homology <AN22>
 F:766-798/Domain: ankryn repeat homology <AN23>

Query Match 8.1%; Score 294; DB 2; Length 1856;
 Best Local Similarity 25.6%; Pred. No. 3, 1e-14;
 Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LQHLTDLIRNHPWSVAHLAVELGIRECFPH--SRIISCANCAENE---EGCTPLHLACR 161
 DB 336 LDHLTPL-----HVAA-----HCGHNVAKVLDKGAKPNSBALNGFTPLHLACK 380
 QY 162 KGGELIVELVOYCHTQMD-----VTDYKGET 188
 DB 381 KKHVRVM-ELLKGTGASIDAVTESGLTPLHVASFMGHLPIVKNLDRGASPNVSVKVEET 439
 QY 189 VPHYAVQGDNSOYLQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLLCNARCI 248
 DB 440 PLHMAARAGHTEVAKYLLQNK-AKVNAKAKDDOTPLHCAARIGHTVMVLLLENNANPNL 498
 QY 249 MGENGY-----PIHSAMKFSQKCAEMIIISM 274
 DB 499 ATTAGHTPLHIAAREGHVETVALLLEKEASQACMTKKGTPLHVAAYGKVAELLER 558
 QY 275 DSSQHSKDPRYGASPLHMA---KNAEMAMLLKRCGNVNSTSSAGNTALHVGMMNRPD 331
 DB 559 DAHP--NAAGKNGLTPLHVAVHHNNNDIVKLLPRGSGSPSPAMNGYTPPLHIAKONQVE 616
 QY 332 CAIVLTHGANADAREGHNTPLHAMSNDNEMIKALIVFGAEVDTPNDPGETPFLAS 391
 DB 617 VARSLLQYGSANASVQGVTPPLHIAQEGHAEVALLSKQANGNLGNKSGLTPLHLVA 676
 QY 392 KIG 394
 DB 677 QEG 679

RESULT 14

ankryn 1, erythrocyte splice form 2 - human
 N/Alternate names: ankryn 2.1, erythrocyte; ankryn-R
 N/Contains: ankryn 2.2, erythrocyte
 C/Species: Homo sapiens (man)
 C/Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004
 C/Accession: A35049
 R/Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.;
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A/Title: cDNA sequence for human erythrocyte ankryn.
 A/Reference number: A35049; MUID:90157370; PMID:1689849
 A/Accession: A35049
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1880 <LMA>
 A/Cross-references: UNIPROT:P16157; GB:M28880
 C/Genetics:
 A/Genes: GDB:ANK1, ANK
 A/Cross-references: GDB:118737; OMIM:182900
 A/Map position: 8p11.2-8p11.2
 C/Superfamily: ankryn; ankryn repeat homology
 C/Keywords: alternative splicing; cytoskeleton
 F:2-1880/Product: ankryn 1, erythrocyte form 2 #status predicted <MAT>
 F:2-1513,1676-1880/Product: ankryn 2.2, erythrocyte #status predicted <MA2>
 F:44-76/Domain: ankryn repeat homology <AN01>
 F:77-109/Domain: ankryn repeat homology <AN02>
 F:110-142/Domain: ankryn repeat homology <AN03>
 F:143-171/Domain: ankryn repeat homology <AN04>
 F:172-204/Domain: ankryn repeat homology <AN05>
 F:205-237/Domain: ankryn repeat homology <AN06>
 F:238-270/Domain: ankryn repeat homology <AN07>

F:271-303/Domain: ankryn repeat homology <AN08>
 F:304-336/Domain: ankryn repeat homology <AN09>
 F:337-369/Domain: ankryn repeat homology <AN10>
 F:370-402/Domain: ankryn repeat homology <AN11>
 F:403-435/Domain: ankryn repeat homology <AN12>
 F:436-468/Domain: ankryn repeat homology <AN13>
 F:469-501/Domain: ankryn repeat homology <AN14>
 F:502-534/Domain: ankryn repeat homology <AN15>
 F:535-567/Domain: ankryn repeat homology <AN16>
 F:568-600/Domain: ankryn repeat homology <AN17>
 F:601-633/Domain: ankryn repeat homology <AN18>
 F:634-666/Domain: ankryn repeat homology <AN19>
 F:667-699/Domain: ankryn repeat homology <AN20>
 F:700-732/Domain: ankryn repeat homology <AN21>
 F:733-765/Domain: ankryn repeat homology <AN22>
 F:766-798/Domain: ankryn repeat homology <AN23>

Query Match 8.1%; Score 294; DB 2; Length 1880;
 Best Local Similarity 25.6%; Pred. No. 3, 1e-14;
 Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LQHLTDLIRNHPWSVAHLAVELGIRECFPH--SRIISCANCAENE---EGCTPLHLACR 161
 DB 336 LDHLTPL-----HVAA-----HCGHNVAKVLDKGAKPNSBALNGFTPLHLACK 380
 QY 162 KGGELIVELVOYCHTQMD-----VTDYKGET 188
 DB 381 KKHVRVM-ELLKGTGASIDAVTESGLTPLHVASFMGHLPIVKNLDRGASPNVSVKVEET 439
 QY 189 VPHYAVQGDNSOYLQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLLCNARCI 248
 DB 440 PLHMAARAGHTEVAKYLLQNK-AKVNAKAKDDOTPLHCAARIGHTVMVLLLENNANPNL 498
 QY 249 MGENGY-----PIHSAMKFSQKCAEMIIISM 274
 DB 499 ATTAGHTPLHIAAREGHVETVALLLEKEASQACMTKKGTPLHVAAYGKVAELLER 558
 QY 275 DSSQHSKDPRYGASPLHMA---KNAEMAMLLKRCGNVNSTSSAGNTALHVGMMNRPD 331
 DB 559 DAHP--NAAGKNGLTPLHVAVHHNNNDIVKLLPRGSGSPSPAMNGYTPPLHIAKONQVE 616
 QY 332 CAIVLTHGANADAREGHNTPLHAMSNDNEMIKALIVFGAEVDTPNDPGETPFLAS 391
 DB 617 VARSLLQYGSANASVQGVTPPLHIAQEGHAEVALLSKQANGNLGNKSGLTPLHLVA 676
 QY 392 KIG 394
 DB 677 QEG 679

RESULT 15

ankryn 1, erythrocyte splice form 1 - human
 N/Alternate names: ankryn 2.1, erythrocyte; ankryn-R
 N/Contains: ankryn 2.2
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C/Accession: S08275; A33219; F02220; A35443
 R/Lux, S.E.; John, K.M.; Bennett, V.
 Nature 344, 36-42, 1990
 A/Title: Analysis of cDNA for human erythrocyte ankryn indicates a repeated structure w/
 A/Reference number: S08275; MUID:90158830; PMID:2137557
 A/Accession: S08275
 A/Molecule type: mRNA
 A/Residues: 1-1881 <LNU>
 A/Cross-references: UNIPROT:P16157; EMBL:X16609; NID:g28701; P1DN:CAA34610.1; P1D:g28702
 A/Accession: A33219
 A/Molecule type: protein
 A/Residues: 2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30, 733-749, 'A', 751-753, 828-833, 'X', 835-855, 'X',
 'X', 1367, 1383-1427, 1601-1630, 1686-1698, 'D', 1700, 1763-1772 <LUX>
 A/Note: 845-Arg and 1392-Thr were also found
 R/Hermann, U.; Barel, M.; Fraide, R.
 Biochem. Biophys. Res. Commun. 204, 453-460, 1994

A:Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
A:Reference number: PC2220; MUID:95071346; PMID:7526850
A:Accession: PC2220
A:Molecule type: protein
A:Residues: 910-929 <HER>
R:Davis, L.H.; Bennett, V.
J. Biol. Chem. 265, 10589-10596, 1990
A:Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
A:Reference number: A35443; MUID:90285190; PMID:2141335
A:Accession: A35443
A:Molecule type: protein
A:Residues: 'X',5,'X',7-12,403-417,'X',419-422,'H',424,'YQ',797-800,'L',802-814,862-863,
C:Genetics:
A:Gene: GDB:ANK1; ANK
A:Cross-references: GDB:118737; OMIM:182900
A:Map position: 8p11.2-8p11.2
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing; phosphoprotein
F:2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>
F:2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>
F:2-827/Domain: 89K #status predicted <DOM1>
F:2-827/Region: anion exchange protein binding
F:44-76/Domain: ankyrin repeat homology <AN01>
F:77-109/Domain: ankyrin repeat homology <AN02>
F:110-142/Domain: ankyrin repeat homology <AN03>
F:143-171/Domain: ankyrin repeat homology <AN04>
F:172-204/Domain: ankyrin repeat homology <AN05>
F:205-237/Domain: ankyrin repeat homology <AN06>
F:238-270/Domain: ankyrin repeat homology <AN07>
F:271-303/Domain: ankyrin repeat homology <AN08>
F:304-336/Domain: ankyrin repeat homology <AN09>
F:337-369/Domain: ankyrin repeat homology <AN10>
F:370-402/Domain: ankyrin repeat homology <AN11>
F:403-435/Domain: ankyrin repeat homology <AN12>
F:436-468/Domain: ankyrin repeat homology <AN13>
F:469-501/Domain: ankyrin repeat homology <AN14>
F:502-534/Domain: ankyrin repeat homology <AN15>
F:535-567/Domain: ankyrin repeat homology <AN16>
F:568-600/Domain: ankyrin repeat homology <AN17>
F:601-633/Domain: ankyrin repeat homology <AN18>
F:634-666/Domain: ankyrin repeat homology <AN19>
F:667-699/Domain: ankyrin repeat homology <AN20>
F:700-732/Domain: ankyrin repeat homology <AN21>
F:733-765/Domain: ankyrin repeat homology <AN22>
F:766-798/Domain: ankyrin repeat homology <AN23>
F:828-1382/Domain: 62K #status predicted <DOM2>
F:828-1382/Region: spectrin binding
F:1383-1881/Domain: 55K #status predicted <DOM3>

Query Match 8.1%; Score 294; DB 1; Length 1881;

Best Local Similarity 25.6%; Pred. No. 3.2e-14; Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LGHLTDLIRNHPMSVAHLAVELGIRCEPHN--SRIISCANCAENE---EGCTPLHACR 161
DB 336 LDHITPL-----HVAA-----HGHHRVAKVLLDKAKPNSBALNGFTPLHIACT 380
QY 162 KGDGEILVELVOYCHTQMD-----VTDYKGET 188
DB 381 KNYRVVM-ELLKTKGASIDAVTESGLTPLVASFVGHLPVKNLLQRGASPNVSNVAKET 439
QY 189 VFHYAVGDNISQVQLLGRNAVAGLNOVNNQGLTPHLACQLGQEMVRVILLCNARCN 248
DB 440 PLHVAAPAGHTEVAKYLLQNR-AKVNAKAKDDQTPHICARIGHITNNVKLLLENNANPNL 498
QY 249 MGPNY-----PIHSAKFSOKCAEMTISM 274
DB 499 ATTAGHTPLIARREHVEVTLALLEKASQACMTKGFPLHVAATYGVAVALLER 556
QY 275 DSSQIHSKDPRYGASPLHMA---KNAEMARMLLRGCNVNSTSAGNTALHVGVRNRF 331
DB 559 DAHP--NAAGNGLTPHVAHVHNNLDIVKLLPRGSPHSPANNGYTPHIAKQNOVE 616

QY 332 CATVLTGANDARGHGNTPLHLSMKNVEMIKALIVGAEDVPNDPFGETPTFLAS 391
DB 617 VANSLLQYGGSANASVQGYTPHLAAQGHAEVALLSKQANGSLGKSGITPLHVA 676
QY 392 KTG 394
DB 677 QEG 679

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Job time: 34.0226 sec

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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:52:25 ; Search time 149.609 Seconds
(without alignments)
2642.105 Million cell updates/sec

Title: US-10-612-668-21
Perfect score: 3620
Sequence: 1 MGFRLVNTFSGVTNLFNS.....GAKELGMVVDCTDPDGR 687

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|--------------|--------------------|
| 1 | 3566.5 | 98.5 | 806 | 1 PA26_HUMAN | O60733 homo sapien |
| 2 | 3566.5 | 98.5 | 806 | 1 CAG30429 | Cag30429 homo sapi |
| 3 | 3289.5 | 91.1 | 752 | 1 PA26_MOUSE | P97819 mus musculu |
| 4 | 3289.5 | 90.9 | 752 | 1 Q7TPX2 | Q7TPX2 mus musculu |
| 5 | 3272 | 90.4 | 807 | 2 Q9JK61 | Q9JK61 mus musculu |
| 6 | 3272 | 90.4 | 807 | 2 AAH57209 | AAH57209 mus muscu |
| 7 | 3257 | 90.0 | 751 | 1 PA26_RAT | P97570 rattus norv |
| 8 | 2210.5 | 61.1 | 756 | 2 Q6DDFO | Q6DDFO xenopus lae |
| 9 | 1977.5 | 54.6 | 818 | 2 Q6NW10 | Q6NW10 brachydanto |
| 10 | 1977.5 | 54.6 | 818 | 2 AAH67375 | AAH67375 brachydan |
| 11 | 1164 | 32.1 | 879 | 2 Q7Q2U1 | Q7Q2U1 anopheles g |
| 12 | 1163.5 | 32.1 | 877 | 2 Q9VTE6 | Q9VTE6 drosophila |
| 13 | 1163.5 | 32.1 | 877 | 2 AAH50194 | AAH50194 drosophi |
| 14 | 1163.5 | 32.1 | 887 | 2 Q7KUD4 | Q7KUD4 drosophila |
| 15 | 1163.5 | 32.1 | 887 | 2 AAH11936 | AAH11936 drosophi |
| 16 | 742 | 20.5 | 386 | 2 Q8MR13 | Q8MR13 drosophila |
| 17 | 647.5 | 17.9 | 1071 | 2 Q20500 | Q20500 caenorhabdi |
| 18 | 629.5 | 17.5 | 1023 | 2 Q62398 | Q62398 caenorhabdi |
| 19 | 629.5 | 17.4 | 1021 | 2 Q81006 | Q81006 caenorhabdi |
| 20 | 458 | 12.7 | 762 | 2 Q95YD2 | Q95YD2 caenorhabdi |
| 21 | 357.5 | 9.9 | 501 | 2 Q9NSJ3 | Q9NSJ3 caenorhabdi |
| 22 | 338 | 9.3 | 843 | 2 P97582 | P97582 rattus norv |
| 23 | 338 | 9.3 | 1219 | 2 Q8C8R3 | Q8C8R3 mus musculu |
| 24 | 332 | 9.2 | 1863 | 2 Q7Z3L5 | Q7Z3L5 homo sapien |
| 25 | 332 | 9.2 | 3924 | 1 ANK2_HUMAN | ANK2_HUMAN |
| 26 | 324.5 | 9.0 | 1004 | 2 Q7JNZ0 | Q7JNZ0 caenorhabdi |
| 27 | 324.5 | 9.0 | 1004 | 2 AAQ91911 | AAQ91911 caenorhab |
| 28 | 324.5 | 9.0 | 1786 | 2 Q17344 | Q17344 caenorhabdi |
| 29 | 324.5 | 9.0 | 1809 | 2 Q17487 | Q17487 caenorhabdi |
| 30 | 324.5 | 9.0 | 1815 | 2 Q17488 | Q17488 caenorhabdi |
| 31 | 324.5 | 9.0 | 1841 | 2 Q8MGQ0 | Q8MGQ0 caenorhabdi |

ALIGNMENTS

| RESULT 1 | PA26_HUMAN | STANDARD, | PRT, | 806 AA. | |
|----------|--|-----------|------|---------|--------|
| AC | O60733; Q75645; Q8N452; Q9UG29; Q9UIT0; Q9Y671; | | | | Q17486 |
| DT | 30-MAY-2000 (Rel. 39, Created) | | | | Q17489 |
| DT | 30-MAY-2000 (Rel. 39, Last sequence update) | | | | Q17490 |
| DT | 01-OCT-2004 (Rel. 45, Last annotation update) | | | | Q17491 |
| DE | 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cat-PLA2) (Group VI phospholipase A2) (GVI PLA2). | | | | Q24241 |
| GN | Name=iPLA2G6; Synonyms=iPLA2; | | | | Q9V4B1 |
| OS | Homo sapiens (Human). | | | | Q8JHU3 |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | Q8JHU3 |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | Q8JHU3 |
| OX | NCBI_TaxID=9606; | | | | Q8JHU3 |
| RN | [1] | | | | Q8JHU3 |
| RP | SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND ANKYRIN-IPLA2-2). | | | | Q8JHU3 |
| RC | TISSUE=B-cell, and Testis; | | | | Q8JHU3 |
| RX | MEDLINE=98079046; PubMed=9417066; | | | | Q8JHU3 |
| RA | Larsson P.K.A., Claesson H.-E., Kennedy B.P.; | | | | Q8JHU3 |
| RT | "Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity."; | | | | Q8JHU3 |
| RL | J. Biol. Chem. 273:207-214(1998). | | | | Q8JHU3 |
| RN | [2] | | | | Q8JHU3 |
| RP | SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2). | | | | Q8JHU3 |
| RC | TISSUE=pancreatic islets; | | | | Q8JHU3 |
| RX | MEDLINE=99194813; PubMed=10092647; | | | | Q8JHU3 |
| RA | Ma Z., Wang X., Nowatke W., Ramanadham S., Turk J.; | | | | Q8JHU3 |
| RT | "Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (iPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the iPLA2 gene on chromosome 22q13.1."; | | | | Q8JHU3 |
| RL | J. Biol. Chem. 274:9607-9616(1999). | | | | Q8JHU3 |
| RN | [3] | | | | Q8JHU3 |
| RP | SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING. | | | | Q8JHU3 |
| RX | MEDLINE=99269033; PubMed=10336645; | | | | Q8JHU3 |
| RA | Larsson Forell P.K.A., Kennedy B.P., Claesson H.-E.; | | | | Q8JHU3 |
| RT | "The human calcium-independent phospholipase A2 gene. Multiple enzymes with different properties from a single gene."; | | | | Q8JHU3 |
| RL | Eur. J. Biochem. 262:575-585(1999). | | | | Q8JHU3 |
| RN | [4] | | | | Q8JHU3 |
| RP | SEQUENCE FROM N.A. (ISOFORM LH-IPLA). | | | | Q8JHU3 |
| RC | TISSUE=Testis; | | | | Q8JHU3 |
| RA | Amoysse W., Winkler U., Mewe H.-W., Gassenhuber J., Wiemann S.; | | | | Q8JHU3 |
| RL | Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases. | | | | Q8JHU3 |
| RN | [5] | | | | Q8JHU3 |
| RP | SEQUENCE FROM N.A. AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND THR-343. | | | | Q8JHU3 |
| RA | Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.; | | | | Q8JHU3 |
| RT | Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.; | | | | Q8JHU3 |
| RL | Sherwood J.K., Sherwood A.M., Leitauer B.J., Nickerson D.A.; | | | | Q8JHU3 |
| RT | "NIH-SNP, environmental genome project. NIH ES15478, Department of Genome Sciences, Seattle, WA (URL: http://esp.gs.washington.edu)."; | | | | Q8JHU3 |
| RL | Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases. | | | | Q8JHU3 |

[6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
 RA Clump M., Smith L.J., Alincough R., Almeida J.P., Babbage A.K.,
 RA Bagdley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
 RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
 RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Copley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
 RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
 RA Gilbert J.G.R., Goward M.E., Graffham D.V., Griffiths M.N.D., Hall C.,
 RA Hall S.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
 RA Laird G.K., Langford C.F., Leverhwa M.A., Lloyd C., Lloyd D.M.,
 RA Martin I.D., Mashreghi-Mohammadi M., Matthews L.H., McLean O.T.,
 RA McCally J., McLaren S., McMurtry A.A., Milne S.A., Northmore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Rose M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minochina S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuayama S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,
 RA Phan Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisoso S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Bemis G., Bentley J., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinde K., Kemp K., Lacroix P., Layman D., Ozerky P., Rottling T.,
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salter S.,
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumarek J.P.,
 RA Peyrard M., Kedia D., Seroussi E., Fransoni I., Tapia I., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Bodentelch H., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tliahun Y., Wright H.,
 RT "The DNA sequence of human chromosome 22."
 RL Nature 402:489-495(1999).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORMS LH-1PLA2 AND SH-1PLA2).
 RC TISSUE=Brain;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Heien F.,
 RA Diatchenko L., Marutka K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiki S., Carninci P., Prange C.,
 RA Raha S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.D., Hulyk S.W.,
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Catalyzes the release of fatty acids from phospholipids.
 CC It has been implicated in normal phospholipid remodeling, nitric
 CC oxide-induced or vasopressin-induced arachidonic acid release and

CC in leukotriene and prostaglandin production. May participate in
 CC fas mediated apoptosis and in regulating transmembrane ion flux in
 CC glucose-stimulated B-cells.
 CC -1- FUNCTION: Isoform ankyrin-1PLA2-1 and isoform ankyrin-1PLA2-2,
 CC which lack the catalytic domain, are probably involved in the
 CC negative regulation of 1PLA2 activity.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a carboxylate.
 CC SUBUNIT: Forms large oligomeric 270-350 kDa structures.
 CC -1- SUBCELLULAR LOCATION: Isoform LH-1PLA2 was found to be membrane
 CC bound. Isoform SH-1PLA2 is cytoplasmic.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=LH-1PLA2;
 CC IsoId=O60733-1; Sequence=Displayed;
 CC Name=SH-1PLA2;
 CC IsoId=O60733-2; Sequence=VSP_000278;
 CC Name=Ankyrin-1PLA2-1;
 CC IsoId=O60733-3; Sequence=VSP_000281, VSP_000282;
 CC Name=Ankyrin-1PLA2-2;
 CC IsoId=O60733-4; Sequence=VSP_000277, VSP_000279, VSP_000280;
 CC TISSUE SPECIFICITY: Four different transcripts were found to be
 CC expressed in a distinct tissue distribution.
 CC -1- SIMILARITY: Contains 7 ANK repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC -----
 DR EMBL: AF064594; AAC97486.1; -;
 DR EMBL: AF102989; AAD41722.1; -;
 DR EMBL: AF102989; AAD41723.1; -;
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DR HSSP; 060778; 10Y3.
DR Genew; HGNC:9039; PLA2G6.

Query Match 98.5%; Score 3566.5; DB 1; Length 806;
Best Local Similarity 92.3%; Pred. No. 5,8e-265;
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;

QY 1 MOFFGRVNTFSGVTNLFSPNFRKVEAVADYSSDRVREGQILFQNTPNRTWDCVLY 60
DB 1 MOFFGRVNTFSGVTNLFSPNFRKVEAVADYSSDRVREGQILFQNTPNRTWDCVLY 60
QY 61 NPNNSGGRFLFOLELEADALVNFHOYSQQLPFYESSPOVLTHTVLOHITDLIRNHPSW 120
DB 61 NPNNSGGRFLFOLELEADALVNFHOYSQQLPFYESSPOVLTHTVLOHITDLIRNHPSW 120
QY 121 SVHLAVELGIRRCFHSRIISCANCAENEGCTPLHACRKDGELVELVOYCHTQMD 180
DB 121 SVHLAVELGIRRCFHSRIISCANCAENEGCTPLHACRKDGELVELVOYCHTQMD 180
QY 181 VTDYKGETVHYAVQGNDSQVQLLGRNVAAGLNVNNOGILFPLHACOLGKQEMRVLL 240
DB 181 VTDYKGETVHYAVQGNDSQVQLLGRNVAAGLNVNNOGILFPLHACOLGKQEMRVLL 240
QY 241 LCNARCNMGPNGYPIHSAMKFSQKCAEMIISDSSQIHSKDPRYGASPLHAKNAEMA 300
DB 241 LCNARCNMGPNGYPIHSAMKFSQKCAEMIISDSSQIHSKDPRYGASPLHAKNAEMA 300
QY 301 RMLKRCGNVSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLSMSK 360
DB 301 RMLKRCGNVSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLSMSK 360
QY 361 DNEMTKALIVFGAEVDPNDPGETPTFLASKIGRLVTRKAILTLRTVGAECFPPHIG 420
DB 361 DNEMTKALIVFGAEVDPNDPGETPTFLASKIGRLVTRKAILTLRTVGAECFPPHIG 420
QY 421 VPAEQSAAHHFPSLEBAOPPIISLNLELOLMHISRAKPAFLIGSRDEKRTDHL 480
DB 421 VPAEQSAAHHFPSLEBAOPPIISLNLELOLMHISRAKPAFLIGSRDEKRTDHL 480
QY 481 LCLDGGGVKGLIIITQLIAIEKASGVAATKDLFDWVAGTSTGGILALAILHKSMAVYRGM 540
DB 481 LCLDGGGVKGLIIITQLIAIEKASGVAATKDLFDWVAGTSTGGILALAILHKSMAVYRGM 540
QY 546 NYDAPEVREPRFNQVNLRRPAPQSDQVWRARSSGAAPTYFRPNGRFLDGLLANNP 605
DB 546 NYDAPEVREPRFNQVNLRRPAPQSDQVWRARSSGAAPTYFRPNGRFLDGLLANNP 605
QY 601 NYDAPEVREPRFNQVNLRRPAPQSDQVWRARSSGAAPTYFRPNGRFLDGLLANNP 660
DB 601 NYDAPEVREPRFNQVNLRRPAPQSDQVWRARSSGAAPTYFRPNGRFLDGLLANNP 660
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DB 606 TLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGSPQVPTCVDFRPSNWEIAKT 665
QY 661 TLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGSPQVPTCVDFRPSNWEIAKT 720
DB 661 TLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGSPQVPTCVDFRPSNWEIAKT 720
QY 666 VFGAKELGKRVVDCCTDPDGR 686
DB 666 VFGAKELGKRVVDCCTDPDGR 686
QY 721 VFGAKELGKRVVDCCTDPDGR 741
DB 721 VFGAKELGKRVVDCCTDPDGR 741

RESULT 2

CAG30429 PRELIMINARY; PRT; 806 AA.
AC CAG30429;
DT 01-JUN-2004 (Tremblrel. 27, Created)
DT 01-JUN-2004 (Tremblrel. 27, Last sequence update)
DT 01-JUN-2004 (Tremblrel. 27, Last annotation update)
DE PLA2G6 protein.
GN PLA2G6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1];
RP SEQUENCE FROM N.A.
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Gingham J.A.,
RA Cole C.G., Goward M.E., Aguado B., Mallia M., Mokrab Y., Huckle B.J.,
RA Beare D.M., Dunham I.,
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR456543; CAG30429.1; -
SQ SEQUENCE 806 AA; 89902 MW; 8E55CDAEB9ACAD8B CRC64;

Query Match 98.5%; Score 3566.5; DB 2; Length 806;
Best Local Similarity 92.3%; Pred. No. 5,8e-265;
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;

QY 1 MOFFGRVNTFSGVTNLFSPNFRKVEAVADYSSDRVREGQILFQNTPNRTWDCVLY 60
DB 1 MOFFGRVNTFSGVTNLFSPNFRKVEAVADYSSDRVREGQILFQNTPNRTWDCVLY 60
QY 61 NPNNSGGRFLFOLELEADALVNFHOYSQQLPFYESSPOVLTHTVLOHITDLIRNHPSW 120
DB 61 NPNNSGGRFLFOLELEADALVNFHOYSQQLPFYESSPOVLTHTVLOHITDLIRNHPSW 120
QY 121 SVHLAVELGIRRCFHSRIISCANCAENEGCTPLHACRKDGELVELVOYCHTQMD 180
DB 121 SVHLAVELGIRRCFHSRIISCANCAENEGCTPLHACRKDGELVELVOYCHTQMD 180
QY 181 VTDYKGETVHYAVQGNDSQVQLLGRNVAAGLNVNNOGILFPLHACOLGKQEMRVLL 240
DB 181 VTDYKGETVHYAVQGNDSQVQLLGRNVAAGLNVNNOGILFPLHACOLGKQEMRVLL 240
QY 241 LCNARCNMGPNGYPIHSAMKFSQKCAEMIISDSSQIHSKDPRYGASPLHAKNAEMA 300
DB 241 LCNARCNMGPNGYPIHSAMKFSQKCAEMIISDSSQIHSKDPRYGASPLHAKNAEMA 300
QY 301 RMLKRCGNVSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLSMSK 360
DB 301 RMLKRCGNVSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLSMSK 360
QY 361 DNEMTKALIVFGAEVDPNDPGETPTFLASKIGRLVTRKAILTLRTVGAECFPPHIG 420
DB 361 DNEMTKALIVFGAEVDPNDPGETPTFLASKIGRLVTRKAILTLRTVGAECFPPHIG 420
QY 421 VPAEQSAAHHFPSLEBAOPPIISLNLELOLMHISRAKPAFLIGSRDEKRTDHL 480
DB 421 VPAEQSAAHHFPSLEBAOPPIISLNLELOLMHISRAKPAFLIGSRDEKRTDHL 480
QY 481 LCLDGGGVKGLIIITQLIAIEKASGVAATKDLFDWVAGTSTGGILALAILHKSMAVYRGM 540
DB 481 LCLDGGGVKGLIIITQLIAIEKASGVAATKDLFDWVAGTSTGGILALAILHKSMAVYRGM 540
QY 546 NYDAPEVREPRFNQVNLRRPAPQSDQVWRARSSGAAPTYFRPNGRFLDGLLANNP 605
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QY 661 TLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGSPQVPTCVDFRPSNWEIAKT 720
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RESULT 3

PA26_MOUSE STANDARD; PRT; 752 AA.
ID PA26_MOUSE
AC P97819; 0991A9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (PLA2) (Cat-
DE PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1) _
RP SEQUENCE FROM N.A.
RC STRAIN=DNA/2;
RX MEDLINE=97236816; PubMed=9079688;
RA Balboa M.A., Balshine J., Jones S.S., Dennis E.A.;
RT "Identity between the Ca²⁺-independent phospholipase A2 enzymes from
RT P3881 macrophages and Chinese hamster ovary cells";
RL J. Biol. Chem. 272:8576-8580(1997).
RN [2]
RP REVISIONS TO 2-3; 9; 11 AND 211.
RA Balboa M.A., Balshine J., Jones S.S., Dennis E.A.;
RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RX SEQUENCE FROM N.A.
RA MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Butcherfield Y.S.N., Krzywiński M.I., Skalska U., Smallue D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Contains 7 ANK repeats.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.1sb-81b.ch/announce/>
CC or send an email to license@1sb-81b.ch).
CC -----
CC EMBL: U88624; AAB4511.2; -.
CC EMBL: BC003487; AA03487.1; -.
CC HSSP: Q60778; IOY3.
CC MGD: MGI:1859152; Pla2g6.
CC InterPro: IPR002110; ANK.
CC Pfam: PF000023; ANK_6.
CC PRINTS: PR01415; ANKYRIN.
CC SMART: SM00248; ANK_6.
CC PROSITE: PSS0088; ANK_REPEAT; 4.
CC PROSITE: PSS0297; ANK_REPEAT_REGION; 1.
CC ANK repeat; Hydrolase; Lipid degradation; Repeat.
FT REPEAT 151 181 ANK 1.
FT REPEAT 185 215 ANK 2.
FT REPEAT 219 248 ANK 3.
FT REPEAT 251 281 ANK 4.
FT REPEAT 286 312 ANK 5.
FT REPEAT 316 345 ANK 6.
FT REPEAT 349 378 ANK 7.

FT ACT SITE 465 465 Potential.
SQ SEQUENCE 752 AA; 83702 MW; AAC3347B0E1292E9 CRC64;
Query Match 91.1%; Score 3299.5; DB 1; Length 752;
Best Local Similarity 90.5%; Pred. No. 1.7e-244;
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QY 241 LCNARCNINMGPGFPIHTANKFQKCAEVIISMDSNQHSKDPKYGASPLHMAKNAEMA 300
DB 241 LCNARCNINMGPGFPIHTANKFQKCAEVIISMDSNQHSKDPKYGASPLHMAKNAEMA 300
QY 301 RMLLKSGCWNSTYSAGNTALHYGVNRNFDCAIVLTHGANADARHGNTPLHLAMSK 360
DB 301 RMLLKSGCVDSTSSSGNTALHYAVNRNFDCAIVLTHGANADARHGNTPLHLAMSK 360
QY 361 DNVEMIKALIVGAEDVTPNDGEPTPLASKIGK-LQDLMHISRAKRAPFIISGRDEX 419
DB 361 DNVEMIKALIVGAEDVTPNDGEPTPLASKIGK-LQDLMHISRAKRAPFIISGRDEX 419
QY 420 RTHDHLCLDGGVKGKLIILILATEKASGVATKOLPMVAGTSGGILALILSKSN 479
DB 420 RSHDHLCLDGGVKGKLIILILATEKASGVATKOLPMVAGTSGGILALILSKSN 480
QY 480 AYVRGMYFPMKDEVFPGSRPYESGPLEFLKREFGHTKTVDKRWLTGTLSDRPA 539
DB 481 AYVRGMYFPMKDEVFPGSRPYESGPLEFLKREFGHTKTVDKRWLTGTLSDRPA 540
QY 540 ELHLFNVYDAPEVREPRFNQVNLRRPAQPSDQVWRAARSSGAAPYFRNGRLDGG 599
DB 541 ELHLFNVYDAPEVREPRFNQVNLRRPAQPSDQVWRAARSSGAAPYFRNGRLDGG 600
QY 600 LLANNPTLAMEIHEHYNDLIRKQANRYKULSTVSIIGTGRSPQVPTCVVFRPSNP 659
DB 601 LLANNPTLAMEIHEHYNDLIRKQANRYKULSTVSIIGTGRSPQVPTCVVFRPSNP 660
QY 660 WEIAKTVFGAKELGKRVVDCCTDPDGR 686
DB 661 WEIAKTVFGAKELGKRVVDCCTDPDGR 687
RESULT 4
Q7TPX2 PRELIMINARY; PRT; 752 AA.
ID 07TPX2;
AC 07TPX2;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Phospholipase A2, group VI.
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1) _
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/He; Tissue=Osteoblast;
RX MEDLINE=2388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marins K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.M., Buttefield Y.S.,
 RA Krzywnicki M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/He; TISSUE=osteoblast;
 RA Strausberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC052845; AHS52845.1; -
 DR GO: GO:0003824; F: catalytic activity; IEA.
 DR GO: GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR002641; Patatin.
 DR Pfam: PF000023; Ank: 6.
 DR Pfam: PF012734; Patatin: 1.
 DR SMART: SM00248; ANK: 6.
 DR PROSITE: PS50088; ANK_REPEAT: 4.
 DR PROSITE: PS50297; ANK_REPEAT_REGION: 1.
 DR ANK repeat.
 SQ SEQUENCE 752 AA; 83717 MW; DAC3347B0E14AFC CRC64;

Query Match 90.9%; Score 3289.5; DB 2; Length 752;
 Best Local Similarity 90.4%; Pred. No. 1e-243;
 Matches 621; Conservative 29; Mismatches 36; Indels 1; Gaps 1;
 QY 1 MOPFGRVNTFSGTNTLFSNPFYKVEAVADVTSDDVREBGGILPONTNRTWDCV 60
 DB 1 MOPFGRVNTLSTVTLFSNPFYKVEAVSLDYSSERREBGGILQNVNTRWDCV 60
 QY 61 NPNRSQSGFRLFOLEBADLVNPFHOYSSQILPFYESSPOVLAHTEVLQHLTDLIRNPSW 120
 DB 61 SPNRPQSGFRLFOLEBADLVNPFHOYSSQILPFYESSPOVLAHTEVLQHLTDLIRNPSW 120
 QY 121 SVAILAVELGIRECFHHSRIISCANCAENEBGCTPLHLACKRGDEILVELVQYCTOMD 180
 DB 121 TVTHIAVELGIRECFHHSRIISCANSTENEBGCTPLHLACKRGDEILVELVQYCHAMD 180
 QY 181 VTQYKGTVFHYAVQGNOSVQILGNNAVAGLVNNOVGLTPHLACOLGKQOMAVYL 240
 DB 181 VTQYKGTVFHYAVQGNOSVQILGNNAVAGLVNNOVGLTPHLACOLGKQOMAVYL 240
 QY 241 LCNARCINMGPNYPIHSAMKFSQKCAEMTISMDSSQIHSKDPYSGAPLHAKNAEMA 300
 DB 241 LCNARCINMGPNYPIHSAMKFSQKCAEMTISMDSSQIHSKDPYSGAPLHAKNAEMA 300
 QY 301 RMLIKRGCVNVSISAGNTALHVGVRNRPFCALVLTGKANADARGHGTPLHLSMSK 360
 DB 301 RMLIKRGCVNVSISAGNTALHVGVRNRPFCALVLTGKANADARGHGTPLHLSMSK 360
 QY 361 DNVEMLRATLVFGABVDTPNDFGETPTLAKIGK-LQDLHGISRRAPAFITLSMDEK 419
 DB 361 DNVEMLRATLVFGABVDTPNDFGETPTLAKIGK-LQDLHGISRRAPAFITLSMDEK 419
 QY 420 RTHDHLCLDGGGVKGLIIOLLIAIEKASGVATKDLFDVAGTSGGIIALAILHLSKSM 479
 DB 420 RTHDHLCLDGGGVKGLIIOLLIAIEKASGVATKDLFDVAGTSGGIIALAILHLSKSM 479
 QY 421 RSHDHLCLDGGGVKGLIIOLLIAIEKASGVATKDLFDVAGTSGGIIALAILHLSKSM 480
 DB 421 RSHDHLCLDGGGVKGLIIOLLIAIEKASGVATKDLFDVAGTSGGIIALAILHLSKSM 480

QY 480 AYKRGVFRKQDEVPRGSRPYESGPLEEFKRFEGHTKMTDVRKPKWLTGTLSDROPA 539
 DB 481 AYKRGVFRKQDEVPRGSRPYESGPLEEFKRFEGHTKMTDVRKPKWLTGTLSDROPA 540
 QY 540 ELHIFRNYDAFETVREPRFNOVNLRRPAPQSPDQVWRAARSSGAAPTYFRPGRFLDGG 599
 DB 541 ELHIFRNYDAFETVREPRFNOVNLRRPAPQSPDQVWRAARSSGAAPTYFRPGRFLDGG 600
 QY 600 LLANNPTLDAMTEIHEYNQDLIRKQANVKKLSIVSISGTGSSPOVPTCYDVFRRPSP 659
 DB 601 LLANNPTLDAMTEIHEYNQDLIRKQANVKKLSIVSISGTGSSPOVPTCYDVFRRPSP 660
 QY 660 WEIAKTVFGAKELGRVNVDCCTDPDGR 686
 DB 661 WEIAKTVFGAKELGRVNVDCCTDPDGR 687
 RESULT 5
 ID Q9JUK61 PRELIMINARY; PRT; 807 AA.
 AC Q9JUK61;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE C22+-independent phospholipase A2 long form (Pla2g6 protein).
 GN Name=Pla2g6;
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NTH/Swiss;
 RA Chiu C.-H., Jackowski S.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MNR1; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marins K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Udén T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz U., Myers R.M., Buttefield Y.S.,
 RA Krzywnicki M.I., Skalka U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MNR1; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF259401; AAF72651.1; -
 DR HSSP: Q60726; 10Y3.
 DR MGD; MGI:1859152; Pla2g6.
 DR GO: GO:0003824; F: catalytic activity; IEA.
 DR GO: GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR002641; Patatin.

DR Pfam; PF00023; Ank; 6.
 DR Pfam; PF01734; Patatin; 1.
 DR PRINTS; PR01415; ANKYRN.
 DR PROSITE; PSS0088; ANK_REPEAT; 4.
 DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
 DR ANK repeat.
 KW ANK repeat.
 SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match 90.4%; Score 3272; DB 2; Length 807;
 Best Local Similarity 83.8%; Pred. No. 2,5e-242;
 Matches 622; Conservative 29; Mismatches 35; Indels 56; Gaps 1;

QY 1 MOFGRLVNTFGSVTLFSPNPRVKEVAADYTSRDRVEEGQLIFONTNRTWDCVLY 60
 DB 1 MOFGRLVNTLSSVTNLFSPNPRVKEVSLTDYSSRVEEGQLILQNVSNRTWDCVLY 60
 QY 61 NPNNSGGRFLFQLELEADALVNFQVSSQLPFYESSPOVLTTEVLOHITDLIRNPSW 120
 DB 61 SPNPSGGRFLFQLESEADALVNFQVSSQLPFYESSPOVLTTEVLOHITDLIRNPSW 120
 QY 121 SVNHLAVELGIRCFPHHSRIISCANCAENEBEGTPLHLACRKGDEILVELVOYCHTQMD 180
 DB 121 TVNHLAVELGIRCFPHHSRIISCANSTENEBEGTPLHLACRKGDEILVELVOYCHTQMD 180
 QY 181 VTQYKETEYFHYAVQGDNSQVTLQLGKNAVAGLVNNOGSLTPHLACQKQKQEMRVLL 240
 DB 181 VTQNKETAFHYAVQGDNPQVTLQLGKNAAGLVNNOGSLTPHLACQKQKQEMRVLL 240
 QY 241 LCNARCNINPQNGPYTHSAKFKSQKCAEMTISMDSQIHSKDPYRGA SPLHAKNAEMA 300
 DB 241 LCNARCNINPQNGPYTHSAKFKSQKCAEMTISMDSQIHSKDPYRGA SPLHAKNAEMA 300
 QY 301 RMLLKGCNVNSTSSAGNTALHGVNMRPDCAILVLTGHGANDARGEHNTPLHLAMSK 360
 DB 301 RMLLKGCVDVSTSSSGNTALHVAVMNRPDCAVLTGAGNAGARGEHNTPLHLAMSK 360
 QY 361 DNVEIMKALIVGAEDVTPNDPGETPTFLASKIGK----- 395
 DB 361 DNNEVMKALIVGAEDVTPNDPGETPTFLASKIGK----- 395
 QY 396 ----- 424
 DB 421 VSTEQSGAAATHPLFSLDRTPPAISLNNLEODLMPISRAKPAFLTSSMRBCKSHDH 480
 QY 425 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGSTGGILALAILHKSMAVMRG 484
 DB 481 LCLDGGGVKGLVITQLLIAIEKASGVATKDLFDWVAGSTGGILALAILHKSMAVMRG 540
 QY 485 MYRPMKDEVFRSGRPYSGPLSEFLKKEFGEHTYMTDKRKPMVLTGTLSDRQPAELHLF 544
 DB 541 VYFRMKDEVFRSGRPYSGPLSEFLKKEFGEHTYMTDKRKPMVLTGTLSDRQPAELHLF 600
 QY 545 RNVDAPEYVPERPNCQVNRPRAPQSPDOUVMRAASGGAAPYFRNGSFLGGILLAN 604
 DB 601 RNVDAPEYVPERPNCQVNRPRAPQSPDOUVMRAASGGAAPYFRNGSFLGGILLAN 660
 QY 605 PTLIDAMTEIHEYNODLIRKQGANVKKLSTIVSLGTRSPQVPTCDVFRPSNPWELAK 664
 DB 661 PTLIDAMTEIHEYNODLIRKQGANVKKLSTIVSLGTRSPQVPTCDVFRPSNPWELAK 720
 QY 665 TVFGAKELGKVVVDCCTDPDGR 686
 DB 721 TVFGAKELGKVVVDCCTDPDGR 742

RESULT 6

AAH57209 PRELIMINARY; PRT; 807 AA.
 AC AAH57209;
 DT 02-MAR-2004 (TEMBLrel. 27, Created)
 DT 02-MAR-2004 (TEMBLrel. 27, Last sequence update)
 DE 02-MAR-2004 (TEMBLrel. 27, Last annotation update)
 DE Plazg6 protein.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Hirschhorn S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Sapichstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Tohiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullan S.J.,
 RA Beek S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.T., Skalska U., Smalios D.E., Schmechel A., Schein J.E.,
 RA Jones S.J., Maiz M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057209; AAH57209.1; -
 SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match 90.4%; Score 3272; DB 2; Length 807;
 Best Local Similarity 83.8%; Pred. No. 2,5e-242;
 Matches 622; Conservative 29; Mismatches 35; Indels 56; Gaps 1;

QY 1 MOFGRLVNTFGSVTLFSPNPRVKEVAADYTSRDRVEEGQLIFONTNRTWDCVLY 60
 DB 1 MOFGRLVNTLSSVTNLFSPNPRVKEVSLTDYSSRVEEGQLILQNVSNRTWDCVLY 60
 QY 61 NPNNSGGRFLFQLELEADALVNFQVSSQLPFYESSPOVLTTEVLOHITDLIRNPSW 120
 DB 61 SPNPSGGRFLFQLESEADALVNFQVSSQLPFYESSPOVLTTEVLOHITDLIRNPSW 120
 QY 121 SVNHLAVELGIRCFPHHSRIISCANCAENEBEGTPLHLACRKGDEILVELVOYCHTQMD 180
 DB 121 TVNHLAVELGIRCFPHHSRIISCANSTENEBEGTPLHLACRKGDEILVELVOYCHTQMD 180
 QY 181 VTQYKETEYFHYAVQGDNSQVTLQLGKNAVAGLVNNOGSLTPHLACQKQKQEMRVLL 240
 DB 181 VTQNKETAFHYAVQGDNPQVTLQLGKNAAGLVNNOGSLTPHLACQKQKQEMRVLL 240
 QY 241 LCNARCNINPQNGPYTHSAKFKSQKCAEMTISMDSQIHSKDPYRGA SPLHAKNAEMA 300
 DB 241 LCNARCNINPQNGPYTHSAKFKSQKCAEMTISMDSQIHSKDPYRGA SPLHAKNAEMA 300
 QY 301 RMLLKGCNVNSTSSAGNTALHGVNMRPDCAILVLTGHGANDARGEHNTPLHLAMSK 360
 DB 301 RMLLKGCVDVSTSSSGNTALHVAVMNRPDCAVLTGAGNAGARGEHNTPLHLAMSK 360
 QY 361 DNVEIMKALIVGAEDVTPNDPGETPTFLASKIGK----- 395
 DB 361 DNNEVMKALIVGAEDVTPNDPGETPTFLASKIGK----- 395
 QY 396 ----- 424
 DB 421 VSTEQSGAAATHPLFSLDRTPPAISLNNLEODLMPISRAKPAFLTSSMRBCKSHDH 480
 QY 425 LCLDGGGVKGLIIQLLIAIEKASGVATKDLFDWVAGSTGGILALAILHKSMAVMRG 484


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DB 481 LLLDGGGKGVGLVITQLLIEKASGATATDLPWVAGTGGIALALHLSKSMYMRG 540
QY 485 MYFRMKDEVFRSGRPYSGPLSEFLKKEFGSHNTMTDVRKPKWLTGTLSDROPALHLF 544
DB 541 VYFRMKDEVFRSGRPYSGPLSEFLKKEFGSHNTMTDVRKPKWLTGTLSDROPALHLF 600
QY 545 RNYDAPETVREPERFNQVNLPRPAQPSDQVWPAARSSGAAPTYFRNGRFLDGGILLAN 604
DB 601 RNYDAPETVREPERFNQVNLPRPAQPSDQVWPAARSSGAAPTYFRNGRFLDGGILLAN 660
QY 605 PTIDAMTEIHEYNODLIRKGOANKVKLSIVSLGTRSPQVPTCVDFRPSNPMLAK 664
DB 661 PTIDAMTEIHEYNODMIRKGOANKVKLSIVSLGTRSPQVPTCVDFRPSNPMLAK 720
QY 665 TVFGAKELGKRVVDCCTDPDGR 686
DB 721 TVFGAKELGKRVVDCCTDPDGR 742

RESULT 7
ID PA26_RAT STANDARD; PRT; 751 AA.
AC P97570;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 01-OCT-2004 (Rel. 45, Last annotation update)
DE 85 KDa calcium-independent phospholipase A2 (EC 3.1.1.4) (PLA2) (Cat-PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=PLA2G6;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreatic islets;
RX MEDLINE=97259008; PubMed=9111009;
RA Ma Z., Ramamadhani S., Kempe K., Chi X.S., Ladenson J., Turk J.;
RT "Pancreatic islets express a Ca2+-independent phospholipase A2 enzyme that contains a repeated structural homologue to the integral membrane protein binding domain of ankyrin.";
RT J. Biol. Chem. 272:11118-11127(1997).
RL J. Biol. Chem. 272:11118-11127(1997).
CC -1- FUNCTION: Catalyzes the release of fatty acids from phospholipids. It has been implicated in normal phospholipid remodeling, nitric oxide-induced or vasopressin-induced arachidonic acid release and in leukotriene and prostaglandin production. May participate in fas mediated apoptosis and in regulating transmembrane ion flux in glucose-stimulated B-cells.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a carboxylate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver, heart and skeletal muscle.
CC -1- SIMILARITY: Contains 7 ANK repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; U51898; AAC53136.1; -.
CC HSSP; Q60798; 10Y3.
CC RGD; 628867; Pla2g6.
CC InterPro: IPR002110; ANK.
CC Pfam; PF00023; ANK; 6.
CC PRINTS; PR01415; ANKYRIN.
CC SMART; SM00248; ANK; 6.
CC PROSITE; PS50088; ANK_REPEAT; 4.
CC PROSITE; PS50297; ANK_REGION; 1.

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KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
FT REPEAT 150 180 ANK 1.
FT REPEAT 184 214 ANK 2.
FT REPEAT 218 247 ANK 3.
FT REPEAT 250 280 ANK 4.
FT REPEAT 285 311 ANK 5.
FT REPEAT 315 344 ANK 6.
FT REPEAT 348 377 ANK 7.
FT ACT SITE 464 464 Potential.
SQ SEQUENCE 751 AA; 83582 MW; 393BBADAVFC99B CRC64;

Query Match 90.0%; Score 3257; DB 1; Length 751;
Best Local Similarity 89.7%; Pred. No. 3, 2e-241;
Matches 616; Conservative 29; Mismatches 40; Indels 2; Gaps 2;

QY 1 MGFGRVINTFGSVTLNPSNPRVKEVAVADYSSQVRVBEGLLIPONTNRTWCVLV 60
DB 1 MGFGRVINTVTLSSVTNLFSPNFRKVESLADYVASSRVEEGQLLLQVNASNRTWCCLV 60
QY 61 NPNSSGFRPLQLELEADALVNFHOYSQQLAPYESSPOVLTETVLOHITDLIRHPSK 120
DB 61 SPNPSQDFRLFQLESEADLVNFFQYSSQLPEYSSQVLHVEVLQ-LTDLIRHPSK 119
QY 121 SVANLAVELGIRECFHSHRIISCANCAENEBCGTPHLACRKDGELIVELYQCHTQND 180
DB 120 TVTHLAVELGIRCFHSHRIITCANSTENBEGTPHLACRKDGSELIVELYQCHQND 179
QY 181 VTDYKGEVFNHVAQDQNSQVTLQGRNVAAGLQVNNQGLTPHLACQKQKQVRL 240
DB 180 VTNDKKEVFNHVAQDQNPQVTLQGLKNASAGLQVNNQGLTPHLACQKQKQVRL 239
QY 241 LCNARCNINQPNQYPLHSMKESQKCAEMTISMSQSHSDQBRGAPLHAKNAEM 300
DB 240 LCNARCNINQPGFPLHTAKESQKCAEMTISMSQSHSDQBRGAPLHAKNAEM 299
QY 301 RMLLKSGCVNVSSTASAGNTALHGVNRNRPDCAIVLITGANADAGEHNTPLHLAMSK 360
DB 300 RMLLKSGCVNVSSTASAGNTALHVAVTRNRPDCMVLTITGANAGAGEHNTPLHLAMSK 359
QY 361 DNEVMKALIVFAGVDTNPDEGTEPTPLASKIGK-LQDLMHISRAKRPAILGSRDEK 419
DB 360 DNEVMKALIVFAGVDTNPDEGTEPTPLASKISKQLODIMPYSRAKRPAILGSRDEK 419
QY 420 RTHDHLCLDGGGVKGLIITQLLIEKASGVATKOLPFWVAGTSGGIALALHLSKSM 479
DB 420 RTHDHLCLDGGGVKGLIITQLLIEKASGVATKOLPFWVAGTSGGIALALHLSKSM 479
QY 480 AYVRGMYFRMKDEVFRSGRPYSGPLSEFLKKEFGSHNTMTDVRKPKWLTGTLSDROPA 539
DB 480 AYVRGMYFRMKDEVFRSGRPYSGPLSEFLKKEFGSHNTMTDVRKPKWLTGTLSDROPA 539
QY 540 ELHLFNNYDAPEVREPERFNQVNLPRPAQPSDQVWPAARSSGAAPTYFRNGRFLDGG 559
DB 540 ELHLFNNYDAPEVREPERFNQVNLPRPAQPSDQVWPAARSSGAAPTYFRNGRFLDGG 559
QY 600 LLANNPTLAMEIHEYNODLIRKGOANKVKLSIVSLGTRSPQVPTCVDFRPSNP 659
DB 600 LLANNPTLAMEIHEYNODMIRKGOANKVKLSIVSLGTRSPQVPTCVDFRPSNP 659
QY 660 WELAKTVFGAKELGKRVVDCCTDPDGR 686
DB 660 WELAKTVFGAKELGKRVVDCCTDPDGR 686

RESULT 8
Q6DDKO PRELIMINARY; PRT; 756 AA.
AC Q6DDKO;
DT 01-OCT-2004 (TReMBLrel. 28, Created)
DT 01-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE 01-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_TaxID=8355;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebin T.B., Tomihyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [13]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Klein S., Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC07558; AAH7558.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 756 AA; 84303 MW; C0278741CA52A71 CRC64;
 Query Match 61.1%; Score 2210.5; DB 2; Length 756;
 Best Local Similarity 59.9%; Pred. NO. 8.5e-161;
 Matches 413; Conservative 120; Mismatches 152; Indels 5; Gaps 2;
 QY 1 MGFGRVNTFSQVTLNFSNPFRKVEAVADYTSDDRESGQLLEFQNTPNRTWCVLV 60
 DB 1 MGFGRVNTFSQVTLNFSNPFRKVEAVADYTSDDRESGQLLEFQNTPNRTWCVLV 60
 QY 61 NPNRSGSGFLFQLELADLVNPHQYSSQLPPYESSPOVLTHTVQLHTDLIRNPSW 120
 DB 61 NPNRSGSGFLFQLELADLVNPHQYSSQLPPYESSPOVLTHTVQLHTDLIRNPSW 120
 QY 121 SVNLVLELGRFPHSRIRISNCANCAENEGCGPPLHAKRKDGELVLYOYCHTMD 180
 DB 121 SVNLVLELGRFPHSRIRISNCANCAENEGCGPPLHAKRKDGELVLYOYCHTMD 180
 QY 121 SLHVAVEIGLRKSRFKNGILRSINSTECGSGTPLLACKDGINCLQELVECCARLD 180
 DB 121 SLHVAVEIGLRKSRFKNGILRSINSTECGSGTPLLACKDGINCLQELVECCARLD 180
 QY 181 VTDYKGTVEFVAVOQDNGSVTLQGLRNAAVAGLNOVNNQGLTPHLACQLGKQEMVVL 240
 DB 181 VTDYKGTVEFVAVOQDNGSVTLQGLRNAAVAGLNOVNNQGLTPHLACQLGKQEMVVL 240
 QY 181 IADQNGETVYHHAQONNPRVIELICVPSGVVNHKSNNETPLHVAACRLKTELVLALL 240
 DB 181 IADQNGETVYHHAQONNPRVIELICVPSGVVNHKSNNETPLHVAACRLKTELVLALL 240
 QY 241 LCNARCNIMPNGYPIHSAKFGKCAEMITISMDSCISKCPRRGASFLHAKAEMA 300
 DB 241 LCNARCNIMPNGYPIHSAKFGKCAEMITISMDSCISKCPRRGASFLHAKAEMA 300
 QY 241 RCHARCDIICDQGPPIHTAMKYSQKCEVBAILDVSAQLHAEBPRYATPIHAKAEMA 300
 DB 241 RCHARCDIICDQGPPIHTAMKYSQKCEVBAILDVSAQLHAEBPRYATPIHAKAEMA 300
 QY 301 RMLLKGGCVNNTSSAGNTALHYGVMBNPDCAIVLLTHANNDAREGHNTPLHLSMK 360
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 QY 301 RLIERGCVNNTSCKTLIDPLHIVKDRPEALMAVLLTNVADPVKGEHNTPLHLSMK 360
 DB 301 RLIERGCVNNTSCKTLIDPLHIVKDRPEALMAVLLTNVADPVKGEHNTPLHLSMK 360

QY 361 DNEMIKALIVFGAEVDPNDPGETPTFLASKIGK-LQDLMLISPRARK----PAFLGSM 415
 DB 361 DNEMIKALIVFGAEVDPNDPGETPTFLASKIGK-LQDLMLISPRARK----PAFLGSM 415
 QY 361 DQELIKALMVFAVDVQGNHDPGETPTGLAARSXKGFDPVYVSTALSGMLVQDVPDR 420
 DB 361 DQELIKALMVFAVDVQGNHDPGETPTGLAARSXKGFDPVYVSTALSGMLVQDVPDR 420
 QY 416 RDEKRTDHLLCLDGGVKGKLLIQLLAIKASGVATDLPFWAGTSGGILALAILH 475
 DB 416 RDEKRTDHLLCLDGGVKGKLLIQLLAIKASGVATDLPFWAGTSGGILALAILH 475
 QY 421 EDGLRKYDRLCLDGGGIRGLVLMQLLIAEKAGAPRIELFPWVGSTSGGILALAIYH 480
 DB 421 EDGLRKYDRLCLDGGGIRGLVLMQLLIAEKAGAPRIELFPWVGSTSGGILALAIYH 480
 QY 476 SKSMVAWRGVPMKQEVFGSRPYESGPLSEPLKXEPGHTMTQVRPKVLTGLTSD 535
 DB 476 SKSMVAWRGVPMKQEVFGSRPYESGPLSEPLKXEPGHTMTQVRPKVLTGLTSD 535
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 DB 481 GPMESVRCLYFMKQEVFGSRPYESGPLSEPLKXEPGHTMTQVRPKVLTGLTSD 540
 QY 536 RQPAELHLPFANYDAPETVREPRNQVNLPPAQPSPDOLVWRAARSSGAAPYFRPGR 595
 DB 536 RQPAELHLPFANYDAPETVREPRNQVNLPPAQPSPDOLVWRAARSSGAAPYFRPGR 595
 QY 541 RHPAELHLPFANYDAPETVREPRNQVNLPPAQPSPDOLVWRAARSSGAAPYFRPGR 600
 DB 541 RHPAELHLPFANYDAPETVREPRNQVNLPPAQPSPDOLVWRAARSSGAAPYFRPGR 600
 QY 596 LDGGLANPTLDAMEIHEYNODLRKQANKVKLSTVLSGTGRSPQVPTCVDR 655
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 QY 601 LDGGLSNPTLDAMEIHEYNODLRKQANKVKLSTVLSGTGRSPQVPTCVDR 660
 DB 601 LDGGLSNPTLDAMEIHEYNODLRKQANKVKLSTVLSGTGRSPQVPTCVDR 660
 QY 656 PSNPWEIAKTVFGAKELGKVVVDCCTDPG 685
 DB 656 PSNPWEIAKTVFGAKELGKVVVDCCTDPG 685
 QY 661 PSNPWEIAKTVFGAKELGKVVVDCCTDPG 690
 DB 661 PSNPWEIAKTVFGAKELGKVVVDCCTDPG 690
 RESULT 9
 ID 06NRYO PRELIMINARY; PRT; 818 AA.
 AC 06NRYO;
 DT 05-JUL-2004 (TREMblrel. 27, Created)
 DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMblrel. 27, Last annotation update)
 DE Zgc:77476.
 GN Name=zgc:77476;
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebin T.B., Tomihyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC067375; AAH67375.1; -;
 DR InterPro: IPR002110; ANK.
 DR InterPro: IPR002641; Patactin.
 DR Pfam: PF00023; Ank; 6.

DR Pfam; PF01734; Paracitin; 1.
 DR PRINTS; PR01415; ANKRYIN.
 DR SMART; SM00248; ANK; 6.
 DR PROSITE; PSS0086; ANK_REPEAT; 4.
 DR PROSITE; PSS0297; ANK_REGION; 1.
 DR ANK repeat.
 SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8BA9 CRC64;

Query Match 54.6%; Score 1977.5; DB 2; Length 818;
 Best Local Similarity 50.5%; Pred. No. 7,7e-143;
 Matches 380; Conservative 122; Mismatches 182; Indels 69; Gaps 4;

QY 1 MOFGRLVNTFGSVTLFNSNPRFVKEVAADYSSDRVEEGQLIFONTPTNTMPCVLV 60
 DB 1 MOFLGRILDTVSSVSLFSPNPRVRYDVQSLDNGKILHQEGRLALYRQOQSMDCLL 60
 QY 61 NPNRSQGFRLQLBLEADALVNFHOYSQSLPFYESSPOVLTHTVLQHLTDLRNHPW 120
 DB 61 CPSPSVLALRMFQVASEBDMNMFQYALKLPFYEMLRPPLKPEMLQPIVDCVRNHPW 120
 QY 121 SVNHLAVELGIRECFHSHRIISCANCAENBEGCTPLHLARKGDEILVELVOYCHTMD 180
 DB 121 SSNHLAVDTGLRDLCKNTYLSQWN-SRDAQGTPLHLACERGDVGCVRLEECQARTD 179
 QY 181 VTDYKGETVFNHVAVOGDSQVOLLGRNNAVAGLQVNNQGLTPHLACQLGKQEMRYVL 240
 DB 180 VKDRNGETPMHCAKQDSALITVELCAQLCAGNELNAAGETPMHLACRGRVGVKGL 239
 QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIIISDSSQHSKDPYRGASPLHAKNAEMA 300
 DB 240 AGGARDIDMNGNFPHTAMKFSKSCAAILSSPNQLAEDPVYGGTFLHAKNAEMS 299
 QY 301 RMLIKGCVNNTSSAGNTALHVGWNRNPDCAIVLITGANDARGEHNTPLHLAMSK 360
 DB 300 RLILDRGCNNVYLSKTSGESPLHLITKRGREAAATLLITGADANIRQDNTALHLAMKL 359
 QY 361 DNVEMLKALIVFGAEDVTPNDPFGETPTFLASKIGK----- 395
 DB 360 DNNDLIKALNVFGADVEANDVGETPGLIARTSKSNRYKLYLMLCISGVVERCHPSSLN 419
 QY 396 -----LQDLMHIS---RARKPAFLGSMDEKRTDHLCLDGGVYKGLI 437
 DB 420 SPTHSLRKAPRPGIGFDIMQVAVAVTAMSRGFVEADGKLTGNKMDRLCLDGGGIGLV 479
 QY 438 IIOGLLAIRKASVATKDLVDWVAGTSGTGLTALILHSSAMVYRGMTFRMDEVPFSG 497
 DB 480 LIOLLAIRKASRPIRELFDWVSGTSGTGLTALILHSGSMBYLRCLYFRMKEOVFKGS 539
 QY 498 RPYESGPLEBFLKREGEHTRKMTDYRKRYMLTGSTSDROPALHLFRNYDARETVREPR 557
 DB 540 RPYESGPLEBFLKREGEHTRKMTDYRKRYMLTGSTSDROPALHLFRNYDARETVREPR 559
 QY 558 FNVGNVLRPPAP-----SDQLVWRARSSGAAPTYFRPN 592
 DB 600 YKSTATFQPLTVFQGWEDDLVLVGYTRPPRKRKRYTDEQJLWRRARSSGAAPTYFRPN 659
 QY 593 GRFLDGLLANNPTLDAMTEIHEYNODLIRKQANVYKSLIYVSLGTGSPPOVPTCV 632
 DB 660 GRFLDGLLANNPTLDAMTEIHEYNODLIRKQANVYKSLIYVSLGTGSPPOVPTCV 719
 QY 653 VFRPSNPWELAKTVFGAKELGKXNVVDCCTPDG 685
 DB 720 VFRPSNPWELAKTVFGAKELGKXNVVDCCTPDG 752

RESULT 10

AAH67375 PRELIMINARY; PRT; 818 AA.
 AC AAH67375;
 DT 24-MAY-2004 (Tremblrel. 27, Created)
 DT 24-MAY-2004 (Tremblrel. 27, Last sequence update)
 DT 24-MAY-2004 (Tremblrel. 27, Last annotation update)
 DE Zgc:77476.

GN ZGC:77476.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_Taxid=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Scheiner C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Caaveira T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Wang C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murray D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maitra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC067375; AAH67375.1; -
 SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8BA9 CRC64;

Query Match 54.6%; Score 1977.5; DB 2; Length 818;
 Best Local Similarity 50.5%; Pred. No. 7,7e-143;
 Matches 380; Conservative 122; Mismatches 182; Indels 69; Gaps 4;

QY 1 MOFGRLVNTFGSVTLFNSNPRFVKEVAADYSSDRVEEGQLIFONTPTNTMPCVLV 60
 DB 1 MOFLGRILDTVSSVSLFSPNPRVRYDVQSLDNGKILHQEGRLALYRQOQSMDCLL 60
 QY 61 NPNRSQGFRLQLBLEADALVNFHOYSQSLPFYESSPOVLTHTVLQHLTDLRNHPW 120
 DB 61 CPSPSVLALRMFQVASEBDMNMFQYALKLPFYEMLRPPLKPEMLQPIVDCVRNHPW 120
 QY 121 SVNHLAVELGIRECFHSHRIISCANCAENBEGCTPLHLARKGDEILVELVOYCHTMD 180
 DB 121 SSNHLAVDTGLRDLCKNTYLSQWN-SRDAQGTPLHLACERGDVGCVRLEECQARTD 179
 QY 181 VTDYKGETVFNHVAVOGDSQVOLLGRNNAVAGLQVNNQGLTPHLACQLGKQEMRYVL 240
 DB 180 VKDRNGETPMHCAKQDSALITVELCAQLCAGNELNAAGETPMHLACRGRVGVKGL 239
 QY 241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMIIISDSSQHSKDPYRGASPLHAKNAEMA 300
 DB 240 AGGARDIDMNGNFPHTAMKFSKSCAAILSSPNQLAEDPVYGGTFLHAKNAEMS 299
 QY 301 RMLIKGCVNNTSSAGNTALHVGWNRNPDCAIVLITGANDARGEHNTPLHLAMSK 360
 DB 300 RLILDRGCNNVYLSKTSGESPLHLITKRGREAAATLLITGADANIRQDNTALHLAMKL 359
 QY 361 DNVEMLKALIVFGAEDVTPNDPFGETPTFLASKIGK----- 395
 DB 360 DNNDLIKALNVFGADVEANDVGETPGLIARTSKSNRYKLYLMLCISGVVERCHPSSLN 419
 QY 396 -----LQDLMHIS---RARKPAFLGSMDEKRTDHLCLDGGVYKGLI 437
 DB 420 SPTHSLRKAPRPGIGFDIMQVAVAVTAMSRGFVEADGKLTGNKMDRLCLDGGGIGLV 479

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QY 438 IIOIIAIEKASGATKOLFDPVAGTSTGGILALAIHLSKMAVMRGMYPRMKDEVERGS 497
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 480 LIIILLALIEGAEAPRIREFLDWISGCTSGIILALIVHSGSMYELKCLYRMEQVFKGS 539
QY 498 RPYESGPLEEELKREFEGENTKMTDVKKPKVMTLGTSLDRQPAELH.FRNDAEIVREPR 557
Db 540 RPYESGPLEEELKREFEGENTKMTDVTHPRVMTSVLADRHGELH.FRNDDPPLAQDP 599
QY 558 FNNNNLRRPAOP-----SPOLVWRARSSGAAPTYFRPN 592
Db 600 YKSTATFQPLTVQGWEDDLIVGYTRPRKRKYTDEQLVWRARSSGAAPTYFRPN 659
QY 593 GRELDGGLANPPLDAMTEIHEYNODLIRKGOANKVKLSIVSLGTSRPOVPYTCVD 652
Db 660 GRLLDGLANPPLDAMTEIHOENKALKRGDEDEVTRLGVVSLGTSRPOVAVNSVD 719
QY 653 VFRSPNPWEIAKTVFGAKELGKRVVDCCTDPDG 685
Db 720 VFRSPNPIELAKTVFGVKELGKMLVDCCTDSG 752

RESULT 11
QY 070201 PRELIMINARY; PRT; 879 AA.
AC 070201;
Dt 01-MAR-2004 (T-EMBLrel. 26, Created)
Dt 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
Dt 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE EBI3359 (Fragment).
GN Name=eb1G3359; ORFNames=ENSANG0000002698;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Mecoptera; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
   EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
   preliminary data.
CC EMBL: AAAB0106968; EMBL3225.1;
CC GO: GO:0003824; F: catalytic activity; IEA.
CC GO: GO:0045735; F: nutrient reservoir activity; IEA.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000560; HisAc_phapthee.
DR Pfam: PF00023; ANK. 6.
DR PRINTS: PR01734; Patatin. 1.
DR PROSITE: PSS0088; ANK_REPEAT. 3.
DR PROSITE: PSS0297; ANK_REPEAT_REGION. 1.
DR PROSITE: PSS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KM ANK repeat.
FT NON_TER 1
FT NON_TER 879
SQ SEQUENCE 879 AA; 96484 MW; 3491E003CF637188 CRC64;

Query Match 32.2%; Score 1164; DB 2; Length 879;
Best Local Similarity 32.1%; Pred. No. 2.8e-80;
Matches 260; Conservative 134; Mismatches 269; Indels 146; Gaps 9;
QY 21 PFVYKAVADVYSSDRVREEGQILFQNTPNR-----TWDCLVAPRNS--OSGRLLFQ 73
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Db 11 PNTVOEAKESYINLPVLOQNESMRLEFAPNPNBDKLVYEIILERHSSTINTSYSLR 70
QY 74 LELEADALVHFHGYSSQLPFYESSPOVLTEVLOHLLDIRHPSVSHALVELGIRE 133
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Db 71 ATTQSAHEEFKEFPHQRLPELVKIVREMYINGLQKCLDVLDINPSSLSLHVAVFNYLTD 130
QY 134 CFHHSRIISCANCAENEGCTPLHLACRKDGELVELVOYCHTQMDVDTYKGETVFHVA 193

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Db 131 YISNPSIIDFLVYAESEEMKTEPLOVAVKANNEFVALLQSNQCNEHLDKNSNSVFHVA 190
QY 194 VQDGNQVQLQILGRNAVAGLGNVNGQLTPRLHACQLGQKQEMVRLVLCNARCNVPG 253
Db 191 A-STTKEMINMLANSTSVLNHCNIDGYTPHLACLADPDCVALLGADTNKRA-RG 248
QY 254 YPIHSAKKSOKGCAEMIISMDSQIHSKDPYGSPLHMAKVAEMARMILKRGCVNST 313
Db 249 AGTSYSKSLPSSNVADFLVS-NPNKLFQDMKGCGTFLHSSSREVLANSIERGCDVNLV 307
QY 314 SSAGNTALVGVKRNRPDCALVLLTNGANADARGEHNTPLHLANSKDNVEIKALIVRG 373
Db 308 NENGQPLHVMVAKRDLCECVALLAHDAEIDVDVNSGNTPLHIAVEKKLPIVQCLVFG 367
QY 374 AEVDTPNDGERTPL-----ASKIGLQDLNH----- 401
Db 368 ADFNKKNKDGKTPRLHVGKDSGSKSMILYILHSYGAKRCEPKSKCPGCCAAGTYNG 427
QY 402 -----ISRA 405
Db 428 IPPAQPETTEGRENHIOQLARTTTSKHSNVSPLSINTIRATIPERERPEVKTVDVSG 487
QY 406 RKPAFLGSM-----RDEKRTHD----- 423
Db 488 RKGSAMMDALLSMFNSKVEAASKPTSTSSSLKXCAGSGQRTDSRRSSCEAGSGE 547
QY 424 -----HLICLDGGGKGLIIOIIAIEKASGATKOLFDPVAGTSTGGIILALAIHSG 477
Db 548 SYNGRRLCLDGGGKGLVLAOMLEIENLAQTPVHLFDVIAGSTGGIILALAIHSG 607
QY 478 SMAVMGMYPRMKDEVFRSGRPYESGPLEEFLKREFEGENTKMTDVKKPKVMTLGTSLDRQ 537
Db 608 TMOGCKCLVLRMKDQAFVGSRPYPSPQLETVLKEGGEFTVMSDIGHPLMTVGVVADR 667
QY 538 PAELH.FRNDAEIVREPRFNONVNLRRPAQSDQLVWRARSSGAAPTYFRPNRFLD 597
Db 668 PVNLHLFRVYEAASDLISIVTPSNRNGQPPPESEQLVWRARATGAASYRFAFGRLD 727
QY 598 GGLANPPLDAMTEIHEYNODLIRKGOANKVKLSIVSLGTSRPOVPYTCVDVFRPS 657
Db 728 GGLANPPLDAMTEIHEYNALHLYIGRASVAVSVSLGTGLTPVDLKEIVDFRD 787
QY 658 NPWEIAKTVFGAKELGKRVVDCCTDPDGR 686
Db 788 SIWATAKVAVGISTITLVDQATASDR 816

RESULT 12
QY 09VT60 PRELIMINARY; PRT; 877 AA.
AC 09VT60;
Dt 01-MAY-2000 (T-EMBLrel. 13, Created)
Dt 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
Dt 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE CG6718-PA.
GN ORFNames=CG6718;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amandick P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Chame M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Avril J.F., Agdayani A., An H.U., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Bayraktoglu L., Beasley E.M.,

```

RA Beeson A.V., Benoe P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borczyk D., Botchan M.R., Bouck J.J., Brokstein P., Brotlier P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA de Pallos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabriellian A.S., Gary N.S., Gelbart W.M., Glasser K.,
RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegami C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Kechum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laek P., Lei Y., Levinsohn A.A., Li U., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Milneron D.,
RA Merklov G., Mishina N.V., Mobarry C., Morris J., Moshtefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murzy D.M., Nelson D.L.,
RA Neilson D.R., Neilson K.A., Nixon K., Nusken D.R., Paley J.M.,
RA Palazzo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Silden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stepieton M., Strong R., Sun E.,
RA Svirskaas R., Teeter C., Turner C., Venker E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassenaar D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodagert, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yen R.F., Zaveri J.S., Zhao N., Zhang G., Zhao Q., Zheng X.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*";
RL Science 287;2185-2195(2000).
[2]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Centiner S.R., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Murry D.M., Nelson C.R.,
RA Paley J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.U.,
RA Svirskaas R., Taber P.E., Wan K., Stepieton M., Sutton G.G., Venker C.,
RA Weinstein G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
melanogaster euchromatic genome sequence";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Caminker S.B.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
a genomic perspective";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22426063; PubMed=12537572;
RA Hidera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Madresky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Betencourt B.R., Centiner S.B., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.B.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
systematic review";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
RN
RP SEQUENCE FROM N.A.
RG FLVBASE;
RL Submitted (SEP-2002) to the EMBL/GenBank/DDB databases.
[6]
RN
RP SEQUENCE FROM N.A.
RG FLVBASE;
RL Submitted (MAR-2004) to the EMBL/GenBank/DDB databases.
DR EMBL; AF003550; AA050194.3; -.

[illegible]

DB 790 TAKLAVGISTGNLVDQATCSGDR 814

RESULT 13

AAFS0194 PRELIMINARY; PRT: 877 AA.

AC AAF50194;

DT 01-APR-2004 (TREMBlrel. 27, Created)

DT 01-APR-2004 (TREMBlrel. 27, Last sequence update)

DE CG6718-PA.

GN CG6718.

OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

OX

RN

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L., Abail J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P., Burtis K.C., Buesam D.A., Butler H., Cadiou E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Deodson K., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M., Durbin K.J., Evans G.L., Fouts D.E., Gaitanaris G., Garg N.S., Gerhart M., Glasser K., Goad C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glesner A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hottel D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Jaffe J.M., Kalush F., Karpen G.H., Ke Z., Kenton J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laoko P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Matcel B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Stryer E., Spradling A.C., Stempleton M., Strong R., Sun B., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wasserman D.A., Weinstein G.M., Wu D., Yang S., Yao Q.A., Ye J., Williams S.M., Woodage J., Worley K.C., Wu D., Yang S., Ye Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN

RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R., Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.B., Wan K., Stempleton M., Sutton G.G., Venter C., Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Miara S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminick J.S., Millburn G.H., Prochman S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O., Stempleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;

RT "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN

RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;

RA Celniker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin: a genomic perspective.";

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN

RP SEQUENCE FROM N.A.

RA FlyBase;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RN

RP SEQUENCE FROM N.A.

RA FlyBase;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AEO03550; AAF50194.3; -

DR FlyBase; FBgn0036053; CG6718.

SQ SEQUENCE 877 AA; 96863 MW; C9DC2CD6C282869B CRC64;

Query Match 32.1%; Score 163.5; DB 2; Length 877;

Best Local Similarity 31.9%; Pred. No. 3e-80;

Matches 257; Conservative 155; Mismatches 248; Indels 165; Gaps 12;

DB 17 LFSPNPRVKEVNAADVTSSPRVREBQGLTFQTPRTRTMDVLRNRSQSGRLFQLEL 76

40 LFAFPP-----NSSNEKAVVEILLQRTSD-----SNTSFLRSPV 78

DB 77 EALALVNFHOSSQLPFRESSPOLVTEVLQHLTDLIRNPSVAHLAVELIGRECFH 136

79 QQAERFNAFLQRLVFVSVIVKEVYNNVNGQLQACALADNPWTSLHLAYFNVLVDYIS 138

DB 137 HSRILSCANCAENEBECSTPLHLACRKGDELVELVQVCTQMDVTDTYKGVTFHYAVQG 196

139 NPKMLQCPDADATLMSFPQLAIKQGHMEVYKALLPL--SKLEHNDINSNSVFHFAA-S 195

DB 197 DNSQVQLQGRNAVAGLNVNNGQLPRHLAQLGQEGQEMVRVLLLCNARCNMGPRGYR 256

196 TTYEILNLIIDKSTVNLNHLNSDGYTPRLHACADLPENVKALLAGANVL--NAKDI 252

DB 257 HSAKFSQKCAEMIISMSQIHSKDPYRGASPLHMAKVAEMARMILKRCNVNSTSSA 316

253 RKYYKTSAPRTTSSPLRTNVSKLYTQDMKYGGRPLMCSRETLHLLIMEGCVNNTNFD 312

DB 317 GNTALHGVNRNFPDCAVLVLTGANAADAGEHGTPLHLANSKDVNEMIKALIVGAEV 376

313 GRTALHYVVARNFECVTLADAEIDVLKDKGNALHIAIEKRLVPIVQCLVVEGCDI 372

DB 377 DTENDFGEP-----TFASKIG----- 394

DB 373 NLNKKQKTPRHVNGVNDASGNKDEILYLHSHVGRCKDTGSKPCPGCAKNYNGIRP 432

DB 395 -----KLQDLMIHSR-----ARKPAFI----- 411

DB 433 EAPESVQGRHITHMLATTSRQMGFLVAAAAGILEKQAPKAPVVDTEKELKQGSIM 492

DB 412 -----LGSNR-----DEKTHDH 424

DB 493 DALLGFTTKVNADEMKEKNSDSLASGQKSAVSSPEQLPSPTPIAAIEGDKPYGRGR 552

DB 425 LLLGDSGVKGLIIQLLAIIEKASGVATKDLFDWVAGTSTGTLALAIHSSSMVMNG 484

Db 553 LUCIDGGGIRGLVLYOMLEIEKLSRTPIIHFMDIAGTSTGILLALALGCKTMRQCMG 612

Qy 485 MYRMDEVRGRGPRPESGLESFLEKRESEHTRKTDVREPKMLTGLSDROPALHLF 544

Db 613 LYLKMEKOCQVGRSPNSEFESILKDMGEFVMMMDIKPKKIMVGVMDRPRVLIHLF 672

Qy 545 RNDVARETVR---EPRFNQVNNLRPPAPQSDOLVWRAARSGAAPYFRNGRFLDGLL 601

Db 673 RNTTASDLIGITYTPINNRI---PPQSEQLVWRAARSGAAPYFRNGRFLDGLL 729

Qy 602 ANNPITDAMTEIHEYNODLIRKQANKVKLSIVSLGTSRSPQVPTCVDFRPSNPM 661

Db 730 ANNPITDAMTEIHEYNMALLASAGRESEDAIVSVVMSLGTHIIVTELKOIDVFRPSIND 769

Qy 662 LATTVGAKELGMVVDCTDPRGR 686

Db 790 TATLAVGISTGIMLVDAQTCSDGR 814

RESULT 14

ID 07KUD4 PRELIMINARY; PRT; 887 AA.

AC 07KUD4; 05-JUL-2004 (T-EMBLrel. 27, Created)

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE CG6718-PB (CG6718-pc).

GN ORFNames=CG6718;

OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

NCBI_taxid=7227;

OK [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10711132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abil J.F., Aghayani A., An H.J., Andrews-Pfannkoch L., Basley E.M.,

RA Ballou R.M., Beasly A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Maye A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,

RA Foslter C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibbegan C.,

RA Jalali M., Kalush F., Kapran G.H., Ke Z., Kemison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasbo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mpherson D.,

RA Merkulov G., Misha N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclad J.M.,

RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Slater B., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter J., Wang A.H., Wang X.,

RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodruff, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195 (2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Paclad J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

RT melanogaster euchromatic genome sequence."

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.,

RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomic perspective."

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Beitzelcort B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

RT systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [5]

RP SEQUENCE FROM N.A.

RG PLYBASE;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RG PLYBASE;

RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: AEO03550; AAN11936.2; -.

DR InterPro: IPR002110; ANK.

DR InterPro: IPR002641; Patatin.

DR Pfam: PF00023; ANK; 5.

DR Pfam: PF01734; Patatin; 1.

DR PRINTS: PR01415; ANKYRIN.

DR SMART: SM00248; ANK; 6.

DR PROSITE: PS50088; ANK_REPEAT; 3.

DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.

DR ANK repeat.

SW SEQUENCE 887 AA; 97776 MW; 1387084E7265B85 CRC64;

Qy Query Match 32.1%; Score 1163.5; DB 2; Length 887;

Db Best Local Similarity 31.9%; Pred. No. 3.1e-80;

Matches 257; Conservative 135; Mismatches 248; Indels 165; Gaps 12;

Qy 17 LFNPRVKEVAVADYSDRVEEGQLLIFQTPRTMDVNLNPNRSGQGRFLQLEL 76

Db 50 LFPAPF-----NSSNEKRAVVEILLQRTSD-----SWTTSLSKRSVP 88

Qy 77 EADALVPHQYSSQLLPYESSPVOLATEVLTDLINHPGWSVAHLAVELGIRECFH 136

Db 89 QGAERERFNAFLQRLPVSIVSEYVNVNGLQACDALADNSPWTSHLIAVFNLDVYLS 148

Qy 137 HSRILICANCAENEBECTPLHLACRGDEILVELVQYCHTQMDVTDYNGEYFHYAVOG 196

Db 149 NPMPLQCVQADADATLMSPPQALIKGHNEMVVALPL--SKLEHLDINSNSVFHYAA-S 205

Qy 197 DNSQVQLLRNNAVAGLQVNNNGLTPHLACQIGKQENVRVLLCNARCNIMGPGYPI 256

DB 206 TTKEIINLIIDKSTVNILNHLNSDGYTPYTHVACIADCKPENYKALLLAGANVL---NAKDI 262
 QY 257 HSAMKPSQKCAEMITISMDSSOHSXDPKRGASPLHWAKVEMARMLTKRCNVNSTSSA 316
 DB 263 RKVYKTSAPTTVSFLRTNVSKLYTQDMKGGTPLHMCSSRETLHALIMGCVNATNFD 322
 QY 317 GNTALHVGWRNRFDCALVLLTGANADARGHNTPLHLAMSKDNVEMIKALIVEGAEV 376
 DB 323 GRTALHVMVARNRNFECVTLTADAEIDVDKDNALHIAIEKKVLPYIOGLVRFCDI 382
 QY 377 DTNDNGERTP-----TFLLASKIG----- 394
 DB 383 MLNKKQCKTPRHVNGDASGNKODEILYILHSVGAKCKDGTGSKCPGCAKNYNGIRP 442
 QY 395 ----KLQDMLHISR-----ARKPAFI----- 411
 DB 443 EABESVQRHIEHMLATTSRQMMGGFGLNAAANGILEKQPAQKPVVDTREKLGOSIM 502
 QY 412 -----LGSNR-----DEKRTDHI 424
 DB 503 DALLGFTTKVNADEMCKENSSDSLASQKSNVSPQLPSPPIAIEIGDKPYGRGR 562
 QY 425 LCLDGGGVKGLIITQILLIIEKASGVATKDLFDWAGTGTGGLALALHKSMAVMRG 464
 DB 563 LCLDGGGRGLVGVQMLLEIKLSRTPIIHMFDMWAGTGTGGLALALGCKTMCQMG 622
 QY 485 MYFRMKDEVFRSGPYESGPLEEFLEKREFGHTMTDVRKPKYMLTGLSDROPAELHLF 544
 DB 623 LYIKMEQCVSGRPNSSEFSLKDNLGEFNMVMDIKPKIMVTCVMDKRPVDLHLF 662
 QY 545 RNYDAPETVR--EPRENQNVNLRPPAPSDQVLWRPARRSGAAPYFRPNGRFLLDGLL 601
 DB 683 RNTYSASDILGIVTPINNRI---PPQPSQGLVWRAPARATGAAPSYFRAFGFLLDGLI 739
 QY 602 ANNPPTDAMTEIHENYODLIRKQANVKKLSIVSGTSGRSQVPTVCVDVRRSPNWE 661
 DB 740 ANNPPTDAMTEIHENYNALRSAGRESAIVSVMSLGTGHIPTVELKDIDVRRPESIMD 799
 QY 662 LAKTVEGAKELGKVVVDCCTDPDGR 686
 DB 800 TALTAVGISTIGLVLDQATCSQGR 824
 RESULT 15
 AANI1936 PRELIMINARY; PRT; 887 AA.
 AC AANI1936;
 DT 01-APR-2004 (TEMBLrel. 27, Created)
 DT 01-APR-2004 (TEMBLrel. 27, Last sequence update)
 DE 01-APR-2004 (TEMBLrel. 27, Last annotation update)
 GN CG6718-PB.
 OS *Drosophila melanogaster* (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; *Drosophila*.
 NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang M., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,
 RA Abryl J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Bevo P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Borzhan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fessler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kul D., Lai Z.,
 RA Laske P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Miliutina N.V., Mobarry C., Morris J., Mosher A.,
 RA Mount S.M., Moy M., Murphy E., Murphy L., Murry D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,
 RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Stroup R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muray D.M., Nelson C.R.,
 RA Geolb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Beltencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426071; PubMed=12537574;
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AEO03550; AANI1936.2; -
 SQ SEQUENCE 887 AA; 97778 MW; 1387084E7265BEE5 CRC64;
 Query Match 32.1%; Score 1163.5; DB 2; Length 887;
 Best Local Similarity 31.9%; Pred. No. 31e-80;
 Matches 257; Conservative 135; Mismatches 248; Indels 165; Gaps 12;

| | | | |
|----|-----|---|-----|
| Qy | 17 | FESNFERKEVAVADYDTSDDRREBQQLIFONTPRRTDVCVLRNRSNOSGRLEQLEH | 76 |
| Dh | 50 | LFAPPE-----NSSNEKGAVEYELLQAPTS-----SNTTSELSRSP | 88 |
| Qy | 77 | EADALVNFHVSQQLPPESSPOVLHTEVLOHLDLIMHPSWVAHLAVEIGRECFH | 136 |
| Dh | 89 | QOEAEERNAPLQRLPVFVSIKEYYNVNGLOXACDALNDPSWTLSHLIAVFNLDVYS | 148 |
| Qy | 137 | HSRIISCANCAENEGCTPPLHACRKGDEILVELYQYCHTQMDVTDYKGETYFHHAVQG | 196 |
| Dh | 149 | NPKMLQCVDOADPAATLMSFPOLAIKQGHMEWYKALLPL--SKLEHLDINSNSVFHYAA-S | 205 |
| Qy | 197 | DNSOVLTLGNAVAGLNVNNQGLTPHLHACLOLGOEWVRYVLLCNARCNIMPGYPI | 256 |
| Dh | 206 | TTKEIINIILDKSTYVNLHNSDGTPTPLVACLADKPEVNAKALLAGANVL--NAKDI | 262 |
| Qy | 257 | HSAMFQSKGCAEMIISMSQIHSKDPYGYASPLHMAKNAEMARMILKRCGNVNSTSA | 316 |
| Dh | 263 | RKVYXTSAPPTVVSFLRTVNSKLYTQDMKYGGTPLHMCSSRETLHALIMEGCVNATNFD | 322 |
| Qy | 317 | GNTALHVGVMRRFPICALVYLLTHGANADARGEHNTPLHLAMSKDNVEMIKLLIVGAV | 376 |
| Dh | 323 | GRTAHVAVARRFECVYLLLAHDAEIDVLDKGNALHIALERKLVPIVQCVLVEGDI | 382 |
| Qy | 377 | DTPNDFGPT-----TFLASKIG----- | 394 |
| Dh | 383 | NLKNXDGKTPRMVGNNDASGNDDDELTYLHVSGARCRDGTSGKPCPGCAKNKNVGIIP | 442 |
| Qy | 395 | ---KLQDLMIHSR-----ARKPAFI----- | 411 |
| Dh | 443 | EAPESVEOREHIEHMLATTSRQMGGFLNAANGILEKQOPAKPVPVVDEKELKQSIM | 502 |
| Qy | 412 | -----LGSMB-----DEKTHDH | 424 |
| Dh | 503 | DALGMFTTKNADEMKKENSDDSLASGOKSAVSSPEOLPSTSPIAIEIGDKPYGRGR | 562 |
| Qy | 425 | LLCLDGGGVKGLIITQLLAIKASGVATKDLFDVAGTSTGGIILALILHKSMAVMRG | 484 |
| Dh | 563 | LLCLDGGGIRGLVQMLLEIKELSTPIIHMDWIAGTSTGGIILALDLCGKTYMQCMG | 622 |
| Qy | 485 | MYFRKADVEVFRSGRPYESGPLEBEFLKREGEHNTKOTDVAKPKMMLTGLSLDRPAELHF | 544 |
| Dh | 623 | LYLBMKEQCFVSGRPNSEFFESILKDNJGEEFVWMDIKRPKIMVGVNADRPVLDLHF | 682 |
| Qy | 545 | RNYDAPEYR---BPRFNQNVMLRPAOPSDOLVMPAARSSGAAPYFRNGRFLDGLL | 601 |
| Dh | 663 | RNYTSASDLGLVTPINNRT---PPQOSEQOLVMPAARATGAAPSYFRAFGFLDGLI | 739 |
| Qy | 602 | ANNPTLDANTEIHEYNOULIRKQANKVKKLSTIVSLGTGRSDQVYTCVDFRPSNPMW | 661 |
| Dh | 740 | ANNPTLDANTEIHEYNMALRSAGRESEALPVSVMSLGTGHIPTVELKQDIDVERPSIWD | 799 |
| Qy | 662 | LAKTVFGAKELGKRMVDDCTPDGR | 686 |
| Dh | 800 | TAKLAVGISTIGNLVDOATCSGGR | 824 |

Search completed: December 15, 2004, 13:13:14
Job time : 153.609 secs

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XX SQ Sequence 687 AA;

Query Match 100.0%; Score 3620; DB 2; Length 687;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFGRLVNTFSGVTNLFSNPFPRKEVAADYTSDDREEGQLIFONTPNRTWDCVLV 60
 DB 1 MOEFGRLVNTFSGVTNLFSNPFPRKEVAADYTSDDREEGQLIFONTPNRTWDCVLV 60

QY 61 NPNSSGFRLLFQLEADALVNFHOYSSQLPFYESSPOVLTEVLOHTLDIRNHPSW 120
 DB 61 NPNSSGFRLLFQLEADALVNFHOYSSQLPFYESSPOVLTEVLOHTLDIRNHPSW 120

QY 121 SVNHLAVEIGIRCEFHHSRIISCANCAENEBEGCTPLHLCKRGDGLVLELVQYCHTQMD 180
 DB 121 SVNHLAVEIGIRCEFHHSRIISCANCAENEBEGCTPLHLCKRGDGLVLELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLLQLRNNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 DB 181 VTDYKGETVFHYAVQGDNSQVLLQLRNNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240

QY 241 LCNARCNIMGPNNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
 DB 241 LCNARCNIMGPNNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300

QY 301 RMLLKGCNNVNSTSSAGNTALHGVNKRNPDCAVLLTTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLLKGCNNVNSTSSAGNTALHGVNKRNPDCAVLLTTHGANADARGEHNTPLHLAMSK 360

QY 361 DNVEIMKALIVFGAEVDPNDPFGETPTFLASKIGKLODLNHSRARKPAFILGSMRDEKR 420
 DB 361 DNVEIMKALIVFGAEVDPNDPFGETPTFLASKIGKLODLNHSRARKPAFILGSMRDEKR 420

QY 421 THNHLCTLDGGYKGLIIQLLAIKASGVATDLPDWAGSTGTGIIALAIHSKMA 480
 DB 421 THNHLCTLDGGYKGLIIQLLAIKASGVATDLPDWAGSTGTGIIALAIHSKMA 480

QY 481 YMGMYFRMDEVFRGSRPYESGPLEEFLKREFEHTKMTDVRKPKMLTGLTSDROPAE 540
 DB 481 YMGMYFRMDEVFRGSRPYESGPLEEFLKREFEHTKMTDVRKPKMLTGLTSDROPAE 540

QY 541 LHLFRYDABETVREPRNQNVMLRPPAOPSDQLWBAASSGAAPTYFRPNGRFLDGL 600
 DB 541 LHLFRYDABETVREPRNQNVMLRPPAOPSDQLWBAASSGAAPTYFRPNGRFLDGL 600

QY 601 LANNPTLDANTEIHEYNQDILRKQANKVKKLSIVSLGTRSPQVVTCDVFRPSNPW 660
 DB 601 LANNPTLDANTEIHEYNQDILRKQANKVKKLSIVSLGTRSPQVVTCDVFRPSNPW 660

QY 661 ELAKTVGAKELGKRVVDCCTDPGRP 687
 DB 661 ELAKTVGAKELGKRVVDCCTDPGRP 687

RESULT 2
 ABB82231
 ID ABB82231 standard; protein; 687 AA.
 AC ABB82231;
 XX 08-JAN-2003 (first entry)
 DE Human cPLA2/B splice variant (clone 19a).
 XX
 XX
 KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KW antiinflammatory; antiarthritic; antipneumatic; antirheumatic; cytosolic;
 KW antiaesthetic; human.
 XX
 OS Homo sapiens.
 XX
 PN US2002106364-A1.

XX PD 08-AUG-2002.
 XX PF 09-AUG-2001; 2001US-00927180.
 XX PR 27-JUL-1994; 94US-00281193.
 XX PR 14-APR-1995; 95US-00422106.
 XX PR 14-APR-1995; 95US-00422420.
 XX PR 26-JUN-1995; 95MO-US008069.
 XX PR 08-NOV-1995; 95US-00555568.
 XX PR 09-SEP-1998; 98US-00149988.
 XX PR 06-MAR-2000; 2000US-00519223.
 XX PA (GEMV) GENETICS INST INC.
 XX PI Jones S, Tang J;
 XX WPI, 2002-739923/80.
 XX DR N-PSDB; ABV73010.
 XX PT Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 PS Claim 6; Page 23-25; 41pp; English.
 CC The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (I),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
 CC 19a)
 XX
 XX SQ Sequence 687 AA;

Query Match 100.0%; Score 3620; DB 5; Length 687;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFGRLVNTFSGVTNLFSNPFPRKEVAADYTSDDREEGQLIFONTPNRTWDCVLV 60
 DB 1 MOEFGRLVNTFSGVTNLFSNPFPRKEVAADYTSDDREEGQLIFONTPNRTWDCVLV 60

QY 61 NPNSSGFRLLFQLEADALVNFHOYSSQLPFYESSPOVLTEVLOHTLDIRNHPSW 120
 DB 61 NPNSSGFRLLFQLEADALVNFHOYSSQLPFYESSPOVLTEVLOHTLDIRNHPSW 120

QY 121 SVNHLAVEIGIRCEFHHSRIISCANCAENEBEGCTPLHLCKRGDGLVLELVQYCHTQMD 180
 DB 121 SVNHLAVEIGIRCEFHHSRIISCANCAENEBEGCTPLHLCKRGDGLVLELVQYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVLLQLRNNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 DB 181 VTDYKGETVFHYAVQGDNSQVLLQLRNNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240

QY 241 LCNARCNIMGPNNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
 DB 241 LCNARCNIMGPNNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300

QY 301 RMLLKGCNNVNSTSSAGNTALHGVNKRNPDCAVLLTTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLLKGCNNVNSTSSAGNTALHGVNKRNPDCAVLLTTHGANADARGEHNTPLHLAMSK 360

Db 301 RMLKRGCVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 Qy 361 DNVEMLKALIVFGAEVDTPEPDPFTPLASKIGKODLMIHSARKPAFLGSMREKR 420
 Db 361 DNVEMLKALIVFGAEVDTPEPDPFTPLASKIGKODLMIHSARKPAFLGSMREKR 420
 Qy 421 THHLLCLDGGVKGKLIILQLLAIERKASGVATKDLFDWVAGSTGGILALAIHSKMA 480
 Db 421 THHLLCLDGGVKGKLIILQLLAIERKASGVATKDLFDWVAGSTGGILALAIHSKMA 480
 Qy 481 YMRGMVFRMKDEYFRGSRPYESGPLEEFLLKREFGEHTKMTDVRKPKVMTLGTLSDRPAE 540
 Db 481 YMRGMVFRMKDEYFRGSRPYESGPLEEFLLKREFGEHTKMTDVRKPKVMTLGTLSDRPAE 540
 Qy 541 LHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600
 Db 541 LHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 600
 Qy 601 LANNPTLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNP 660
 Db 601 LANNPTLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNP 660
 Qy 661 ELAKTVFGAKELGKRVVDCCTDPDGRP 687
 Db 661 ELAKTVFGAKELGKRVVDCCTDPDGRP 687
 RESULT 3
 AAM17848 standard; protein; 688 AA.
 AAM17848:
 DT 07-AUG-1997 (first entry)
 XX Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
 XX Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
 KM Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
 KM inflammation; inhibitor; antiinflammatory.
 OS Homo sapiens.
 XX MO9717448-A2.
 PD 15-MAY-1997.
 XX 07-NOV-1996; 96WO-US017794.
 PF 08-NOV-1995; 95US-00555568.
 PR (GENEY) GENETICS INST INC.
 PA Jones S, Tang J;
 PI WPI; 1997-281037/25.
 DR N-PSDB; AAT68826.
 XX Calcium independent phospholipase A2/B - used to reduce inflammation in a
 PT mammalian subject.
 PS Claim 12; Page 54-56; 74pp; English.
 CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAM17848) is
 CC characterised by activity in the absence of calcium, by activity in a
 CC mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl-
 CC phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
 CC lack of stimulation by ATP, and by including in its sequence at least one
 CC of the amino acid sequences given in AAM17839-44). It is an
 CC alternatively spliced variant of another isolated polypeptide (AAM17846)
 CC and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes
 CC (AAM17845, AAM17847) have also been identified. sPLA2/B enzymes are
 CC thought to be involved in the release of arachidonic acid in specific
 CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host

CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
 CC drugs which inhibit the arachidonic acid cascade
 XX Sequence 688 AA:
 Qy 1 MGFPGRLVNTFSQVTLNFSNPRFKVAVADYSSDRVREEGGLIFONTNRTWCVLV 60
 Db 1 MGFPGRLVNTFSQVTLNFSNPRFKVAVADYSSDRVREEGGLIFONTNRTWCVLV 60
 Qy 61 NPNRSOSGFRPLFPLELEADALVNFHYSQQLPFYESSPOVLTLYLQHTDILRNHPSW 120
 Db 61 NPNRSOSGFRPLFPLELEADALVNFHYSQQLPFYESSPOVLTLYLQHTDILRNHPSW 120
 Qy 121 SVAHLAVELGIRRCFHSRIISCANCAENEGCTPLHACRKDGELIVELVQYCHTOMD 180
 Db 121 SVAHLAVELGIRRCFHSRIISCANCAENEGCTPLHACRKDGELIVELVQYCHTOMD 180
 Qy 181 VTQKGETVFHVAVQGDNSQVTLQGRNVAAGLNQVNNQGLTFPLHACQLGKQEMRVLL 240
 Db 181 VTQKGETVFHVAVQGDNSQVTLQGRNVAAGLNQVNNQGLTFPLHACQLGKQEMRVLL 240
 Qy 241 LCNARCNIMGPNQVPIHSAMKFSQKCAEMTISMDSSQHSKDPYRGASPLHAKNAEMA 300
 Db 241 LCNARCNIMGPNQVPIHSAMKFSQKCAEMTISMDSSQHSKDPYRGASPLHAKNAEMA 300
 Qy 301 RMLKRGCVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 Db 301 RMLKRGCVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
 Qy 361 DNVEMLKALIVFGAEVDTPEPDPFTPLASKIGK-LQDLMIHSARKPAFLIGSMREKR 419
 Db 361 DNVEMLKALIVFGAEVDTPEPDPFTPLASKIGK-LQDLMIHSARKPAFLIGSMREKR 419
 Qy 420 RTHDHLCLDGGVKGKLIILQLLAIERKASGVATKDLFDWVAGSTGGILALAIHSKMA 479
 Db 420 RTHDHLCLDGGVKGKLIILQLLAIERKASGVATKDLFDWVAGSTGGILALAIHSKMA 479
 Qy 480 AYMRGMVFRMKDEYFRGSRPYESGPLEEFLLKREFGEHTKMTDVRKPKVMTLGTLSDRPA 539
 Db 480 AYMRGMVFRMKDEYFRGSRPYESGPLEEFLLKREFGEHTKMTDVRKPKVMTLGTLSDRPA 539
 Qy 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 599
 Db 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRAARSSGAAPTYFRPNGRFLDGG 599
 Qy 600 LANNPTLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNP 659
 Db 600 LANNPTLDAMTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNP 659
 Qy 660 WEIAKTVFGAKELGKRVVDCCTDPDGRP 687
 Db 660 WEIAKTVFGAKELGKRVVDCCTDPDGRP 687
 RESULT 4
 ABB82232
 ID ABB82232 standard; protein; 688 AA.
 XX ABB82232:
 AC 08-JAN-2003 (first entry)
 XX Human cPLA2/B splice variant (clone 19b).
 DE Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
 KM antiinflammatory; antiarthritic; antipsoaritic; antirheumatic; cytosolic;
 KM antiaesthetic; human.
 XX Homo sapiens.
 OS

XX US2002106364-A1.
 PN
 XX
 PD 08-AUG-2002.
 XX
 PF 09-AUG-2001, 2001US-00927180.
 XX
 XX 27-JUL-1994; 94US-00281193.
 PR 14-APR-1995; 95US-00422106.
 PR 14-APR-1995; 95US-00422120.
 PR 26-JUN-1995; 95MO-US008069.
 PR 08-NOV-1995; 95US-00555568.
 PR 09-SEP-1998; 98US-00149988.
 PR 06-MAR-2000; 2000US-00519223.
 XX
 PA (GEM) GENETICS INST INC.
 PI Jones S, Tang J;
 XX
 XX WPI; 2002-739923/80.
 DR N-PDB; ABV73011.
 XX
 PT Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 PS
 PS Claim 6; Page 28-30; 41pp; English.
 XX
 CC The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (I),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
 CC 19b)
 CC
 SQ Sequence 688 AA.

Query Match 99.6%; Score 3606.5; DB 5; Length 688;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAVADYTSDDVREGQLLFQNTPNRTWCVLV 60
 DB 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAVADYTSDDVREGQLLFQNTPNRTWCVLV 60
 QY 61 NPNSOSGFFLPOLLEADALVNPHOVSSQLLPFYESSPOVLTEVLOHLLTDLRNHP 120
 DB 61 NPNSOSGFFLPOLLEADALVNPHOVSSQLLPFYESSPOVLTEVLOHLLTDLRNHP 120
 QY 121 SVNHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
 DB 121 SVNHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
 QY 181 VYDKGETVHYAVOGNSQVLOLGRNNAVAGLNQVNNQGLTPHLACQCGKQEMRVLL 240
 DB 181 VYDKGETVHYAVOGNSQVLOLGRNNAVAGLNQVNNQGLTPHLACQCGKQEMRVLL 240
 QY 241 LCNARCNIMGPNGPITHSAKFOSKCAEMIIISMSQHSKDPKRYGASPLHNAKAEMA 300
 DB 241 LCNARCNIMGPNGPITHSAKFOSKCAEMIIISMSQHSKDPKRYGASPLHNAKAEMA 300

QY 301 RMLKRGCVNNTSSAGNTALHVGVRNRPDCAIVLLTHGANADAGEHNTPLHLSMK 360
 DB 301 RMLKRGCVNNTSSAGNTALHVGVRNRPDCAIVLLTHGANADAGEHNTPLHLSMK 360
 QY 361 DNVEMLKALIVPAEVDTPNDPEETPTFLASKIGK-LDPLMHSRARKPAFLIGSRDEK 419
 DB 361 DNVEMLKALIVPAEVDTPNDPEETPTFLASKIGK-LDPLMHSRARKPAFLIGSRDEK 420
 QY 420 RTHDHLCLDGGGVKLLIIQLLIAEKASGVATKDLFPMVAGTSTGCLALAILHLSKM 479
 DB 421 RTHDHLCLDGGGVKLLIIQLLIAEKASGVATKDLFPMVAGTSTGCLALAILHLSKM 480
 QY 480 AYRGMVFYKDKDVEFGSPRYSBGPLEFLKRGEGHTKTDYRKRVMLTGLSROPA 539
 DB 481 AYRGMVFYKDKDVEFGSPRYSBGPLEFLKRGEGHTKTDYRKRVMLTGLSROPA 540
 QY 540 ELHLFNNYAPETVREPRFQNNVLRPPAPSPQLVWRARSSGAPTYFRPGRFLDDG 599
 DB 541 ELHLFNNYAPETVREPRFQNNVLRPPAPSPQLVWRARSSGAPTYFRPGRFLDDG 600
 QY 600 LLANNPTLDAMTEIHENODLIRKQANKVKLSIVSISGTGRSPQVPYTCVDVFRSPNP 659
 DB 601 LLANNPTLDAMTEIHENODLIRKQANKVKLSIVSISGTGRSPQVPYTCVDVFRSPNP 660
 QY 660 WEIAKTVFGAKELGKRVVDCCTDDGGRP 687
 DB 661 WEIAKTVFGAKELGKRVVDCCTDDGGRP 688

RESULT 5
 ADD93407
 ID ADD93407 standard; protein; 784 AA.
 XX
 XX ADD93407;
 AC
 AC
 DT 29-JAN-2004 (first entry)
 XX
 XX
 DE Human lipid-associated molecule LIPM-14 polypeptide.
 XX
 XX Human; lipid-associated molecule; LIPM-14; neuroprotective; relaxant;
 KW antihypertoid; antidiabetic; cytostatic; dermatological; immunosuppressive;
 KW antiinflammatory; thymometric; antiallergic; cerebroprotective;
 KW gastrointestinal; hepatotropic; nephroprotective; anticonvulsant;
 KW antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;
 KW virucide; uterapathic; antirheumatic; cardiant; cardiovascular; anti-HIV;
 KW neurotopic.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2003083081-A2.
 PN
 XX
 XX 09-OCT-2003.
 PD
 XX
 XX 27-MAR-2003; 2003MO-US009755.
 PF
 XX
 XX 29-MAR-2002; 2002US-0368722P.
 PR 03-MAY-2002; 2002US-0377576P.
 PR 05-JUL-2002; 2002US-039334P.
 PR 27-SEP-2002; 2002US-0414269P.
 XX
 XX (INCY-) INCYTE CORP.
 PA
 XX Emerling BM, Margulis JP, Chawla NK, Lee SY, Duggan BM, Warren BA;
 PI Baughn MR, Lee EA, Griffin JA, Kahle AE, Elliott VS, Chang H;
 PI Lee S, Ramkumar J, Bulloch SA, Hafalia Aub, Khare R, Jiang X;
 PI Jackson AA;
 DR WPI; 2003-788347/74.
 DR N-PDB; ADD93426.
 XX
 XX New LIPM polypeptides, useful for diagnosing, preventing, and treating
 PT disorders associated with abnormal expression or activity of LIPM, e.g.
 PT neuromuscular, immunological, cardiovascular disorders, cancer and/or

PT Infections.
 XX Claim 69, Page 206-207, 238pp; English.
 PS
 XX The present sequence is the protein sequence of human lipid-associated
 CC molecule LIPAM-14 (Incyte polypeptide 751262CD1), a protein that shows
 CC homology to human Ca2+-independent phospholipase A2 short isoform. This
 CC is one of 19 LIPAM polypeptides of the invention. The invention relates
 CC to these novel LIPAMs and the nucleic acids encoding them, and to the use
 CC of nucleic acids and proteins in the diagnosis, treatment and prevention
 CC of disorders associated with abnormal expression or activity of LIPAM
 CC such as neurodegenerative disorders (e.g. Parkinson's disease,
 CC Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy,
 CC cataractia), endocrine disorders (e.g. diabetes, Grave's disease), cancers
 CC (e.g. leukemia, cervical or breast cancers), immunological disorders
 CC (e.g. scleroderma, systemic lupus erythematosus, allergies),
 CC gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g.
 CC Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal,
 CC parasitic, protozoal, helminthic), cardiovascular disorders (e.g.
 CC atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention
 CC also relates to the assessment of the effects of exogenous compounds on
 CC the expression of nucleic acids and LIPAMs. The invention provides
 CC expression vectors, host cells, antibodies, agonists and antagonists,
 CC transgenic organisms, and arrays and microarrays of the polynucleotides.
 CC
 XX
 SQ Sequence 784 AA;
 Query Match 99.3%; Score 3593.5; DB 7; Length 784;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 684; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 QY 1 MOPFGRVNTFSGVTNLFSPNFRKVEAVAVADYSSDRVREGGQLIFONTPNRTWDCV 60
 DB 33 MOPFGRVNTFSGVTNLFSPNFRKVEAVAVADYSSDRVREGGQLIFONTPNRTWDCV 92
 QY 61 NPNRSQGFRLFOLELEADALVNFHOYSSQLPFYESSPOVLTHTVLOHTLDIRNHP 120
 DB 93 NPNRSQGFRLFOLELEADALVNFHOYSSQLPFYESSPOVLTHTVLOHTLDIRNHP 152
 QY 121 SVHLAVELGIRCEFHHSRIISCANCAENBEGCTPLHLACRKDGILVELVOYCHTOMD 180
 DB 153 SVHLAVELGIRCEFHHSRIISCANCAENBEGCTPLHLACRKDGILVELVOYCHTOMD 212
 QY 181 VTQYKGETVTHYAVQGNQSVTLQLGRNAVAGLNQVNNQGITPLHLACOLGKQEMRVLL 240
 DB 213 VTQYKGETVTHYAVQGNQSVTLQLGRNAVAGLNQVNNQGITPLHLACOLGKQEMRVLL 272
 QY 241 LCNARCNIMGPNNGPIHSAMKFSQKCAEMTISMSQIHSKDRYCGASPLHAKNAEMA 300
 DB 273 LCNARCNIMGPNNGPIHSAMKFSQKCAEMTISMSQIHSKDRYCGASPLHAKNAEMA 332
 QY 301 RMLKRGCVNSTSSAGNTALHVGWNRNPDCAIVLLTGHANADARGEHTPLHLAMSK 360
 DB 333 RMLKRGCVNSTSSAGNTALHVGWNRNPDCAIVLLTGHANADARGEHTPLHLAMSK 392
 QY 361 DNVEMITALIVFGAEVTPNDPFGETPTPLASKIKK-LQDLMLHTRAKKPAITLISMD 419
 DB 393 DNVEMITALIVFGAEVTPNDPFGETPTPLASKIKKIGROLDMLHTRAKKPAITLISMD 452
 QY 420 RTDHDLCLDGGGKGLIIQLLAIEKASGATKDFDWVAGSTGGIATLALILHKS 479
 DB 453 RTDHDLCLDGGGKGLIIQLLAIEKASGATKDFDWVAGSTGGIATLALILHKS 512
 QY 480 AYNGMFRMKDEVFRSGRPYESGLEFLKRGEGHTKMTDVAKPKVMTLGTLSDR 539
 DB 513 AYNGMFRMKDEVFRSGRPYESGLEFLKRGEGHTKMTDVAKPKVMTLGTLSDR 572
 QY 540 ELHIFRYVADPETHREPRFNQVNLPRPAQSDOLVNRRAASSGAATYPRPNRFLD 599
 DB 573 ELHIFRYVADPETHREPRFNQVNLPRPAQSDOLVNRRAASSGAATYPRPNRFLD 632
 QY 600 LLANPTLDMTEIHEYNODLIRKGOANKVKGLSIIVSLGTGRSPQVPTCVDFRPSNP 659

DB 633 LLANPTLDMTEIHEYNODLIRKGOANKVKGLSIIVSLGTGRSPQVPTCVDFRPSNP 692
 QY 660 WEIAKTVFGAKELGKRVVDCCTPDGR 686
 DB 693 WEIAKTVFGAKELGKRVVDCCTPDGR 719
 RESULT 6
 AAE25968
 ID AAE25968 standard; protein; 806 AA.
 AC AAE25968;
 DT 15-NOV-2002 (first entry)
 DE Human PLA2 group VI (Ca2+-independent) protein.
 XX Human; antisense; phospholipase A2; infection; inflammation; tumour;
 KW antisense therapy; PLA2 protein.
 OS Homo sapiens.
 PN US6410325-B1.
 PD 25-JUN-2002.
 PF 09-MAY-2001, 2001US-00851896.
 PR 09-MAY-2001, 2001US-00851896.
 PA (ISIS-) ISIS PHARM INC.
 PI Bennett CF, Freier SM, Watt AT;
 XX WPI: 2002-616513/66.
 DR N-PSDB; AAD42941.
 PT Novel antisense compounds useful for inhibiting gene expression of human
 PT phospholipase A2, group VI and for treating diseases associated with
 PT expression of phospholipase A2, group VI.
 PS Disclosure; Col 109-116; 72pp; English.
 CC The present invention relates to novel antisense compounds which inhibit
 CC the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
 CC The invention is useful for inhibiting the expression of PLA2, group VI
 CC (Ca2+-independent) in human cells or tissues and for treating an animal,
 CC particularly a human suspected of having or being prone to a disease or
 CC condition associated with expression of human PLA2, group VI (Ca2+-
 CC independent). It is useful for diagnostics, therapeutics and as research
 CC reagent, e.g. prophylactically to prevent or delay infection, tumour
 CC formation or inflammation. The present sequence is human PLA2 group VI
 CC (Ca2+-independent) protein
 CC
 XX
 SQ Sequence 806 AA;
 Query Match 98.5%; Score 3566.5; DB 5; Length 806;
 Best Local Similarity 92.3%; Pred. No. 0;
 Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;
 QY 1 MOPFGRVNTFSGVTNLFSPNFRKVEAVAVADYSSDRVREGGQLIFONTPNRTWDCV 60
 DB 1 MOPFGRVNTFSGVTNLFSPNFRKVEAVAVADYSSDRVREGGQLIFONTPNRTWDCV 60
 QY 61 NPNRSQGFRLFOLELEADALVNFHOYSSQLPFYESSPOVLTHTVLOHTLDIRNHP 120
 DB 61 NPNRSQGFRLFOLELEADALVNFHOYSSQLPFYESSPOVLTHTVLOHTLDIRNHP 120
 QY 121 SVHLAVELGIRCEFHHSRIISCANCAENBEGCTPLHLACRKDGILVELVOYCHTOMD 180
 DB 121 SVHLAVELGIRCEFHHSRIISCANCAENBEGCTPLHLACRKDGILVELVOYCHTOMD 180
 QY 181 VTQYKGETVTHYAVQGNQSVTLQLGRNAVAGLNQVNNQGITPLHLACOLGKQEMRVLL 240

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Db      181 VTQYKGETVFHYAVQGDNSQVLTQLGRNAVAGLNQVNNQGLTPLHLACQLGKQGMVRVLL 240
Qy      241 LCNARCNINPNGYPPIHSAMKFSQKCAEMTISMSDSQIHSKOPRYASPLHAKNAEMA 300
Db      241 LCNARCNINPNGYPPIHSAMKFSQKCAEMTISMSDSQIHSKOPRYASPLHAKNAEMA 300
Qy      301 RMLLKSGCWNSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db      301 RMLLKSGCWNSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Qy      361 DNVEIMKALIVFGAEVDTENDFGETPTFLASKIGK-----LQDLMIHSRARKPAFTILGSMRDEKRTDHL 425
Db      361 DNVEIMKALIVFGAEVDTENDFGETPTFLASKIGK-----LQDLMIHSRARKPAFTILGSMRDEKRTDHL 425
Qy      396 -----LQDLMIHSRARKPAFTILGSMRDEKRTDHL 425
Db      421 VPABQGSAAHPHPSLERAPPPISLNNLELQDLMIHSRARKPAFTILGSMRDEKRTDHL 480
Qy      426 LCDGGGVKGLIITQLLIAIEKASGVATKDLFDWVAGTSTGGLIALALILHSKSMAYMRGM 485
Db      481 LCDGGGVKGLIITQLLIAIEKASGVATKDLFDWVAGTSTGGLIALALILHSKSMAYMRGM 540
Qy      486 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKWMLTGLSDROPABELHLFR 545
Db      541 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKWMLTGLSDROPABELHLFR 600
Qy      546 NYAPETVAREPRNQNVLNLRPPAOPSDQLVWRARSSGAAPTYFRNGRPLDGGLLANNP 605
Db      601 NYAPETVAREPRNQNVLNLRPPAOPSDQLVWRARSSGAAPTYFRNGRPLDGGLLANNP 660
Qy      606 TLDAWTEIHEYNODLIRKQGANVKKLSIVSLGTGRSPQVPTCVDFRSPNPMELAKT 665
Db      661 TLDAWTEIHEYNODLIRKQGANVKKLSIVSLGTGRSPQVPTCVDFRSPNPMELAKT 720
Qy      666 VFGAKELGKRVVDDCTDPDGR 686
Db      721 VFGAKELGKRVVDDCTDPDGR 741

RESULT 7
AD019776 ID AD019776 standard; protein; 806 AA.
AC AD019776;
XX
DT 12-AUG-2004 (first entry)
DE Human PRO polypeptide #350.
XX
KW Human; PRO; immune related disorder; systemic lupus erythematosus;
KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
KW diabetes mellitus; renal disease; demyelinating disease;
KW central nervous system; peripheral nervous system;
KW demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX
OS Homo sapiens.
XX
PN MO2004043361-A2.
XX
PD 27-MAY-2004.
XX
PF 06-NOV-2003; 2003MO-US035268.
XX
PR 08-NOV-2002; 2002US-0425235P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Feng S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM,
PI Wood WI, Wu TD,

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XX      WPI; 2004-42067/39.
DR      N-PSDB; AD019775.
XX
PT      Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT      treating an immune related disorder such as systemic lupus erythematosus,
PT      rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT      spondyloarthritis.
XX
PS      Claim 7; SEQ ID NO 700; 1731bp; English.
XX
CC      The invention relates to human PRO polypeptides and the polynucleotides
CC      encoding them. The polypeptides and polynucleotides are useful for
CC      treating and diagnosing immune related disorders in mammals. The immune
CC      related disorders include systemic lupus erythematosus, rheumatoid
CC      arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC      sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC      haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC      mellitus, immune-mediated renal disease, demyelinating diseases of the
CC      central or peripheral nervous system, demyelinating polyneuropathy,
CC      Guillain-Barre syndrome and chronic inflammatory demyelinating
CC      polyneuropathy. This sequence represents a human PRO polypeptide of the
CC      invention.
XX
SQ      Sequence 806 AA;
XX
Query Match      98.5%; Score 3566.5; DB 8; Length 806;
Best Local Similarity 92.3%; Pred. No. 0;
Matches 684; Conservative 1; Mismatches 1; Indels 55; Gaps 1;
Qy      1 MOFFGRLVNTFSQVTLFNSNPRVKEVAVADYSSDRVBEGLILFQTPNRTMDCVLY 60
Db      1 MOFFGRLVNTFSQVTLFNSNPRVKEVAVADYSSDRVBEGLILFQTPNRTMDCVLY 60
Qy      61 NPNRSQSGRRLRLLEADALVNFHOYSQQLBFYSSPOVLTETLQHLTDILRNHPSM 120
Db      61 NPNRSQSGRRLRLLEADALVNFHOYSQQLBFYSSPOVLTETLQHLTDILRNHPSM 120
Qy      121 SVNLAVELGIRCFHHSRIISCANCAENBEGCTPLHLACRKDGSEILVELVQYCHTQMD 180
Db      121 SVNLAVELGIRCFHHSRIISCANCAENBEGCTPLHLACRKDGSEILVELVQYCHTQMD 180
Qy      181 VTQYKGETVFHYAVQGDNSQVLTQLGRNAVAGLNQVNNQGLTPLHLACQLGKQGMVRVLL 240
Db      181 VTQYKGETVFHYAVQGDNSQVLTQLGRNAVAGLNQVNNQGLTPLHLACQLGKQGMVRVLL 240
Qy      241 LCNARCNINPNGYPPIHSAMKFSQKCAEMTISMSDSQIHSKOPRYASPLHAKNAEMA 300
Db      241 LCNARCNINPNGYPPIHSAMKFSQKCAEMTISMSDSQIHSKOPRYASPLHAKNAEMA 300
Qy      301 RMLLKSGCWNSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db      301 RMLLKSGCWNSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Qy      361 DNVEIMKALIVFGAEVDTENDFGETPTFLASKIGK-----LQDLMIHSRARKPAFTILGSMRDEKRTDHL 425
Db      361 DNVEIMKALIVFGAEVDTENDFGETPTFLASKIGK-----LQDLMIHSRARKPAFTILGSMRDEKRTDHL 425
Qy      396 -----LQDLMIHSRARKPAFTILGSMRDEKRTDHL 425
Db      421 VPABQGSAAHPHPSLERAPPPISLNNLELQDLMIHSRARKPAFTILGSMRDEKRTDHL 480
Qy      426 LCDGGGVKGLIITQLLIAIEKASGVATKDLFDWVAGTSTGGLIALALILHSKSMAYMRGM 485
Db      481 LCDGGGVKGLIITQLLIAIEKASGVATKDLFDWVAGTSTGGLIALALILHSKSMAYMRGM 540
Qy      486 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKWMLTGLSDROPABELHLFR 545
Db      541 YFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKWMLTGLSDROPABELHLFR 600
Qy      546 NYAPETVAREPRNQNVLNLRPPAOPSDQLVWRARSSGAAPTYFRNGRPLDGGLLANNP 605
Db      601 NYAPETVAREPRNQNVLNLRPPAOPSDQLVWRARSSGAAPTYFRNGRPLDGGLLANNP 660

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QY 606 TLDMATEIHYNODLIRKGOANKVKLSIVSLGTGRSPVPYTCVDFRPSNPWEIAKT 665
 DB 661 TLDMATEIHYNODLIRKGOANKVKLSIVSLGTGRSPVPYTCVDFRPSNPWEIAKT 720
 QY 666 VFGAKELGKRVVDCCTDPDGR 686
 DB 721 VFGAKELGKRVVDCCTDPDGR 741

RESULT 8
 AAR83018 standard; protein; 752 AA.

XX AAR83018;
 XX 15-JUN-1996 (first entry)
 XX
 XX Calcium-independent cytosolic phospholipase-A2/B enzyme.

KM CHO, calcium-independent cytosolic phospholipase-A2/B; enzyme;
 KM phospholipase-A2; phospholipase-B; drug screening; anti-inflammatory;
 KW antibody.

XX Criceulius griseus.

XX USS466595-A.

XX 14-NOV-1995.

XX 27-JUL-1994; 94US-00281193.

XX 27-JUL-1994; 94US-00281193.

XX (GEMY) GENETICS INST INC.

XX Tang J, Jones S;

XX WPI; 1996-009526/01.

XX N-PSDB; AAT05842.

PT Isolated polynucleotide encoding cytosolic phospholipase A2/B - for
 PT producing enzyme for use in screening anti-inflammatory agents and prodn.
 PT of antibodies.

XX Claim 5; Col 15-22; 24pp; English.

XX The enzyme may be produced recombinantly in host cells such as animal
 CC cells, insect cells, eukaryotes, prokaryotes, etc. The protein may also
 CC be expressed in transgenic animals (e.g. milk of transgenic cow). The
 CC protein is used to screen for agents which inhibit phospholipase activity
 CC for use as anti-inflammatory agents. These agents can be used to treat
 CC e.g. Rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease
 CC and other disease mediated by increased levels of prostaglandins,
 CC leukotriene or platelet activating factor. The enzyme can also be used
 CC for the production of antibodies for use as research or diagnostic tools

XX Sequence 752 AA;

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOFFGLVNTFSGVTNLSNPFVKEVAVADYSSDRVREGQILFQNTENRTWDCVLY 60
 DB 1 MOFFGLVNTLSSVTNLSNPFVKEISVADYTSHERVREGQILFQNSNRTWDCILV 60
 QY 61 NPNRSQSGFRLFOLEADALVNFQYSSQLLPYESSPOLYHTYVQHLTDLRNPN 120
 DB 61 SPRNPHSGFRLFOLEADALVNFQYSSQLLPYESSPOLYHTYVQHLTDLRNPN 120
 QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGGEIVELVQYCHTQMD 180
 DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGGEIVELVQYCHTQMD 180

DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGSEIVELVQYCHTQMD 180
 QY 181 VPDYKSETPHYAVVOGDNQOVLOLGRNAVAGLNQNNQGLTPHLACQKQKEMRYLL 240
 DB 181 VPDYKSETPHYAVVOGDNQOVLOLGRNAVAGLNQNNQGLTPHLACQKQKEMRYLL 240
 QY 241 LCNARCNINQNGPYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPRIYASPLHAKNAEMA 300
 DB 241 LCNARCNINQNGPYPIHSAMKFSQKCAEMIIISMDSSQIHSKDPRIYASPLHAKNAEMA 300
 QY 301 RMLKRGCVNVTSSAGNTALHGVNRPDCAIVLTHGANADAGEHNTPLHLAMSK 360
 DB 301 RMLKRGCVNVTSSAGNTALHGVNRPDCAIVLTHGANADAGEHNTPLHLAMSK 360
 QY 361 DNVEMIKALIVGAEDTPDPEGETPTPLASKIGK-LQDLMHSRARKAFILISMRDEK 419
 DB 361 DNVEMIKALIVGAEDTPDPEGETPTPLASKIGK-LQDLMHSRARKAFILISMRDEK 419
 QY 420 RTDHLCLDGGGVKGLIIQLLIAIEKASGVATKOLPMVAGTSTGGILALAILHASKM 479
 DB 420 RTDHLCLDGGGVKGLIIQLLIAIEKASGVATKOLPMVAGTSTGGILALAILHASKM 479
 QY 480 AYMRGMYFRMKQEVFRGSRPYESGPLEEFLKREGEHTKOTDVKRKNMLTGLSDROPA 539
 DB 480 AYMRGMYFRMKQEVFRGSRPYESGPLEEFLKREGEHTKOTDVKRKNMLTGLSDROPA 539
 QY 540 ELHLFRNYDAPEVFRPRFRQNVNLRPPAPQSPQLVWRARSSGAPTYFRPRGRILDDG 559
 DB 540 ELHLFRNYDAPEVFRPRFRQNVNLRPPAPQSPQLVWRARSSGAPTYFRPRGRILDDG 559
 QY 600 LLANNPTLDAMTEIHYNODLIRKGOANKVKLSIVSLGTGRSPVPYTCVDFRPSNP 659
 DB 600 LLANNPTLDAMTEIHYNODLIRKGOANKVKLSIVSLGTGRSPVPYTCVDFRPSNP 659
 QY 660 WELAKTVFGAKELGKRVVDCCTDPDGR 686
 DB 660 WELAKTVFGAKELGKRVVDCCTDPDGR 687

RESULT 9
 AAM01479
 ID AAM01479 standard; protein; 752 AA.
 XX AAM01479;
 AC 25-MAR-2003 (revised)
 DT 12-FEB-1997 (first entry)
 DE Calcium-independent cytosolic phospholipase A2/B.
 XX cPLA2/B; calcium-independent cytosolic phospholipase A2/B;
 KM arachidonic acid; 1-palmitoyl-2-[14C]-arachidonyl-phosphatidylcholine;
 KM anti-inflammatory; screen; rheumatoid arthritis.
 XX Synthetic.
 OS
 XX USS554511-A.
 PN 10-SEP-1996.
 PD 14-APR-1995; 95US-00422420.
 PF 27-JUL-1994; 94US-00281193.
 PR (GEMY) GENETICS INST INC.
 XX Tang J, Jones S;
 XX WPI; 1996-424653/42.
 DR N-PSDB; AAT44578.
 PT Prodn. of a Ca-independent cytosolic phospholipase A(2)/B - by culturing
 PT host cells contg. the phospholipase gene, useful for screening anti-

PT inflammatory agents for treating e.g. rheumatoid arthritis.
 XX
 PS Claim 1; Col 15-22; 24pp; English.
 XX

CC The present sequence is that of a calcium-independent cytosolic
 CC phospholipase A2/B (cPLA2/B) enzyme. cPLA2/B is important in the release
 CC of arachidonic acid in specific tissues characterized by unique membrane
 CC phospholipids. The invention provides a process for producing such an
 CC enzyme. The enzyme has a mol. wt. of 86 kD on SDS-PAGE and the presence
 CC of one or more amino acid sequences selected from AAM01480-92, cPLA2/B
 CC has activity in a mixed micelle assay with 1-palmitoyl-2-[14C]-
 CC arachidonyl-1-phosphatidylcholine. The enzyme is useful for screening anti-
 CC -inflammatory agents mediated by the arachidonic acid cascade, for
 CC treating, e.g. rheumatoid arthritis (Updated on 25-MAR-2003 to correct PF
 CC field.)
 CC
 XX
 SQ Sequence 752 AA;

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOPFGSLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREBQGLIFQNTPRNTWCULV 60
 DB 1 MOPFGSLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREBQGLIFQNTPRNTWCULV 60
 QY 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSQVLAHTEVLOHLDLIRNHPSW 120
 DB 61 SPNPHSGRFLFQLEADALVNFHOYSQQLPFYESSQVLAHTEVLOHLDLIRNHPSW 120
 QY 121 SVNHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
 DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
 QY 181 VTDYKGETVPHYAVOGDNSQVQLQLGKNAVAGLNQVNNQGLTPHLACOLGKQEMRVLL 240
 DB 181 VTDNKETAHYAVOGDNSQVQLQLGKNASAGLNQVNNQGLTPHLACOLGKQEMRVLL 240
 QY 241 LCNARCNMGPNVPIHSAMKFSQKGAEMIIISDSSQHSKDPYKASPLHAKNAEMA 300
 DB 241 LCNARCNMGPNVPIHSAMKFSQKGAEMIIISDSSQHSKDPYKASPLHAKNAEMA 300
 QY 301 RMLKRGCVNSTSSAGNTALHVGVMNRPDCAI VILLTGANADANGHGNTPLHLAMSK 360
 DB 301 RMLKRGCVNSTSSAGNTALHVGVMNRPDCAI VILLTGANADANGHGNTPLHLAMSK 360
 QY 361 DNVEMLKALIVGAEDVTPNDPGEPTFLASKTIGK-LQDLMIHSRAKPAFLIGSMRDEK 419
 DB 361 DNVEMLKALIVGAEDVTPNDPGEPTFLASKTIGK-LQDLMIHSRAKPAFLIGSMRDEK 419
 QY 420 RTDHDLCLDGGGVKGLIIITQLIAIEKASGAVTKDLFDVAVAGTSTGIIALAILHSSKM 479
 DB 420 RTDHDLCLDGGGVKGLIIITQLIAIEKASGAVTKDLFDVAVAGTSTGIIALAILHSSKM 479
 QY 480 AYVRGMVFRMKDEVFRRSGRPYESGPLEEFLKREFGEHTKMTDVKRPMVLTGTLSDRQPA 539
 DB 480 AYVRGMVFRMKDEVFRRSGRPYESGPLEEFLKREFGEHTKMTDVKRPMVLTGTLSDRQPA 539
 QY 540 EHLFPNNYAPRVVREPRFNQNNLRPPAPSPQVLRARSSGAAPTYRPRGRFLDGG 599
 DB 540 EHLFPNNYAPRVVREPRFNQNNLRPPAPSPQVLRARSSGAAPTYRPRGRFLDGG 599
 QY 600 ILANNPTLDAMTEIHEYNODLIRKQANVKKLSIVSLGTGRSPQVPTCVVFRPSNP 659
 DB 600 ILANNPTLDAMTEIHEYNODLIRKQANVKKLSIVSLGTGRSPQVPTCVVFRPSNP 659
 QY 660 WEIAKTVFGAKELGKVVVDCCTDPDGR 686
 DB 660 WEIAKTVFGAKELGKVVVDCCTDPDGR 686
 QY 661 WEIAKTVFGAKELGKVVVDCCTDPDGR 687
 DB 661 WEIAKTVFGAKELGKVVVDCCTDPDGR 687

RESULT 10
 AAM13163

ID AAM13163 standard; protein; 752 AA.

XX AAM13163;

DT 17-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 20-MAY-1997 (first entry)

DE Ca-independent phospholipase A2/B protein.

KM Ca-independent phospholipase A2/B; Chinese hamster ovary cell; probe;
 KM chromatography; DEAE anion exchange; hydrophobic interaction; lambda;
 KM heparin Toyopearl; chromatocoussing; eukaryotic expression vector; COS;
 KM CHO; inhibitor; anti-inflammatory agent; arachidonic acid cascade.

OS Crictetus griseus; ovary cells.

PN US5589170-A.

PD 31-DEC-1996.

PF 14-APR-1995; 95US-00422106.

PR 27-UTL-1994; 94US-00281193.

PA (GEMV) GENETICS INST INC.

PI Tang J, Jones S;

XX WPI; 1997-076789/07.

DR N-PSDB; AAT59199.

PT Compn. comprising calcium-independent phospholipase enzyme - for
 screening for anti-inflammatory agents.

PS Claim 5; Col 15-22; 24pp; English.

XX This is the amino acid sequence of the Ca-independent phospholipase A2/B
 CC from Chinese hamster ovary cells. The protein was isolated from these
 CC cells by conventional chromatographic methods e.g. DEAE anion exchange,
 CC hydrophobic interaction, heparin Toyopearl and Mono P 5/20
 CC chromatocoussing chromatography. The purified protein has mol. wt. of 86
 CC kD and an optimum pH 6. The protein was used for amino acid sequencing
 CC from which pools of degenerate probes were synthesised. The probes were
 CC used to screen a CHO cell cDNA library in lambda ZAPII vector. Of 400000
 CC recombinant phages screened, 12 positive plaques were isolated. One of
 CC these, designated clone 9, contained this sequence. The phospholipase
 CC gene can be inserted into eukaryotic vectors for expression in COS or CHO
 CC cells. The protein, or peptides derived from it e.g. AAM13164-76, can be
 CC used to identify phospholipase inhibitors that can be used as anti-
 CC inflammatory agents, esp. against components of the arachidonic acid
 CC cascade. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT
 CC -2003 to standardise OS field)

XX
 SQ Sequence 752 AA;

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOPFGSLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREBQGLIFQNTPRNTWCULV 60
 DB 1 MOPFGSLVNTFSGVTNLFSPNPRVKEVAVADYSSDRVREBQGLIFQNTPRNTWCULV 60
 QY 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSQVLAHTEVLOHLDLIRNHPSW 120
 DB 61 SPNPHSGRFLFQLEADALVNFHOYSQQLPFYESSQVLAHTEVLOHLDLIRNHPSW 120
 QY 121 SVNHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
 DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDEILVELVOYCHTQMD 180
 QY 181 VTDYKGETVPHYAVOGDNSQVQLQLGKNAVAGLNQVNNQGLTPHLACOLGKQEMRVLL 240
 DB 181 VTDNKETAHYAVOGDNSQVQLQLGKNASAGLNQVNNQGLTPHLACOLGKQEMRVLL 240

```

Db      181 VTGNKGETAHYAVVQGNNSQVQLQLGKNASAGLNQVAKGSLTPLHLACQKQKQEMRVLL 240
Qy      241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMTISMDSSQIHSKDPYRGASPLHAKNAEMA 300
Db      241 LCNARCNWMPGSGPIHTAMKFSQKCAEMTISMDSSQIHSKDPYRGASPLHAKNAEMA 300
Qy      301 RMLKRGCVNNTSSAGNTALHGVNMRPDCALVLLTHGANADARGEHNTPLHLAMSK 360
Db      301 RMLKRGCVNNTSSAGNTALHGVNMRPDCALVLLTHGANADARGEHNTPLHLAMSK 360
Qy      361 DNVEMLKALIVFGAEVDPNDPGETPTPLASKIGK-LQDLMIHSRAKPAFIISMRDEK 419
Db      361 DNVEMLKALIVFGAEVDPNDPGETPTPLASKIGK-LQDLMIHSRAKPAFIISMRDEK 420
Qy      420 RTDHLCLDGGGVKGLIIITQLIAIEKASGAVATKDLFDVAVGTSGIILALAILHSSKM 479
Db      421 RIHDHLCLDGGGVKGLIIITQLIAIEKASGAVATKDLFDVAVGTSGIILALAILHSSKM 480
Qy      480 AYNRGMVFRMKDVEFGSRPYESGPLEEFLKREGEHTKMTDVAKKPVMLTGLISDRQPA 539
Db      481 AYNRGMVFRMKDVEFGSRPYESGPLEEFLKREGEHTKMTDVAKKPVMLTGLISDRQPA 540
Qy      540 ELHLFRNYDAPETVREPRFNQNNVLRPPAOPSDQVLRARSSGAFTYFRPNRFLDGG 599
Db      541 ELHLFRNYDAPETVREPRFNQNNVLRPPAOPSDQVLRARSSGAFTYFRPNRFLDGG 600
Qy      600 LLAANNPTLDMTEIHEYNODLIRKQGNKYKLSIVSLGTGRSPQVPTCVDFRPSNP 659
Db      601 LLAANNPTLDMTEIHEYNODMIRKQGNKYKLSIVSLGTGRSPQVPTCVDFRPSNP 660
Qy      660 WEIAKTVFGAKELGKRVVDDCTDPDGR 686
Db      661 WEIAKTVFGAKELGKRVVDDCTDPDGR 687

RESULT 11
AAW17849
ID      AAW17849 standard; protein; 752 AA.
XX
AC      AAW17849;
XX
DT      27-AUG-2003 (revised)
XX
DT      07-AUG-1997 (first entry)
XX
DE      Hamster cytosolic phospholipase A2/B.
XX
KM      Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
XX      inflammation; inhibitor; antiinflammatory; CHO.
XX
OS      Cricetus.
XX
FH      Key
FT      Active-site
XX
FT      Location/Qualifiers
XX      465
XX      /note= "mutagenesis of Ser-465 results in loss of
XX      activity"
XX
PN      MO9717448-A2.
XX
PD      15-MAY-1997.
XX
PF      07-NOV-1996; 96MO-US017794.
XX
PR      08-NOV-1995; 95US-00555568.
XX
PA      (GEMV ) GENETICS INST INC.
XX
PI      Jones S, Tang J;
XX
DR      WPI, 1997-281037/25.
XX
DR      N-PSDB; AAT68827.
XX
PT      Calcium independent phospholipase A2/B - used to reduce inflammation in a

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PT      mammalian subject.
XX
XX      Example 4; Page 33-36; 74pp; English.
XX
CC      A novel hamster cytosolic phospholipase A2/B (sPLA2/B) (AAW17849) is
CC      thought to be involved in the arachidonic acid cascade. Its amino acid
CC      sequence was deduced from a cDNA clone (AAT68827) obt'd. from a CHO-CDX
CC      cDNA library. The recombinant enzyme has been expressed in CHO and COS
CC      host cells. Human sPLA2/B polypeptides (see also AAW17845-48) have also
CC      been isolated. These can be used to screen for inhibitors useful as
CC      antiinflammatory agents that block the arachidonic acid cascade in
CC      mammals. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX      Sequence 752 AA;
XX
Qy      Query Match      91.2%; Score 3302.5; DB 2; Length 752;
Qy      Best Local Similarity 90.4%; Pred. No. 0;
Qy      Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
Db      1 MOPFGLVMTFSGVTLFSPNPFYKEVAVADYSSDRVREBQGLIFONTPNRTMPCVLY 60
Db      1 MOPFGLVMTLSSVTLFSPNPFYKEISVADYSHSRVREBQGLIFONASNTMDCILV 60
Qy      61 NPNNSQGFRLFQLELEADALVNFHOYSQQLPFYESSPOVLTTEVLQHLTDLIRNHPSW 120
Db      61 SPNHPHSGFRLFQLESEADALVNFQPSQQLPFYESSQVVLHVEVLQHLSDLIRSHPSW 120
Qy      121 SVNHLAVEIGIRECFHHSRIISCANCAENBEGCTPLHACKKDGILVELVQYCHTQND 180
Db      121 TVTHLAVEIGIRECFHHSRIISCANSTENEBGCTPLHACKKDSILVELVQYCHAQND 180
Qy      181 VTQKGETAHYAVVQGNNSQVQLQLGRNAVAGLNQVNNQGLPTPLHACQKQKQEMRVLL 240
Db      181 VTQKGETAHYAVVQGNNSQVQLQLGKNASAGLNQVAKGSLTPLHLACQKQKQEMRVLL 240
Qy      241 LCNARCNIMGPNGYPIHSAMKFSQKCAEMTISMDSSQIHSKDPYRGASPLHAKNAEMA 300
Db      241 LCNARCNWMPGSGPIHTAMKFSQKCAEMTISMDSSQIHSKDPYRGASPLHAKNAEMA 300
Qy      301 RMLKRGCVNNTSSAGNTALHGVNMRPDCALVLLTHGANADARGEHNTPLHLAMSK 360
Db      301 RMLKRGCVNNTSSAGNTALHGVNMRPDCALVLLTHGANADARGEHNTPLHLAMSK 360
Qy      361 DNVEMLKALIVFGAEVDPNDPGETPTPLASKIGK-LQDLMIHSRAKPAFIISMRDEK 419
Db      361 DNVEMLKALIVFGAEVDPNDPGETPTPLASKIGK-LQDLMIHSRAKPAFIISMRDEK 420
Qy      420 RTDHLCLDGGGVKGLIIITQLIAIEKASGAVATKDLFDVAVGTSGIILALAILHSSKM 479
Db      421 RIHDHLCLDGGGVKGLIIITQLIAIEKASGAVATKDLFDVAVGTSGIILALAILHSSKM 480
Qy      480 AYNRGMVFRMKDVEFGSRPYESGPLEEFLKREGEHTKMTDVAKKPVMLTGLISDRQPA 539
Db      481 AYNRGMVFRMKDVEFGSRPYESGPLEEFLKREGEHTKMTDVAKKPVMLTGLISDRQPA 540
Qy      540 ELHLFRNYDAPETVREPRFNQNNVLRPPAOPSDQVLRARSSGAFTYFRPNRFLDGG 599
Db      541 ELHLFRNYDAPETVREPRFNQNNVLRPPAOPSDQVLRARSSGAFTYFRPNRFLDGG 600
Qy      600 LLAANNPTLDMTEIHEYNODLIRKQGNKYKLSIVSLGTGRSPQVPTCVDFRPSNP 659
Db      601 LLAANNPTLDMTEIHEYNODMIRKQGNKYKLSIVSLGTGRSPQVPTCVDFRPSNP 660
Qy      660 WEIAKTVFGAKELGKRVVDDCTDPDGR 686
Db      661 WEIAKTVFGAKELGKRVVDDCTDPDGR 687

RESULT 12
AAW81825
ID      AAW81825 standard; protein; 752 AA.
XX
AC      AAW81825;

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XX 02-FEB-1999 (first entry)
DT Chinese hamster calcium independent cPLA2/B protein.
XX
XX
XX
XX Calcium independent; cytosolic phospholipase A2/B; cPLA2/B; screening;
KM anti-inflammatory; arachidonic acid cascade; Chinese hamster.
XX
XX Crictetus griseus.
XX
XX US840511-A.
PN
XX
XX 24-NOV-1998.
PD
XX
XX 23-OCT-1996; 96US-00735716.
PF
XX
XX 27-JUL-1994; 94US-00281193.
PR
XX 14-APR-1995; 95US-00422106.
PR (GEMV ) GENETICS INST INC.
XX
XX Tang J, Jones S;
PI
XX WPI; 1999-034032/03.
XX N-PSDB; AAV64840.
DR
XX Screening assay for phospholipase inhibitors - using specified
PT phospholipase polypeptide.
XX
XX Claim 1b; Col 21-24; 24pp; English.
PS
XX This sequence represents a novel calcium independent cytosolic
CC phospholipase A2/B enzyme isolated from Chinese hamster ovary cells. This
CC protein can be used for screening unknown compounds for anti-inflammatory
CC activity mediated by the arachidonic acid cascade
XX
XX Sequence 752 AA.
SQ
Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 62; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
QY 1 MGFGRGLVNTFSQVNTLFSNPPRYKAVAVADYSSDVRREGGQILFQNTPNRTWDCVLY 60
DB 1 MGFGRGLVNTFSQVNTLFSNPPRYKAVAVADYSSDVRREGGQILFQNTPNRTWDCVLY 60
QY 61 NPNRSOSGPRFLFOLELEADALVNFHOVSSQLLPYESSPOVLTREVYQHLTDLRNPSW 120
DB 61 SPNNPNSGPRFLFOLELEADALVNFHOVSSQLLPYESSPOVLTREVYQHLTDLRNPSW 120
QY 121 SVALAVELQIRRCFHHRSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
DB 121 TVTHLAVELQIRRCFHHRSRIISCANSTENEGCTPLHLACRKDGSELIVELVOYCHAQMD 180
QY 181 VTYYKGETVHYAVQGNQVQLQGERNAVAGLQVNNQGITPLHLACQIGKQEMRVVL 240
DB 181 VTNNKETATAYAVQGNQVQLQGERNAVAGLQVNNQGITPLHLACQIGKQEMRVVL 240
QY 241 LCNARCNIMGPNGPYHSNPKFSOKGCAEMIIISDSSQHSKOPRYGASPLHAKNAEMA 300
DB 241 LCNARCNIMGPNGPYHSNPKFSOKGCAEMIIISDSSQHSKOPRYGASPLHAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHGVNMRPDCAILVLTTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKGCNVNSTSSAGNTALHGVNMRPDCAILVLTTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMLKALVFGAEVDTPNDPFGTPTPLASKIGK-LQDLMHISRAKRPPIISGMDK 419
DB 361 DNVEMLKALVFGAEVDTPNDPFGTPTPLASKIGK-LQDLMHISRAKRPPIISGMDK 419
QY 420 RTDHLCLDGGGKGLIITQILAIKASGVAITKDLFDVAVAGSTGGIILALILHSKSM 479
DB 421 RTDHLCLDGGGKGLIITQILAIKASGVAITKDLFDVAVAGSTGGIILALILHSKSM 480

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QY 480 AYMRGMYFRMKDEVFGSRAPYESGPLLEBFLKREFGHTTQWTDYRKPKVMTGTLSDRQPA 539
DB 481 AYMRGVYFRMKDEVFGSRAPYESGPLLEBFLKREFGHTTQWTDYRKPKVMTGTLSDRQPA 540
QY 540 ELHLFRNYDAPEVIRPRFRQNNLAPPAQPSQLYWRARSSGAPTYFRPRGRFLDGG 599
DB 541 ELHLFRNYDAPEVIRPRFRQNNLAPPAQPSQLYWRARSSGAPTYFRPRGRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNODLIRKGOANKVKLSIVSLGTGRSPQVPTCVDFVFRSPN 659
DB 601 LLANNPTLDAMTEIHEYNODLIRKGOANKVKLSIVSLGTGRSPQVPTCVDFVFRSPN 660
QY 660 WELAKTVFGAKELGKRVVDCCTDPDGR 686
DB 661 WELAKTVFGAKELGKRVVDCCTDPDGR 687
RESULT 13
ABB82215
ID ABB82215 standard; protein; 752 AA.
XX
XX ABB82215;
AC
XX 08-JAN-2003 (first entry)
DT
XX Calcium independent phospholipase A2/B (cPLA2/B) (clone 9).
XX
XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
KM anti-inflammatory; antiarthritic; antipneumatic; antirheumatic; cytosolic;
KM antileukemic.
XX
XX Unidentified.
XX US2002106364-A1.
PN
XX 08-AUG-2002.
PD
XX
XX 09-AUG-2001; 2001US-00927180.
PF
XX
XX 27-JUL-1994; 94US-00281193.
PR 14-APR-1995; 95US-00422106.
PR 14-APR-1995; 95US-00422106.
PR 26-JUN-1995; 95WO-US008069.
PR 08-NOV-1995; 95US-00555568.
PR 09-SEP-1998; 98US-00149988.
PR 06-MAR-2000; 2000US-00519223.
XX
XX (GEMV ) GENETICS INST INC.
XX
XX Jones S, Tang J;
PI
XX WPI; 2002-739923/80.
XX N-PSDB; ABV73007.
DR
XX Novel composition comprising purified mammalian calcium independent
PT phospholipase enzyme, useful for the screening of inhibitors of
XX phospholipase activity, is active in the absence of calcium.
XX
XX Example 4; Page 10-12; 41pp; English.
XX
XX The invention relates to a purified mammalian calcium independent
CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
CC characterized by activity in the absence of calcium and has a molecular
CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying an
CC inhibitor of phospholipase activity which involves combining (I),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated

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CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (1) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a cPLA2/B enzyme (clone 9)

XX Sequence 752 AA;

Query Match 91.2%; Score 3302.5; DB 5; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOFFGRVNTFSGVTNLFSPNPRKVEAVADYSSDVRBEGQLIFONTPNRTWDCVLY 60
 DB 1 MOFFGRVNTLSSVTNLFSPNPRKVEAVADYSSDVRBEGQLIFONTPNRTWDCVLY 60
 QY 61 NPNRSQGFRLFOLEADALVNFHQSOLLPFYSSPOVLTETVLOHLTDLIRNHPW 120
 DB 61 SPNPSGDFRLFOLESADALVNFHQSOLLPFYSSPOVLTETVLOHLSDLIRNHPW 120
 QY 121 SVNHLAVELGIRCFHHSRIISCANCAENBEGCTPLHACKRKGDEILVELVOYCHTOMD 180
 DB 121 TVTHLAVELGIRCFHHSRIISCANSTENEGCTPLHACKRKGDEILVELVOYCHTOMD 180
 QY 181 VTQYKGETVHYAVQDGNQVQLQGLGRNAVAGLNQVNNQGLTPLHLACQKQEMVRL 240
 DB 181 VTQYKGETVHYAVQDGNQVQLQGLGRNAVAGLNQVNNQGLTPLHLACQKQEMVRL 240
 QY 241 LCNARCINMGPNNGYPIHSAKFSGKCAEMIISSDSSQHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCINMGPNNGYPIHSAKFSGKCAEMIISSDSSQHSKDPYRGASPLHAKNAEMA 300
 QY 301 RMLIKRGCVNVSSTSSAGNTALHGVNENRPPDCAVLLTHGANADARCEHGTPLHLSMSK 360
 DB 301 RMLIKRGCVNVSSTSSAGNTALHGVNENRPPDCAVLLTHGANADARCEHGTPLHLSMSK 360
 QY 361 DNEMITKALVFGAEVTPNDPFGETPTPLASKIGK-LQDLMHSRARKPAFIIGSMDEK 419
 DB 361 DNEMITKALVFGAEVTPNDPFGETPTPLASKIGK-LQDLMHSRARKPAFIIGSMDEK 419
 QY 420 RTDHLCLDGGGVKGIILQGLAIKASGVATKDLFDWVAGTSGIILALILHSKSM 479
 DB 420 RTDHLCLDGGGVKGIILQGLAIKASGVATKDLFDWVAGTSGIILALILHSKSM 479
 QY 480 AYNGMTFRMKDVFRCSPRESGPLEPLKREFGERTKMTDVKPYVMTLGTLSDRQA 539
 DB 480 AYNGMTFRMKDVFRCSPRESGPLEPLKREFGERTKMTDVKPYVMTLGTLSDRQA 539
 QY 540 ELHLFRYVDAPEVTRERFNONVNLBPAPSDQLVWRARSSGAATYFRPNRFLDGG 599
 DB 540 ELHLFRYVDAPEVTRERFNONVNLBPAPSDQLVWRARSSGAATYFRPNRFLDGG 599
 QY 600 LLANNPTLDAMTEIHEYNODLIRKQANKYKLSIVSLGTGRSPQVPTCVDFRPSNP 659
 DB 600 LLANNPTLDAMTEIHEYNODLIRKQANKYKLSIVSLGTGRSPQVPTCVDFRPSNP 659
 QY 660 WEHLAKTVFGAKELGKMYVDCCTPDGR 686
 DB 660 WEHLAKTVFGAKELGKMYVDCCTPDGR 686
 QY 661 WEHLAKTVFGAKELGKMYVDCCTPDGR 687
 DB 661 WEHLAKTVFGAKELGKMYVDCCTPDGR 687

RESULT 14
 ADD6244
 ID ADD6244 standard; protein; 751 AA.

XX ADD6244;

XX 29-JAN-2004 (first entry)

XX Rat Protein P97570, SEQ ID NO 11919.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX XX
 XX Rattus norvegicus.
 OS
 PN W02003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002MO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI
 PI Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; P97570.
 PT
 PT New composition comprising two or more isolated polypeptides, useful for
 PS preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 751 AA;

Query Match 90.4%; Score 3257; DB 7; Length 751;
 Best Local Similarity 89.7%; Pred. No. 0;
 Matches 616; Conservative 29; Mismatches 40; Indels 2; Gaps 2;

QY 1 MOFFGRVNTFSGVTNLFSPNPRKVEAVADYSSDVRBEGQLIFONTPNRTWDCVLY 60
 DB 1 MOFFGRVNTLSSVTNLFSPNPRKVEAVADYSSDVRBEGQLIFONTPNRTWDCVLY 60
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 DB 61 SPNPSGDFRLFOLESADALVNFHQSOLLPFYSSPOVLTETVLOHLSDLIRNHPW 119
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Db 600 LLANNPFLDAMTEIHEYNQDMIRKQANKYKLSIVSLGTRSPQVPTCVDFRPSNP 659
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Db 660 WELAKTVFGAKELGKRVVDDCTDPDGR 686

RESULT 15
ADE60532
ID ADE60532 standard; protein; 751 AA.
AC ADE60532;
DT 29-JAN-2004 (first entry)
DE Rat Protein P97570, SEQ ID NO 6441.
OS Rat; pain: neuronal tissue; gene therapy; spinal segmental nerve injury;
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX Rattus norvegicus.
XX PN MO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WC-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO ) GEN HOSPITAL CORP.
XX PA (FARB ) BAYER AG.
XX PI WOOLF C, D'URSO D, Befort K, Costigan M;
XX DR WPI, 2003-268312/26.
XX DR GENBANK; P97570.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX PS Claim 1, Page, 1017pp; English.
```

```
XX CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPD at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 751 AA;
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Query Match 90.0%; Score 3257; DB 7; Length 751;
Best Local Similarity 89.7%; Pred. No. 0;
Matches 616; Conservative 29; Mismatches 40; Indels 2; Gaps 2;
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Qy 1 MOFFGRVNTFGSVTLFSPNPRVEKAVADYSSDRVREEGQLIFONTPTWQCVV 60
Db 1 MOFFGRVNTLSSVTNLFSPNPRFAKESLADYASSRVEEGQLILQNASNTWQCDLV 60
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Db 61 SPNPSQDRFLRQLEADAVLVNFQYSSQLPFYESSQVLAHVLO-LTDIRNHPM 119
Qy 121 SVAHAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKDGSIIVELVOYCTQND 180
Db 120 TVTHLAVELGIRECFHHSRIITCANSTENEBGCTPLHLACRKDSEIIVELVOYCAQMD 179
Qy 181 VTPYKRETPHYAVQGDNPVQLDLGKNASAGLQVNNQGLTPLHLACQWQKQEMRVLL 240
Db 180 VTNNKGTAFHYAVQGDNPVQLDLGKNASAGLQVNNQGLTPLHLACQWQKQEMRVLL 239
Qy 241 LCNARCNIMGPNPGPIHSAKMFQKGCACEMTISMDSSQIHSKDPYASPLHAKNAEMA 300
Db 240 LCNARCNIMGPGGPIHTAMKFSQKGCACEMTISMDSSQIHSKDPYASPLHAKNAEMA 299
Qy 301 RMLLKRCGVNSTSSAGNTALHGVNRRPDCAILVLTGKANADARGEHNTPLHLAMSK 360
Db 300 RMLLKRCGVNSTSSAGNTALHVAVTNRFPDCVWVLLTGYKANAGARGEHNTPLHLAMSK 359
Qy 361 DNVEMLKALVFGAEVDTPNDPGEPTPLASKIGK-LQDLMHSRARKPAFIISMRDEK 419
Db 360 DNNEMLKALVFGAEVDTPNDPGEPTPLASKISKQLODIMPVSRARKPAFIISMRDEK 419
Qy 420 RTDHLCLDGGGKGLIIQLLAIKASGVAATKDLFDWVAGSTGGIALLIHSKSM 479
Db 420 RTDHLCLDGGGKGLVITQLLAIKASGVAATKDLFDWVAGSTGGIALLIHSKSM 479
Qy 480 AYNRGMVFRMKDEVFRGSRPYESGPLEEPLKREFGHTKMTDVRKPKVMTGTLSDRQPA 539
Db 480 AYNRGMVFRMKDEVFRGSRPYESGPLEEPLKREFGHTKMTDVKPKVMTGTLSDRQPA 539
Qy 540 ELHLFRNYDAPEYVRERPNQVNLPRPAPSDQVWRAARSSGAATYFRPNGRFLDGG 599
Db 540 ELHLFRNYDAPEYVRERPNQVNLPRPAPSDQVWRAARSSGAATYFRPNGRFLDGG 599
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| Qy | 600 | LLANNPTLDAMTEIHEYNODLIRKQANRYKXISIVVSLCTGRSPQVPTCYDVFPRSPNP | 659 |
| Db | 600 | LLANNPTLDAMTEIHEYNODMIRKGOENKVKLSIVVSLGTGKSPQVPTCYDVFPRSPNP | 659 |
| Qy | 660 | WEIAKTVFGAKELGKRVVDCCTDPDGR | 686 |
| Db | 660 | WEIAKTVFGAKELGKRVVDCCTDPDGR | 686 |

Search completed: December 15, 2004, 13:08:08
 Job time : 142.101 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:52:55 ; Search time 17.7917 Seconds
(without alignments)
2130.736 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 2078 | 99.7 | 851 | 2 | T12503 hypothetical prote |
| 2 | 332 | 15.9 | 3924 | 2 | S37431 ankyrin 2, neuroma |
| 3 | 318 | 15.3 | 2039 | 2 | T15347 ankyrin-related un |
| 4 | 313.5 | 15.0 | 1549 | 2 | T13940 ankyrin - fruit fl |
| 5 | 296 | 14.2 | 4377 | 2 | A55575 ankyrin 3, long sp |
| 6 | 294 | 14.1 | 1856 | 2 | B35049 ankyrin 1, erythro |
| 7 | 294 | 14.1 | 1880 | 2 | A35049 ankyrin 1, erythro |
| 8 | 294 | 14.1 | 1881 | 1 | SJH0K ankyrin 1, erythro |
| 9 | 293 | 14.1 | 1765 | 2 | T42714 ankyrin 3, splice |
| 10 | 293 | 14.1 | 1940 | 2 | T42715 ankyrin 3, splice |
| 11 | 293 | 14.1 | 1943 | 2 | T42716 ankyrin 3, splice |
| 12 | 293 | 14.1 | 1961 | 2 | T42716 ankyrin 3, splice |
| 13 | 285 | 13.7 | 1848 | 2 | S37771 ankyrin, erythrocy |
| 14 | 285 | 13.7 | 1862 | 2 | T49502 ankyrin - mouse |
| 15 | 281.5 | 13.5 | 397 | 2 | T46445 hypothetical prote |
| 16 | 258 | 12.4 | 1023 | 2 | T26261 hypothetical prote |
| 17 | 255.5 | 12.3 | 1411 | 2 | S30355 alpha-latrotoxin |
| 18 | 249 | 11.9 | 791 | 2 | T42691 hypothetical prote |
| 19 | 248.5 | 11.9 | 1435 | 2 | T32930 hypothetical prote |
| 20 | 244 | 11.7 | 247 | 2 | D84448 probable ankyrin l |
| 21 | 237 | 11.4 | 1401 | 2 | S11527 alpha-latrotoxin p |
| 22 | 236 | 11.3 | 2437 | 2 | S42612 transmembrane prot |
| 23 | 234 | 11.2 | 1423 | 1 | T37275 death-associated p |
| 24 | 233 | 11.2 | 1436 | 1 | A82149 hypothetical prote |
| 25 | 231 | 11.1 | 934 | 1 | H71274 probable ankyrin- |
| 26 | 225 | 10.8 | 1071 | 2 | T22327 hypothetical prote |
| 27 | 218.5 | 10.5 | 368 | 2 | T18184 ankyrin repeat pro |
| 28 | 216.5 | 10.4 | 633 | 2 | T27499 hypothetical prote |
| 29 | 216.5 | 10.4 | 1184 | 2 | T00253 gene Ankhzn protel |

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| 30 | 215 | 10.3 | 907 | 2 | I50404 p50B/p97 (Lyt-10) |
| 31 | 213.5 | 10.2 | 933 | 2 | S17233 transcritpion fact |
| 32 | 213 | 10.2 | 1662 | 2 | T14151 inv protein - mous |
| 33 | 212 | 10.2 | 1062 | 2 | T30255 inverain - mouse |
| 34 | 208.5 | 10.0 | 606 | 2 | AC2508 hypothetical prote |
| 35 | 206.5 | 9.9 | 2352 | 2 | T30201 Notch homolog prot |
| 36 | 206 | 9.9 | 2531 | 2 | A46019 notch-1 protein - |
| 37 | 205 | 9.8 | 662 | 2 | E84725 ankyrin-like prote |
| 38 | 205 | 9.8 | 900 | 2 | A42024 transcritpion fact |
| 39 | 202 | 9.7 | 664 | 2 | A56695 notch2 protein hom |
| 40 | 202 | 9.7 | 2471 | 2 | A49128 cell-fate determin |
| 41 | 201 | 9.6 | 1031 | 2 | T43458 hypothetical prote |
| 42 | 200.5 | 9.6 | 2584 | 2 | T24158 hypothetical prote |
| 43 | 199.5 | 9.6 | 2606 | 2 | T24157 notch protein homo |
| 44 | 199.5 | 9.6 | 2531 | 2 | S18188 notch protein homo |
| 45 | 199.5 | 9.6 | 2553 | 2 | A40043 notch protein homo |

ALIGNMENTS

| | |
|--|---|
| RESULT 1 | |
| T12503 | hypothetical protein DKFZp434A102.1 - human (fragment) |
| C:Species: | Homo sapiens (man) |
| C:Date: | 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999 |
| C:Accession: | T12503 |
| R:Amorize, W. ; Wilkner, U. ; News, H.W. ; Gassenhuber, J. ; Wiemann, S. | submitted to the protein Sequence Database, June 1999 |
| A:Reference number: | Z17527 |
| A:Accession: | T12503 |
| A>Status: | preliminary |
| A:Molecule type: | mRNA |
| A:Residues: | 1-851 <AMS> |
| A:Cross-references: | EMBL:AL080187 |
| A:Experimental source: | adult testis; clone DKFZp434A102 |
| C:Genetics: | |
| A>Note: | DKFZp434A102.1 |
| Query Match | 99.7% ; Score 2078 ; DB 2 ; Length 851 ; |
| Best Local Similarity | 99.7% ; Pred. No. 1.6e-168 ; |
| Matches 393 ; Conservative | 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ; |
| QY | 1 MGFGRVLTFTSGVTNLFPSNPFVKEVAADYTSSDRVEEGQLIFONTPNRTWCVLV 60 |
| DB | 46 MGFGRVLTFTSGVTNLFPSNPFVKEVAADYTSSDRVEEGQLIFONTPNRTWCVLV 105 |
| QY | 61 NPNNSQSGFRLLPQLLEADALVNFHQQSSQLLPFYESSPOVLHTEVLOHLDLIRNHPGW 120 |
| DB | 106 NPNNSQSGFRLLPQLLEADALVNFHQQSSQLLPFYESSPOVLHTEVLOHLDLIRNHPGW 165 |
| QY | 121 SVAHLAVELGIRECFHSHRIISCANCAENEBEGTPLHLACRKDGGLVLELVGYCTQMD 180 |
| DB | 166 SVAHLAVELGIRECFHSHRIISCANCAENEBEGTPLHLACRKDGGLVLELVGYCTQMD 225 |
| QY | 181 VVDYKGETVPHVAVQDNGSOVLQLGRNAVAGLNQVNNQGLPLHLACOLGKQEMRVLL 240 |
| DB | 226 VVDYKGETVPHVAVQDNGSOVLQLGRNAVAGLNQVNNQGLPLHLACOLGKQEMRVLL 285 |
| QY | 241 LCNARCNINMGPNYPPIHSAKMSQKCAEMIISMDSQIHSKDPRIYGAASPLHAKNAEMA 300 |
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| QY | 301 RMLIKRGCVNVSSTSSAGNTALHVGVRNRPDCAIYVLTGANAADARGEGNTPLHLAMSK 360 |
| DB | 346 RMLIKRGCVNVSSTSSAGNTALHVGVRNRPDCAIYVLTGANAADARGEGNTPLHLAMSK 405 |
| QY | 361 DNVEMTKALIVGAEVDPNDGEPTPLASKIG 394 |
| DB | 406 DNVEMTKALIVGAEVDPNDGEPTPLASKIG 439 |
| RESULT 2 | |

S37431
 ankyrin 2, neuronal long splice form - human
 N/Alternate names: ankyrin B, 40K splice form; ankyrin-B; brain ankylrin; non-erythroid
 N/Contains: ankylrin 2, short form
 C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
 C/Accession: S37431, A39643, B39643, A40334, A49462, S14533, S14569
 R/Chan, M.
 Submitted to the EMBL Data Library, September 1993
 A/Reference number: S37431
 A/Accession: S37431
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-3924 <CHA>
 A/Cross-references: UNIPROT:Q01484; EMBL:Z26634; NID:9406287; PIDN:CAA81387.1; PID:9406287
 R/Otto, E.; Kunitomo, M.; McLaughlin, T.; Bennett, V.
 J. Cell Biol. 114, 241-253, 1991
 A/Title: Isolation and characterization of cDNAs encoding human brain ankylrins reveal a
 A/Reference number: A39643; MUID:91302466; PMID:1830053
 A/Accession: A39643
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-2077 <OT1>
 A/Cross-references: GB:X56957
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 A/Status: preliminary
 A/Molecule type: mRNA
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 A/Cross-references: EMBL:X56958
 R/Tee, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,
 Genomic 10, 858-866, 1991
 A/Title: Isolation and chromosomal localization of a novel nonerythroid ankylrin gene.
 A/Reference number: A40334; MUID:92009921; PMID:1833308
 A/Accession: A40334
 A/Molecule type: DNA
 A/Residues: 463-474, 'PE', 477-495 <TSE>
 A/Cross-references: GB:M37123; NID:gl78647; PIDN:AAA62828.1; PID:gl78648
 R/Chan, W.; Kordeli, B.; Bennett, V.
 J. Cell Biol. 123, 1463-1473, 1993
 A/Title: 440-kD ankylrinB: structure of the major developmentally regulated domain and se
 A/Reference number: A49462; MUID:94075409; PMID:8253844
 A/Accession: A49462
 A/Status: preliminary; nucleic acid sequence not shown
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 A/Cross-references: GDB:127607; OMIM:106410
 A/Map position: 4q25-4q27
 C/Superfamily: ankylrin; ankylrin repeat homology
 C/Keywords: alternative splicing
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F;727-759/Domain: ankyrin repeat homology <AN21>
F;760-792/Domain: ankyrin repeat homology <AN22>
F;793-825/Domain: ankyrin repeat homology <AN23>

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|---------------------------|--------|--------------------|------------|--------------|
| Query Match | 15.9%; | Score 332; | DB 2; | Length 3924; |
| Best Local Similarity | 27.3%; | Pred. No. 4.8e-19; | | |
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QY      142 SCANC-----AENEBCCTPLHLACRKGDEILVELVOY----- 174
D      371 VAAHCHEVETLKLLDKRANPVARALNFTPLHACKNRIKWEILLVYKGASIOAITES 430
QY      175 ----CH-----TQMDVTQYKBEVTFHYAVOGDSOVLQGLGRNAVAG 212
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QY      213 LQNVNNGQLTPHLACQLGQOEMVAVLLLCNARCNIMGPNQY-PHISAMFQSOKCAEMI 271
D      490 VDAAREEPTPLHISRLGKETIYQULLQHMALHDAATNGYTPLHISAREQVDVASVL 549
QY      272 ISMDSQIHSDKPRYGASPLHWAK--NAEMARMLKRGCVNVTSSAGATLHVGMRN 328
D      550 --LEAGAHSLATKKGFPTPLHVAAYGSLDVAKLLQGRRAADBSAGKGLTPHVAAYHD 6070
QY      329 REPCEAVLLTHGAMDAGEHGNTPLHLAMSKDNVENMICALIVGCAVDTPNDPGEIPTF 388
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QY      389 LASKIG 394
D      668 LASQBG 673

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RESULT 3

ankyrin-related unc-44 - *Caenorhabditis elegans*

C/Date: 20-Sep-1999 #sequence revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T15347, T15346, T15344, T15345, B57282, B57283, C57282

R;Gattung, S.

A:Description: The sequence of *C. elegans* cosmid B0350.

A;Reference number: Z18332

A/Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A;CROSS-references: UNIP

A;Accession: T15346

A;Molecule type: DNA

A;Residues: 1-1000,'

A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208875; PIDN:AAA93445.1

A;Accession: T15344

[illegible]

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<GA3>  
M/NOBJLUCB: 4 1 / 40 / AM / 1.000 - 1.000 / ANNNNNNNNNN / 1.000 - 1.000 / XNNNNNNNNNNNNNNNNNNNN
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A;C:Cross-references:

A:Status: preliminary: translated from GB/EMBL/DBJ

A: Molecule type: DNP

PTBRSVEPEEERHSHOHEDHEGST' <GA4>
A;KEBIADUEH: I-I/I/18, KWEEBENKL, I/12/, U, ES, 1942, FSAFUNKS, 1950, 1960, 1965, 1970-1971, EVERE

A;CROSS-References: EMBL:U300/1; NID:gl2088/1; FID:gl2088/6; FIDN:AA453440.1
R:Otsuka. A.T.: Franco. B.: Yang. B.: Shih. K.H.: Tang. H.Z.: Zhang. Y.Y.: E

U. Cell Biol. 129, 1081-1092, 1995

A:Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in *Cad*
 A:Reference number: A57282; MUID:95263663; PMID:7744557
 A:Accession: A57282
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-852; 'GGG', 856-1000, 'SKLQHT', 1002-1119, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'H
 A:SHRD', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHIS' <OTS>
 A:Cross-references: GB:U21734; NID:g790607; PIDN:AAA65854.1; PID:g790608
 A:Accession: B57282
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'H
 A:V', 1945-1947, 'VW', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPRRASVEBEHNS', 1984-1985, 'EDHES', 1
 A:Cross-references: GB:U21731
 A:Accession: C57282
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 194, 'P', 196, 'I', 198, 'DC', 201, 'G', 409, 'AV', 412, 'Q', 414, 824, 'S', 826, 'ER', 829, 'E
 A:4', 'TIV', 1828, 'ESNS', 1833, 'OV', 1836, 'E', 1934-1935, 'EOS', 1939, 'ESSES', 1944, 'REDDGTVTT', 194
 A:Cross-references: GB:U21732; NID:g790603; PIDN:AAA65853.1; PID:g790604
 C:Genetics:
 A:Gene: C5SP:unc-44
 A:introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979
 C:Superfamily: ankyrin; ankyrin repeat homology
 F:164-192/Domain: ankyrin repeat homology <AN04>
 F:358-390/Domain: ankyrin repeat homology <AN1>
 F:391-423/Domain: ankyrin repeat homology <AN11>

Query Match 15.3%; Score 318; DB 2; Length 2039;
 Best Local Similarity 33.6%; Pred. No. 3.1e-18;
 Matches 86; Conservative 49; Mismatches 105; Indels 16; Gaps 6;

Qy 147 AENEBCCTPLHACRKGDEILVELVOYCHTQMDVTDYKGETVFNHAYVAGQDNGSQTQLLG 206
 Db 420 ATTESGLTPLHVAAPFGAIVIVYLQ-Q-CAKDPVETVREGTPLHAAKQMDVVRVLI 478
 Qy 207 RNAAVAGLQVNNQGLTPPLHACQLGKQWVRVLLCNARCNIMGPNY-PIHSAMKFSOK 265
 Db 479 RKG-ANVDQARELOTPPLHASKRGNTDIYLLQAGANSATTRDYSPLHAAEGOE 537
 Qy 266 GCAEMTISDSSQIHSKD---PRYASPLHMAK--NAEMAMLLKKGCVNSTSSAGN 318
 Db 538 EVAIGILLD-----HNADKTLTKKGTPLHLSKKGNEVLVALLERGPVDEIGNQV 591
 Qy 319 TALHVGWNRNRCALVLTGANDARGEHGTPLHANSKNVEMKALIVFGAEVDT 378
 Db 592 TPLHVAHYVNDKVMILLENGASAKAAKGYTPLHIAKKQMEIASLTLOPKADPNA 651
 Qy 379 PNDGFTPTPLASKIG 394
 Db 652 KSRAGFTPLHLSAQBEG 667

RESULT 4

T13940
 ankyrin - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*
 C:date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C:Accession: T13940

R:pubreul, R.R.; Yu, J.
 Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994

A:Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in *Drosoph*

A:Reference number: Z17820; MUID:95024098; PMID:7937942

A:Accession: T13940

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-1549 <DUB>

A:Cross-references: UNIPROT:Q24241; EMBL:L35601; NID:9557083; PID:9557084; PIDN:AA037208

C:Genetics:

A:Cross-references: FlyBase:FBgn0011747

Query Match 15.0%; Score 313.5; DB 2; Length 1549;
 Best Local Similarity 23.9%; Pred. No. 5.1e-18;

Matches 114; Conservative 68; Mismatches 144; Indels 151; Gaps 16;

Qy 45 IIFONTNRTWCULVNPKNSSGFRPLFOLEBADLVNPROXSOLL-----PFRESSP 99
 Db 319 LIQONAP-----ILTKRTGSLALHM-----AAQGEHEAALLLDNKAPEDEVTV 364
 Qy 100 QVL-----HFEVLQHLTDLIRNHP-----WSVAHLA-----VELGIRECPH 136
 Db 365 DYTLHVAHAGCHVAKVAKLDDYKANPAPALNGFTPLHIAKCKKRIKIVELLIK--H 421
 Qy 137 HSRITSCANCAENBECTPLHACRKGDEILVELVOYCHTQMDVTDYKGETVFNHAYVAG 196
 Db 422 GANI-----GATTESGLTPLHVAAPFGAIVIVYLQ-Q-CAKDPVETVREGTPLHAAKQMDVVRVLI 478
 Qy 197 DNSQVQLLGRNAV-----AGLQVNNQGLTPPLHACQLGKQWVRVLLCNARCNIMGPN 252
 Db 476 NQADIRILLRSKAKDAIVREGOTPLHVASRLGNINIMLLQHGAEINAQNDKXSALH 535
 Qy 211 -----AGLQVNNQGLTPPLHACQLGKQWVRVLLCNARCNIMGPN 252
 Db 536 IAAKGEENIVOLVLENGAENNAVTKKGTPLHIAKCKKQNVQVQLLQNGASIDPQGN 595
 Qy 253 GY-PIHSAMKFSOKGCAEMTISDSS-----QI--HSKD- 283
 Db 596 DVTPLHVAHYVNDKVMILLENGASAKAAKGYTPLHIAKKQMEIASLTLOPKADPNA 651
 Qy 284 ---PRYASPLHMAK--NAEMAMLLKKGCVNSTSSAGNTALHVGWNRNRCALVLTG 337
 Db 656 NIISKSGFPLHIAAGQGVNDVQVLEYG-ISAARKGLTPLHVAOEGHVLVQOILL 714
 Qy 338 THGANDARGEHGTPLHANSKNVEMKALIVFGAEVDTNPDGFTPTPLASKIG 394
 Db 715 EHGANSERTRNGYTPPLHVAHYVNDKVMILLENGASAKAAKGYTPLHIAKKQMEIASLTLOPKADPNA 771

RESULT 5

A55575

ankyrin 3, long splice form - human

N:Alternate names: ankyrin G

C:Species: Homo sapiens (man)

C:date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004

C:Accession: A55575

R:Kordeli, E.; Lambert, S.; Bennett, V.

J. Biol. Chem. 270, 2352-2359, 1995

A:Title: Ankyrin-G, A new ankyrin gene with neural-specific isoforms localized at the ax

A:Reference number: A55575; MUID:95138209; PMID:7836469

A:Accession: A55575

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-4377 <KOR>

A:Cross-references: UNIPROT:Q12955; GB:U13616; NID:9608024; PIDN:AAA64834.1; PID:9608025

C:Genetics:

A:Gene: GDB:ANK3

A:Cross-references: GDB:424503; OMIM:600465

A:Map position: 10q21-10q21

C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

C:Keywords: alternative splicing; periplasmic membrane protein

F:106-138/Domain: ankyrin repeat homology <AN01>

F:106-138/Domain: ankyrin repeat homology <AN02>

F:139-171/Domain: ankyrin repeat homology <AN03>

F:172-200/Domain: ankyrin repeat homology <AN04>

F:201-233/Domain: ankyrin repeat homology <AN05>

F:234-266/Domain: ankyrin repeat homology <AN06>

F:267-299/Domain: ankyrin repeat homology <AN07>

F:300-332/Domain: ankyrin repeat homology <AN08>

F:333-365/Domain: ankyrin repeat homology <AN09>

F:366-398/Domain: ankyrin repeat homology <AN10>

F:399-431/Domain: ankyrin repeat homology <AN11>

F:432-464/Domain: ankyrin repeat homology <AN12>

F:465-497/Domain: ankyrin repeat homology <AN13>

F:498-530/Domain: ankyrin repeat homology <AN14>

F:531-563/Domain: ankyrin repeat homology <AN15>

F:564-596/Domain: ankyrin repeat homology <AN16>

F:597-629/Domain: ankysin repeat homology <AN17>
 F:630-662/Domain: ankysin repeat homology <AN18>
 F:634-666/Domain: ankysin repeat homology <AN19>
 F:696-728/Domain: ankysin repeat homology <AN20>
 F:729-761/Domain: ankysin repeat homology <AN21>
 F:762-794/Domain: ankysin repeat homology <AN22>
 F:795-827/Domain: ankysin repeat homology <AN23>

Query Match 14.2%; Score 296; DB 2; Length 4377;
 Best Local Similarity 29.2%; Pred. No. 6, Se-16;
 Matches 81; Conservative 54; Mismatches 130; Indels 12; Gaps 6;

QY 124 HLAVELGIRECFHRSRIISGCAENEGCTPLHLACRKGDELVELVOYCHTQMDVTD 183
 Db HISARLGKADIVQQLQGGASPNAAATSGYTPHLHSREGEHVAFLDH-GASISITT 552
 QY 184 YKEETVPHVAQGDNSQVLLQGRNAVAGLVANNQGLTPHLACQLGKDEMRVLLCN 243
 Db KKGFPTLHVAAKQKLEVNALLQKS-ASPDAAKSGSLTPHLVAAHYDNKVALLLDDG 621
 QY 244 ARGNMGPNQY-PHSAMKFSQKCAEMII--SMDSQHSKDPYVGSPLHNAK--NA 297
 Db 622 ASHMAAAKNGYTPHLPAKGNQMDIATTLLEGADANA---TROGIASVHLAAQEGH 677
 QY 298 EMARMLKRGCVNSTSSAGNTALHVGVMKRPDCALVLLTHGANDARGEHNTPLHLA 357
 Db 678 DMVSLILGRNAVNLNKSGLTPLHLAAGEDRVAVVELVQGAHVDAQTKMGYTPHLVG 737
 QY 358 MSKDNVEMIKALVFGAEVDTPNDPFGFTPTFLASKIG 394
 Db 738 CHYGNITKIVNLLQHSKAVNAKTKNGYTPHLQAQOG 774

RESULT 6

B35049
 ankysin 1, erythrocyte splice form 3 - human

N/Alternate names: ankysin 2.1, erythrocyte; ankysin-R
 N/Contains: ankysin 2.2, erythrocyte
 C/Species: Homo sapiens (man)

C/Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998

C/Accession: B35049
 R/Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A/Title: CDNA sequence for human erythrocyte ankysin.

A/Reference number: A35049; MUID:90175370; PMID:1689849

A/Accession: B35049

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1856 <LAM>

C/Genetics:

A/Gene: GDB:ANK1; ANK

A/Cross-references: GDB:118737; OMIM:182900

A/Map position: 8p11.2-8p11.2

C/Superfamily: ankysin; ankysin repeat homology

C/Keywords: alternative splicing

F:2-1856/Product: ankysin 1, erythrocyte form 3 #status predicted <MA1>

F:2-1513,1676-1856/Product: ankysin 2.2, erythrocyte #status predicted <MA2>

F:44-76/Domain: ankysin repeat homology <AN01>

F:77-109/Domain: ankysin repeat homology <AN02>

F:110-142/Domain: ankysin repeat homology <AN03>

F:143-171/Domain: ankysin repeat homology <AN04>

F:172-204/Domain: ankysin repeat homology <AN05>

F:205-237/Domain: ankysin repeat homology <AN06>

F:238-270/Domain: ankysin repeat homology <AN07>

F:271-303/Domain: ankysin repeat homology <AN08>

F:304-336/Domain: ankysin repeat homology <AN09>

F:337-369/Domain: ankysin repeat homology <AN10>

F:370-402/Domain: ankysin repeat homology <AN11>

F:403-435/Domain: ankysin repeat homology <AN12>

F:436-468/Domain: ankysin repeat homology <AN13>

F:469-501/Domain: ankysin repeat homology <AN14>

F:502-534/Domain: ankysin repeat homology <AN15>

F:535-567/Domain: ankysin repeat homology <AN16>

F:568-600/Domain: ankysin repeat homology <AN17>
 F:601-633/Domain: ankysin repeat homology <AN18>
 F:634-666/Domain: ankysin repeat homology <AN19>
 F:667-699/Domain: ankysin repeat homology <AN20>
 F:700-732/Domain: ankysin repeat homology <AN21>
 F:733-765/Domain: ankysin repeat homology <AN22>
 F:766-798/Domain: ankysin repeat homology <AN23>

Query Match 14.1%; Score 294; DB 2; Length 1856;
 Best Local Similarity 25.6%; Pred. No. 3e-16;
 Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LQHLTDLIRNHSWSVAHLAVELGIRECFH--SRIISGCAENF--EGCTPLHLACR 161
 Db 336 LDHLTLP-----HVA-----HCGHHRVAKVLLDKAKAPNSRALNGFTPLHIACK 380
 QY 162 KEGDELVELVOYCHTQMD-----VTQKGET 188
 Db 381 KKHVRV--ELLKTGASIDAVTESGLTPHLVASFQGLPVLKXNLLORGASPNVSNVKEI 439
 QY 189 VFHYAVQGDNSQVLLQGRNAVAGLVANNQGLTPHLACQLGKDEMRVLLCNARCN 248
 Db 440 PLHMAARAGHTVPAKYLQNK-AKVNAKAKDDQTPHLCAARIGHTMVVLLLENNAPVL 498
 QY 249 MGENGY-----PIHSAMKFSQKCAEMITSM 274
 Db 499 ATTAGTTPHLIAREGHVETVALLLEKASQAQMTKGFPTPLHVAAKYKVRVAELLER 558
 QY 275 DSSQHSKDPYVGSPLHNA---KNAEMARMLKRGCVNSTSSAGNTALHVGVMKRPD 331
 Db 559 DHP--NAAKGNLTPHLVAVHNNNDIVKLLPLRGSGHSPAMNGYTPHLPAKNOYE 616
 QY 332 CAIVLLTHGANDARGEHNTPLHLMSKDNVEMIKALVFGAEVDTPNDPFGFTPTFLAS 391
 Db 617 VARSLLQYGSANAAESVQGTTPHLAAGHAEVALLSKQANGVLGKSGTTPHLVA 676
 QY 392 KIG 394
 Db 677 QEG 679

RESULT 7

A35049
 ankysin 1, erythrocyte splice form 2 - human

N/Alternate names: ankysin 2.1, erythrocyte; ankysin-R
 N/Contains: ankysin 2.2, erythrocyte
 C/Species: Homo sapiens (man)

C/Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 09-Jul-2004

C/Accession: A35049

R/Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A/Title: CDNA sequence for human erythrocyte ankysin.

A/Reference number: A35049; MUID:90175370; PMID:1689849

A/Accession: A35049

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-1880 <LAM>

A/Cross-references: UNIPROT:P16157; GB:M28880

C/Genetics:

A/Gene: GDB:ANK1; ANK

A/Cross-references: GDB:118737; OMIM:182900

A/Map position: 8p11.2-8p11.2

C/Superfamily: ankysin; ankysin repeat homology

C/Keywords: alternative splicing; cytoskeleton

F:2-1880/Product: ankysin 1, erythrocyte form 2 #status predicted <MA1>

F:2-1513,1676-1880/Product: ankysin 2.2, erythrocyte #status predicted <MA2>

F:44-76/Domain: ankysin repeat homology <AN01>

F:77-109/Domain: ankysin repeat homology <AN02>

F:110-142/Domain: ankysin repeat homology <AN03>

F:143-171/Domain: ankysin repeat homology <AN04>

F:172-204/Domain: ankysin repeat homology <AN05>

F:205-237/Domain: ankysin repeat homology <AN06>

F:238-270/Domain: ankysin repeat homology <AN07>

F:271-303/Domain: ankryn repeat homology <AN08>
 F:304-336/Domain: ankryn repeat homology <AN09>
 F:337-369/Domain: ankryn repeat homology <AN10>
 F:370-402/Domain: ankryn repeat homology <AN11>
 F:403-435/Domain: ankryn repeat homology <AN12>
 F:436-468/Domain: ankryn repeat homology <AN13>
 F:469-501/Domain: ankryn repeat homology <AN14>
 F:502-534/Domain: ankryn repeat homology <AN15>
 F:535-567/Domain: ankryn repeat homology <AN16>
 F:568-600/Domain: ankryn repeat homology <AN17>
 F:601-633/Domain: ankryn repeat homology <AN18>
 F:634-666/Domain: ankryn repeat homology <AN19>
 F:667-699/Domain: ankryn repeat homology <AN20>
 F:700-732/Domain: ankryn repeat homology <AN21>
 F:733-765/Domain: ankryn repeat homology <AN22>
 F:766-798/Domain: ankryn repeat homology <AN23>

Query Match 14.1%; Score 294; DB 2; Length 1880;
 Best Local Similarity 25.6%; Pred. No. 3e-16;
 Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LOHLDLIRNHPMSVAHLAVELGIRECFH--SRIISCANCAENE---EGCTPLHLACR 161
 DB 336 LDHLLPL-----HVA-----HCGHRAVAKVLKDGAKPNSBALNGFTPLHIACK 380
 QY 162 KGDGLVLEVOYCHTQMD-----VTDYKGET 188
 DB 381 KHNVRW-ELLKTGASIDAVTESGLTPLHVASFMGHLPIVKNLLORGASPNVSNKVER 439
 QY 189 VPHYAVQDNGSOYLQILGRNVAAGLNQVNNQGLTPLHLACOLGKQEMVRVLLCNARCNI 248
 DB 440 PLHMAARAGHTVAKYLQNK-AKVNAKAKADDPPLHCAARIGHTMVKLLNNANPNL 498
 QY 249 MGENGY-----PIHSANKFSQKCAEMITSM 274
 DB 499 ATTAGHTPLHIAAREGHVETVALLLEKESQACWTKKGFPLHVAAKYGVRAVELLER 558
 QY 275 DSSQHSKDPRYGASPLHMA---KNAEMAMLLKRCGNVNSTSSAGNTALHVGWENRFD 331
 DB 559 DAHP--NAAGKGLTPLHVAVHNHNDIVKLLPRGSGPSPMNGYTPPLHIAKQNOVE 616
 QY 332 CAIVLTGHNADARGHGNTPLHLMASKDNVENIKALIVFGAEVDPDPNFGSTPTFLAS 391
 DB 617 VARSLIQGGSANABESVQVTPPLHLAQGBAEMVALLLSKQANGNLGNKSGTLPLHLVA 676
 QY 392 KIG 394
 DB 677 QEG 679

RESULT 8
 SUBUK
 ankryn 1, erythrocyte splice form 1 - human
 N:Alternate names: ankryn 2.1, erythrocyte; ankryn-R
 N:Contains: ankryn 2.2
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C:Accession: S08275; A33219; PC2220; A35443
 R:Lux, S.E.; John, K.M.; Bennett, V.
 Nature 344, 36-42, 1990
 A:Title: Analysis of cDNA for human erythrocyte ankryn indicates a repeated structure
 A:Reference number: S08275; MUID:90158830; PMID:2137557
 A:Accession: S08275
 A:Molecule type: mRNA
 A:Residues: 1-1881 <UNI>
 A:Cross-references: UNIPROT:P16157; EMBL:X16609; NID:G28701; PIDN:CAA34610.1; PID:G28702
 A:Accession: A33219
 A:Molecule type: protein
 A:Residues: 2-7, 'X', '9-17', 'X', '19-20', 'T', '22-30', '733-749', 'A', '751-753', '828-833', 'X', '835-855', 'X', 'X', '1367', '1383', '1427', '1601', '1630', '1686-1698', 'D', '1700', '1765-1772 <LUX>
 A:Note: 845-Arg and 1392-Thr were also found
 R:Hermann, J.; Barel, M.; Frade, R.
 Biochem. Biophys. Res. Commun. 204, 453-460, 1994

A:Title: Human erythrocyte ankryn, a cytoskeleton component, generates the p57 membrane
 A:Reference number: PC2220; MUID:95071348; PMID:7526850
 A:Accession: PC2220
 A:Molecule type: protein
 A:Residues: 910-929 <HER>
 R:Davis, L.H.; Bennett, V.
 J. Biol. Chem. 265, 10589-10596, 1990
 A:Title: Mapping the binding sites of human erythrocyte ankryn for the anion exchanger
 A:Reference number: A35443; MUID:90285190; PMID:214135
 A:Accession: A35443
 A:Molecule type: protein
 A:Residues: 'X', '5', 'X', '7-12', '403-417', 'X', '419-422', 'H', '424', 'LQ', '797-800', 'L', '802-814', '862-863', 'C:Genetics:
 A:Gene: GDB:ANK1; ANK
 A:Cross-references: GDB:118737; OMIM:182900
 A:Map position: 8p11.2-8p11.2
 C:Superfamily: ankryn; ankryn repeat homology
 C:Keywords: alternative splicing; phosphoprotein
 F:2-1881/Product: ankryn 1, erythrocyte form 1 #status predicted <MAT1>
 F:2-1512,1675-1881/Product: ankryn 2.2, erythrocyte #status predicted <MAT2>
 F:2-827/Domain: 89K #status predicted <DOM1>
 F:2-827/Region: anion exchange protein binding
 F:44-76/Domain: ankryn repeat homology <AN01>
 F:77-109/Domain: ankryn repeat homology <AN02>
 F:110-142/Domain: ankryn repeat homology <AN03>
 F:143-171/Domain: ankryn repeat homology <AN04>
 F:172-204/Domain: ankryn repeat homology <AN05>
 F:205-237/Domain: ankryn repeat homology <AN06>
 F:238-270/Domain: ankryn repeat homology <AN07>
 F:271-303/Domain: ankryn repeat homology <AN08>
 F:304-336/Domain: ankryn repeat homology <AN09>
 F:337-369/Domain: ankryn repeat homology <AN10>
 F:370-402/Domain: ankryn repeat homology <AN11>
 F:403-435/Domain: ankryn repeat homology <AN12>
 F:436-468/Domain: ankryn repeat homology <AN13>
 F:469-501/Domain: ankryn repeat homology <AN14>
 F:502-534/Domain: ankryn repeat homology <AN15>
 F:535-567/Domain: ankryn repeat homology <AN16>
 F:568-600/Domain: ankryn repeat homology <AN17>
 F:601-633/Domain: ankryn repeat homology <AN18>
 F:634-666/Domain: ankryn repeat homology <AN19>
 F:667-699/Domain: ankryn repeat homology <AN20>
 F:700-732/Domain: ankryn repeat homology <AN21>
 F:733-765/Domain: ankryn repeat homology <AN22>
 F:766-798/Domain: ankryn repeat homology <AN23>
 F:828-1382/Domain: 62K #status predicted <DOM2>
 F:828-1382/Region: spectrin binding
 F:1383-1881/Domain: 55K #status predicted <DOM3>

Query Match 14.1%; Score 294; DB 1; Length 1881;
 Best Local Similarity 25.6%; Pred. No. 3e-16;
 Matches 93; Conservative 57; Mismatches 119; Indels 94; Gaps 10;

QY 107 LOHLDLIRNHPMSVAHLAVELGIRECFH--SRIISCANCAENE---EGCTPLHLACR 161
 DB 336 LDHLLPL-----HVA-----HCGHRAVAKVLKDGAKPNSBALNGFTPLHIACK 380
 QY 162 KGDGLVLEVOYCHTQMD-----VTDYKGET 188
 DB 381 KHNVRW-ELLKTGASIDAVTESGLTPLHVASFMGHLPIVKNLLORGASPNVSNKVER 439
 QY 189 VPHYAVQDNGSOYLQILGRNVAAGLNQVNNQGLTPLHLACOLGKQEMVRVLLCNARCNI 248
 DB 440 PLHMAARAGHTVAKYLQNK-AKVNAKAKADDPPLHCAARIGHTMVKLLNNANPNL 498
 QY 249 MGENGY-----PIHSANKFSQKCAEMITSM 274
 DB 499 ATTAGHTPLHIAAREGHVETVALLLEKESQACWTKKGFPLHVAAYGVRAVELLER 558
 QY 275 DSSQHSKDPRYGASPLHMA---KNAEMAMLLKRCGNVNSTSSAGNTALHVGWENRFD 331
 DB 559 DAHP--NAAGKGLTPLHVAVHNHNDIVKLLPRGSGPSPMNGYTPPLHIAKQNOVE 616

QY 332 CAIYLTGHANADARGEHNTPELTILAMSKNVEMITKALIVGAEVDHNDRGETPTFLAS 391
 Db 617 VARSLLQYGGSSANASVGVTPPLHMAQGEHAENVALLHSKQANGNIGKNSGLTPLHVA 676
 QY 392 KIG 394
 Db 677 QEG 679

RESULT 9

T42714
ankyrin 3, splice form 2 - mouse
C:/Species: Mus musculus (house mouse)
C:/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:/Accession: T42714
R:/Peperer, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L
J. Cell Biol. 130, 313-330, 1995
A:/Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain..
A:/Reference number: Z22237; MUID:95340633; PMID:7615634
A:/Accession: T42714
A:/Status: Preliminary; translated from GB/EMBL/DBJ
A:/Molecule type: mRNA
A:/Residues: 1-1765 <PET>
A:/Cross-references: UNIPROT:O61307; EMBL:L40632; NID:g710548; PID:g710551; PIDN:AAB01605
A:/Experimental source: strain C57BL/6J; kidney
C:/Genetics:
A:/Gene: Ank3
A:/Map position: 10
A:/introns: 1587/1
A:/Superfamily: ankyrin; ankyrin repeat homology
A:/Keywords: alternative splicing

| | Query March 14.1% | Score 293.7 | DB 2: | Length 1765: |
|----|-------------------|------------------|---|--------------------|
| | Similarity 29.2% | Pred. 3.4e-16: | | |
| | Matches 81: | Conservative 55: | Mismatches 125: | Indels 16: Gaps 7: |
| Qy | 124 HLAVELG---- | IRCEFHHSRIIS | CANCAENEGCTPLHLACRKGDEITVELVQYCHTQM | 179 |
| Db | 421 HVAAFMGVNIIV | SQLMHH---- | GASPTNTNVRGETALHMAARSCQAEVRYLVO-DGQNV | 475 |
| Qy | 180 DVTQYKGGTVEHY | VQGDNSQVLL | IGRNAVAGNQVNNQGLTPPLHLACQLGKQEMRYVL | 239 |
| Db | 476 EAKAKDDOTPLH | ISARLKGADIV | QQLQCG-A\$PRAATTSGETPLHLAARGCHGDVAFL | 534 |
| Qy | 240 LLCNARCINIM | PNGY-PIHSAMKFS | QKGCAMETISDSSQIHSKDPYRGASPLHWA---K | 295 |
| Db | 535 LDHGASLITTKK | GGTTPHLHVA | KYGLKLEVASILLQK\$A\$P--DAAGSGLTPHLVAHAHYD | 592 |
| Qy | 296 NAEVARMILK | RGCVNNTSS | SAGNTALHYGVNRNPFDCATIVLLTGANADARAGEHNTPLH | 355 |
| Db | 593 NQKVALLLDD | QASPHAAKRG | YTPPLHLAACKNQMDITSLIEYGADANNVTRQGIASVH | 652 |
| Qy | 356 LAMSKDNVEM | KALIVGAEV | DTDPNDFGETPFLASK | 392 |
| Db | 653 LAAQEGHVDNV | SLLSRNANVNL | SNKSGLTPPLHLAAQ | 689 |

```

RESULT 10
T42715
ankyrin 3, splice form 3 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
A/Accession: T42715
R/Petercz, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, L
J. Cell Biol. 130, 313-330, 1995
A/Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.
A/Reference number: Z22237; MUID:95340633; PMID:7615634
A/Accession: T42715
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1940 <PET>

```

A:Cross-references: UNIPROT:061307; EMBL:L40632; NID:9710548; PID:9710549; PION:AA01604.
A:Experimental source: strain C57BL/6J, kidney
C:Gene: Ank3
C:Gene: Ank3
A:Map position: 10
A:introns: 834/71
C:Superfamily: ankyrin, ankyrin repeat homology
C:Keywords: alternative splicing

| | | | | |
|-----------------------|-------|--------------|--------|----------------|
| Query Match | 14.1% | Score 293 | DB 2 | length 1940 |
| Best Local Similarity | 29.2% | Pred. No. 3 | 8e-16 | |
| Matches | 81 | Conservative | 55 | Mismatches 125 |
| | | | Indels | 16 |
| | | | Gaps | 7 |

| | | | | | |
|----|-----|-----------------|--|---------------------------------------|-----|
| QY | 124 | HLAVELG---- | IRECFHHSRIIS | CANCAENBEGCTPLHLCRKGDEIVELVQYCHTQM | 179 |
| | | | | | |
| DB | 421 | HVAALFMGHVNIYS | QLMHH---- | GASPTNTNVGETALHMAARSGOAEVARYLVO-DGAQV | 475 |
| | | | | | |
| QY | 160 | DVTVDKGETVFVYAV | QOGRNSOVLGLGRNAVAGLNVNQGLPLHLACOLGKOEMRVL | 239 | |
| | | | | | |
| DB | 476 | EKKAKDDQTPHLHIS | ARLGKADIVQQLLOOG-ASPNAATTSGYTPPLHIAAREGHEVDVAFL | 534 | |
| | | | | | |
| QY | 240 | LLCNARCNIMGNGY- | PIHSAMKFSQKGAEMIISDSSQIHSKDPRYGASPLHWA-- | K 295 | |
| | | | | | |
| DB | 535 | LDHGASLSTTTKKG | CTPLHVAAKYKGLLEVASLLQKSASP-- | DAAGSGGLTPPLHVAHYD 592 | |
| | | | | | |
| QY | 236 | NAEMARMILLKRG | CNNVSTSGAGNTLHVGVMMNRHPCALYLLTHGANADRGEGHNPFLH | 355 | |
| | | | | | |
| DB | 593 | NOKVALLLLDQGA | SHPAAAKNGCTPLHIAAKKQNMQIMLTSLLRYGADANNAVTTQGISVH | 652 | |
| | | | | | |
| QY | 356 | LAMSKDNVEMIKAL | IVFGAEVDTPNDFGETPTFLASK | 392 | |
| | | | | | |
| DB | 653 | LAAGQGVDMVSL | LLSRNANVNLNKSGLTPTPLHAAQ | 689 | |
| | | | | | |

RESULT 11
 T42713
 ankryrin 3, splice form 1 - mouse
 C.Species: Mus musculus (house mouse)
 C.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C.Accession: T42713
 J.Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yalamas, M.; Turtzo, L.
 J. Cell Biol. 130, 313-330, 1995
 A.Title: Ank3 (epithelial ankryrin), a widely distributed new member of the ankryrin gene 1
 the repeat domain.
 A.Reference number: Z22237, MUID:95340633, PMID:7615634
 A.Accession: T42713
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-1943 <P>
 A.Cross-references: UNIPROT:Q61307, EMBL:L40632, NID:G710548, PID:G710550, PIDN:AA01606
 A.Experimental source: strain C57BL/6J; kidney
 C.Genetics:
 A.Gene: Ank3
 A.Map position: 10
 A.Introns: 855/1
 C.Function:
 A.Description: supposed to play an important role in the polarized distribution of many
 A.Note: major kidney ankryrin
 C.Superfamily: ankryrin; ankryrin repeat homology
 C.Keywords: alternative splicing

[illegible]

A;Accession: I49502

A;Accession: I49502

A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1662 <RES>
A/Cross-references: UNIPROT:Q02357; GB:M84756; NID:g191939; PDB:AAA37236.1; PID:g191940
C/Genetics:
A/Name: Ank-1
C/Superfamily: ankyrin; ankyrin repeat homology
C/Keywords: alternative splicing
F/40-72/Domain: ankyrin repeat homology <AN02>
F/73-105/Domain: ankyrin repeat homology <AN02>
F/106-138/Domain: ankyrin repeat homology <AN03>
F/139-167/Domain: ankyrin repeat homology <AN04>
F/168-200/Domain: ankyrin repeat homology <AN05>
F/201-233/Domain: ankyrin repeat homology <AN06>
F/234-266/Domain: ankyrin repeat homology <AN07>
F/267-299/Domain: ankyrin repeat homology <AN08>
F/300-332/Domain: ankyrin repeat homology <AN09>
F/333-365/Domain: ankyrin repeat homology <AN10>
F/366-398/Domain: ankyrin repeat homology <AN11>
F/399-431/Domain: ankyrin repeat homology <AN12>
F/432-464/Domain: ankyrin repeat homology <AN13>
F/465-497/Domain: ankyrin repeat homology <AN14>
F/498-530/Domain: ankyrin repeat homology <AN15>
F/531-563/Domain: ankyrin repeat homology <AN16>
F/564-596/Domain: ankyrin repeat homology <AN17>
F/597-629/Domain: ankyrin repeat homology <AN18>
F/630-662/Domain: ankyrin repeat homology <AN19>
F/663-695/Domain: ankyrin repeat homology <AN20>
F/696-728/Domain: ankyrin repeat homology <AN21>
F/729-761/Domain: ankyrin repeat homology <AN22>
F/762-794/Domain: ankyrin repeat homology <AN23>

Query Match 13.7%; Score 285; DB 2; Length 1662;
Best Local Similarity 25.6%; Pred. No. 1.7e-15;
Matches 93; Conservative 55; Mismatches 121; Indels 94; Gaps 10;

QY 107 LQHLIDLNNHPSVAHLAVELGIRECFHH--SRIISCANCAENE--EGTTPHLACR 161
DB 332 LDHLTPPL-----HVAA-----HCGHHRVAKYLLDKAKPRNSRALNGFTPLHIACK 376
QY 162 KGDGELIVELVQYCHTQM-----VTDYKGET 188
DB 377 KQHIRFW-ELLKTGASIDAVTESGLTPHLVASFCHLPVKNLQFGASPNVSNVET 435
QY 189 VFHYAVQGNDSQYLQILGRNAVGLNQVNNQGLTPHLACQLGKQEMVRLICNARCN 248
DB 436 PLHMARAGHTBAXKYLQNK--AKANAKAKDDOTPLHCAARIGHTGMVKLLLENGASPNL 494
QY 249 MGPNGY-----PIHSAMKFSQKCAEMIISM 274
DB 495 ATTAGHTPLHTARBGHVDLTALLLEKASQACMTKKGFTPLHVAKYGVRLAEILLH 554
QY 275 DSSQIHSKDPRYGASPLHMA---KNAEMARMLKGCNVNSTSSAGNTALHYGVMMNRPD 331
DB 555 DNHPR--NAAGKGLTPHLVAVHNHNDIYVLLPRGSGPHSPAMNGYTPHLIAKONQTE 612
QY 332 CAIVLLTHGANLARGEHGNTPLHLSKQNVEMIKALIVFGAEVDTPNDFGETPTFLAS 391
DB 613 VARSLQYGSANAEVQGTTPHLHLAGQSHTEMVALLLSKQANGNLGNKSGLTPLHIVS 672
QY 392 KTG 394
DB 673 QEG 675

RESULT 15
T46445
hypothetical protein DKFp434B2328.1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T46445
R./Blöcker, H.; Boeher, M.; Brandt, P.; Mewes, H.W.; Gaassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000

A/Reference number: Z23032
A/Accession: T46445
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-397 <AAA>
A/Cross-references: UNIPROT:Q9NTA1; EMBL:AL137448
A/Experimental source: adult testis; clone DKFp434B2328
C/Genetics:
A/Note: DKFp434B2328.1

Query Match 13.5%; Score 281.5; DB 2; Length 397;
Best Local Similarity 30.7%; Pred. No. 4.2e-16;
Matches 86; Conservative 48; Mismatches 135; Indels 11; Gaps 7;

QY 121 SVANHLAVEGIRECFHSHRIISCANCAENEBCGTPHLAC--RKGDELIVELVQYCHTQM 179
DB 53 SLHLAVELVQGEBCAKWLLNNANPRLSNRRSGTPLHMAVERVRG--VVELLARKISV 110
QY 180 DVTDYKGETVFHYAVQ--GNSQVLLQILGRNAVGLNQVNNQGLTPHLACQLGKQEMRV 238
DB 111 NAKDEQMTALHFAQNGDESSTRLLEKX--ASVNEVDFEGRTPMHVAQCHQGENIVRI 168
QY 239 LLLCNARCMIMPNGY--PIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHMAK-- 295
DB 169 LIRRGVDSVLQGDAMLPLHYAAMOGHLPVILAKQGVSVNAQ--TLDGRTPLHLAQR 227
QY 296 -NAEMARMLKGCNVNSTSSAGNTALHYGVMMNRPDCAIVLLTHGANLARGEHGNTPL 354
DB 228 GHYRVARILLIDCSDVNVGSLAQTPHLVAAETGHTSTARLLHNRGAKGEAVTSQGYTAL 287
QY 355 HLAMSDNVEMIKALIVFGAEVDTPNDFGETPTFLASKTG 394
DB 288 HLAARNGHATVTLVVEERADVLRGRLNQTLNHLAAHG 327

Search completed: December 15, 2004, 13:14:15
Job time : 18.7917 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 15, 2004, 12:52:25 ; Search time 85.8019 Seconds
(without alignments)
2642.105 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084

Sequence: 1 MGPFGLVNTFGVTNLFPSN.....EVDTPNDPGETPTPLSKIG 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues
Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|------------|----------------------|
| 1 | 2078 | 99.7 | 806 | 1 | PA26_HUMAN | 060733 homo sapien |
| 2 | 2078 | 99.7 | 806 | 1 | CAG30429 | CAG30429 homo sapi |
| 3 | 1842 | 88.4 | 752 | 1 | PA26_MOUSE | P97819 mus musculu |
| 4 | 1842 | 88.4 | 807 | 2 | Q9JKE1 | Q9JKE1 mus musculu |
| 5 | 1842 | 88.4 | 807 | 2 | AAH57209 | AAH57209 mus muscu |
| 6 | 1832 | 87.9 | 752 | 2 | Q7TPX2 | Q7TPX2 mus musculu |
| 7 | 1808.5 | 86.8 | 751 | 1 | PA26_RAT | P97570 rattus norv |
| 8 | 1176 | 56.4 | 756 | 2 | Q6DDKO | Q6DDKO xenopus lae |
| 9 | 1037.5 | 49.8 | 818 | 2 | Q6NMW0 | Q6NMW0 brachydanio |
| 10 | 1037.5 | 49.8 | 818 | 2 | AAH67375 | AAH67375 brachydan |
| 11 | 512 | 23.6 | 879 | 2 | Q7QZU1 | Q7QZU1 anopheles g |
| 12 | 494.5 | 23.7 | 877 | 2 | Q9VTE0 | Q9VTE0 drosophila |
| 13 | 494.5 | 23.7 | 877 | 2 | AAFS0194 | AAFS0194 drosophila |
| 14 | 494.5 | 23.7 | 887 | 2 | Q7KDD4 | Q7KDD4 drosophila |
| 15 | 494.5 | 23.7 | 887 | 2 | Q7KDD4 | Q7KDD4 drosophila |
| 16 | 338 | 16.2 | 843 | 2 | AAH11936 | AAH11936 rattus norv |
| 17 | 338 | 16.2 | 843 | 2 | P97582 | P97582 rattus norv |
| 18 | 332 | 15.9 | 1219 | 2 | Q8C8R3 | Q8C8R3 mus musculu |
| 19 | 332 | 15.9 | 1219 | 2 | Q7Z315 | Q7Z315 homo sapien |
| 20 | 332 | 15.9 | 1219 | 2 | Q7Z315 | Q7Z315 homo sapien |
| 21 | 318 | 15.3 | 1004 | 2 | Q7JUN0 | Q7JUN0 caenorhabd |
| 22 | 318 | 15.3 | 1004 | 2 | AAQ91911 | AAQ91911 caenorhab |
| 23 | 318 | 15.3 | 1004 | 2 | AAQ91911 | AAQ91911 caenorhab |
| 24 | 318 | 15.3 | 1809 | 2 | Q17344 | Q17344 caenorhabd |
| 25 | 318 | 15.3 | 1809 | 2 | Q17344 | Q17344 caenorhabd |
| 26 | 318 | 15.3 | 1841 | 2 | Q8MOC0 | Q8MOC0 caenorhabd |
| 27 | 318 | 15.3 | 1867 | 2 | Q17486 | Q17486 caenorhabd |
| 28 | 318 | 15.3 | 2039 | 2 | Q17489 | Q17489 caenorhabd |
| 29 | 318 | 15.3 | 6994 | 2 | Q17343 | Q17343 caenorhabd |
| 30 | 313.5 | 15.0 | 1549 | 2 | Q17490 | Q17490 caenorhabd |
| 31 | 313.5 | 15.0 | 1549 | 2 | Q24241 | Q24241 drosophila |
| | | | | | Q9V4B1 | drosophila |

ALIGNMENTS

| | | | | | |
|----|-------|------|------|---|------------|
| 32 | 310 | 14.9 | 1009 | 2 | Q8SWY2 |
| 33 | 310 | 14.9 | 1159 | 2 | Q9NCP8 |
| 34 | 310 | 14.9 | 1571 | 2 | Q7KH92 |
| 35 | 310 | 14.9 | 1571 | 2 | AAFS0525 |
| 36 | 305.5 | 14.7 | 792 | 2 | Q7Q172 |
| 37 | 304.5 | 14.6 | 820 | 2 | Q8JHU3 |
| 38 | 301 | 14.4 | 786 | 2 | Q9ERK0 |
| 39 | 301 | 14.4 | 786 | 2 | AAH57871 |
| 40 | 298 | 14.3 | 2622 | 2 | Q70511 |
| 41 | 296 | 14.2 | 1088 | 2 | Q13484 |
| 42 | 296 | 14.2 | 4377 | 1 | ANK3_HUMAN |
| 43 | 295.5 | 14.2 | 1145 | 2 | Q7PEZ8 |
| 44 | 295.5 | 14.2 | 1501 | 2 | Q70K03 |
| 45 | 295 | 14.2 | 1887 | 2 | Q7Z3G4 |

ALIGNMENTS

| | | | |
|----------|--|-----------|--------------|
| RESULT 1 | PA26_HUMAN | STANDARD; | PRT; 806 AA. |
| ID | PA26_HUMAN | | |
| AC | 060733; 075645; 08N452; 09UG29; 09UIT0; 09Y671; | | |
| DT | 30-MAY-2000 (Rel. 39, Created) | | |
| DT | 30-MAY-2000 (Rel. 39, Last sequence update) | | |
| DT | 01-OCT-2004 (Rel. 45, Last annotation update) | | |
| DE | 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cal-PLA2) (Group VI phospholipase A2) (GVI PLA2). | | |
| GN | Name=PLA2G6; Synonyms=iPLA2; | | |
| OS | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| OX | NCBI_TaxID=9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2; ANKYRIN-IPLA2-1 AND ANKYRIN-IPLA2-2). | | |
| RC | TISSUE=B-cell, and Testis; | | |
| RX | MEDLINE=98079046; PubMed=9417066; | | |
| RA | Larsson P.K.A., Claesson H.-E., Kennedy B.P.; | | |
| RT | "Multiple splice variants of the human calcium-independent phospholipase A2 and their effect on enzyme activity."; | | |
| RL | J. Biol. Chem. 273:207-214(1998). | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. (ISOFORMS LH-IPLA2 AND SH-IPLA2). | | |
| RC | TISSUE=Pancreatic islets; | | |
| RX | MEDLINE=99194813; PubMed=10092647; | | |
| RA | Ma Z., Wang X., Nowatke W., Ramanadham S., Turk J.; | | |
| RT | "Human pancreatic islets express mRNA species encoding two distinct catalytically active isoforms of group VI phospholipase A2 (iPLA2) that arise from an exon-skipping mechanism of alternative splicing of the transcript from the iPLA2 gene on chromosome 22q13.1."; | | |
| RL | J. Biol. Chem. 274:9607-9616(1999). | | |
| RN | [3] | | |
| RP | SEQUENCE FROM N.A. AND ALTERNATIVE SPLICING. | | |
| RX | MEDLINE=99269033; PubMed=10336645; | | |
| RA | Larsson Forell P.K.A., Kennedy B.P., Claesson H.-E.; | | |
| RT | "The human calcium-independent phospholipase A2 gene. Multiple enzymes with distinct properties from a single gene."; | | |
| RL | Eur. J. Biochem. 262:575-585(1999). | | |
| RN | [4] | | |
| RP | SEQUENCE FROM N.A. (ISOFORM LH-IPLA). | | |
| RC | TISSUE=Testis; | | |
| RA | Ansoyge W., Witkner U., Mewes H.-W., Gassenhuber J., Wiemann S.; | | |
| RL | Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases. | | |
| RN | [5] | | |
| RP | SEQUENCE FROM N.A., AND VARIANTS ILE-58; GLY-63; GLN-70; ASN-183 AND THR-343. | | |
| RA | Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.; | | |
| RA | "NIH8-SNPs, environmental genome project, NIH8 ES15478, Department of Genome Sciences, Seattle, WA (URL: http://esp.gs.washington.edu)."; | | |
| RL | Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases. | | |

DR HSSP; 060778; 10Y3.
DR Genew; HGNC:9039; PLA2G6.

Query Match 99.7%; Score 2078; DB 1; Length 806;
Best Local Similarity 99.7%; Pred. No. 1.9e-162;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPFGVLVNTFGSVTLFSPNPRVKEVAVADYSSDRVREEGQLIFONTPNRTWCVLV 60
DB 1 MOPFGVLVNTFGSVTLFSPNPRVKEVAVADYSSDRVREEGQLIFONTPNRTWCVLV 60
QY 61 NPNRNSGGRFLFQLELEADALVNFHOYSQQLPFYESSPOLVTEVLOHLDLIRNHPN 120
DB 61 NPNRNSGGRFLFQLELEADALVNFHOYSQQLPFYESSPOLVTEVLOHLDLIRNHPN 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKDGSELVELVQYCHTOMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKDGSELVELVQYCHTOMD 180
QY 181 VVDYKGETVPHYAVOGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
DB 181 VVDYKGETVPHYAVOGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
QY 241 LCNARCNINGPNQYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNINGPNQYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTGANADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVGAEVDPNDPDEPTPLASKIG 394
DB 361 DNVEMIKALIVGAEVDPNDPDEPTPLASKIG 394

RESULT 2

CAG30429 PRELIMINARY; PRT; 806 AA.
AC CAG30429; CAG30429; PRT; 806 AA.
DT 01-JUN-2004 (TrEMBLrel. 27, Created)
DT 01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
DE PLA2G6 protein.
GN PLA2G6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A.,
RA Cole C.G., Goward M.E., Aguado B., Mallia M., Mokrab Y., Huckle E.J.,
RA Beate D.M., Dunham I.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; C9456543; CAG30429.1; -; 8E5CDAEB9ACAD8B CRC44;
SQ SEQUENCE 806 AA; 89902 MW; 8E5CDAEB9ACAD8B CRC44;

Query Match 99.7%; Score 2078; DB 2; Length 806;
Best Local Similarity 99.7%; Pred. No. 1.9e-162;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOPFGVLVNTFGSVTLFSPNPRVKEVAVADYSSDRVREEGQLIFONTPNRTWCVLV 60
DB 1 MOPFGVLVNTFGSVTLFSPNPRVKEVAVADYSSDRVREEGQLIFONTPNRTWCVLV 60
QY 61 NPNRNSGGRFLFQLELEADALVNFHOYSQQLPFYESSPOLVTEVLOHLDLIRNHPN 120
DB 61 NPNRNSGGRFLFQLELEADALVNFHOYSQQLPFYESSPOLVTEVLOHLDLIRNHPN 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKDGSELVELVQYCHTOMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKDGSELVELVQYCHTOMD 180

QY 181 VVDYKGETVPHYAVOGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240

DB 181 VVDYKGETVPHYAVOGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240

QY 241 LCNARCNINGPNQYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300

DB 241 LCNARCNINGPNQYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300

QY 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTGANADARGEHNTPLHLAMSK 360

DB 301 RMLKRGCVNVTSSAGNTALHVGVRNRPDCAIVLLTGANADARGEHNTPLHLAMSK 360

QY 361 DNVEMIKALIVGAEVDPNDPDEPTPLASKIG 394

DB 361 DNVEMIKALIVGAEVDPNDPDEPTPLASKIG 394

RESULT 3

PA26_MOUSE STANDARD; PRT; 752 AA.
AC P97819; Q99LA9; PRT; 752 AA.
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE 85 kDa calcium-independent phospholipase A2 (EC 3.1.1.4) (iPLA2) (Cal-
PLA2) (Group VI phospholipase A2) (GVI PLA2).
GN Name=Pla2g6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RX MEDLINE=97236816; PubMed=9079688;
RA Balboa M.A., Balsinde J., Jones S.S., Dennis E.A.;
RT "Identity between the Ca2+-independent phospholipase A2 enzymes from
RT J. Biol. Chem. 272:8576-8580(1997).
RL [2]
RN REVISIONS TO 2-3; 9; 11 AND 211.
RP Balboa M.A., Balsinde J., Jones S.S., Dennis E.A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Mak S.T., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lounellano N.A., Peters G.J., Abramson R.D., Millar S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maria M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Contains 7 ANK repeats.

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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; U88624; AAB48511.2; -
 DR EMBL; BC003487; AAH03487.1; -
 DR HSSP; Q60778; IOY3.
 DR MGD; MG1:1859152; Pla2g6.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF00023; ANK; 6.
 DR PRINTS; PR01415; ANKYRIN.
 DR SMART; SM00248; ANK; 6.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR ANK repeat; Hydrophobic; Lipid degradation; Repeat.
 KM ANK repeat; 181 ANK 1.
 FT REPEAT 181 ANK 1.
 FT REPEAT 185 ANK 2.
 FT REPEAT 219 ANK 3.
 FT REPEAT 251 ANK 4.
 FT REPEAT 286 ANK 5.
 FT REPEAT 316 ANK 6.
 FT REPEAT 349 ANK 7.
 FT ACT SITE 465 Potential.
 SQ SEQUENCE 752 AA; 83702 MW; AAC347B0E1292E9 CRC64;

Query Match 88.4%; Score 1842; DB 1; Length 752;
 Best Local Similarity 87.8%; Pred. No. 5e-143;
 Matches 345; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSQVNTLFSNPRFVKEVAADYTSDDRVREBQGLILFQNTPRNTDVCVLY 60
 DB 1 MOFGRLVNTLSSVTNLFSPNPRFVKEVSLTDYVSSRRVREBQGLILQVNSRNTDVCVLY 60
 QY 61 NPNRSGSGRLFOLELEADALVNFHOYSQQLPFYSSFOVLTETVLOHITLDIRHPSW 120
 DB 61 SPNPSQSGRLFOLESEADALVNFQFSSQLPFYESSVOVLTETVLOHITLDIRHPSW 120
 QY 121 SYAHLAVEIGIRCEFHHSRIISCAEENBEGTPLHLCKRGDGHIVELVOYCHTOMD 180
 DB 121 TYTHLAVEIGIRCEFHHSRIISCAEENBEGTPLHLCKRGDGHIVELVOYCHTOMD 180
 QY 181 VTDYKGETVFNVAQDQNSQVLTQLGRNVAAGVNNQGLTPHLACQIGKQEWVRL 240
 DB 181 VTDNKGETAFHVAQDQNPVLTQLGKNSAGVNNQGLTPHLACQIGKQEWVRL 240
 QY 241 LCNARCNINGPNQYPIHSAKESQKCAEMTISMSQIHSKDPHYGASPLHWAKAENA 300
 DB 241 LCNARCNINGPNQYPIHSAKESQKCAEMTISMSQIHSKDPHYGASPLHWAKAENA 300
 QY 301 RMLLKRGCVNNTSSAGNTALHGVNRNRPDCAIVLTGANGADAGEHNTPLHMSK 360
 DB 301 RMLLKRGCVNNTSSAGNTALHGVNRNRPDCAIVLTGANGADAGEHNTPLHMSK 360
 QY 361 DNVEIMKALIVFGAEVDTPNDFGETPTFLASKI 393
 DB 361 DNMEWIKALIVFGAEVDTPNDFGETPTFLASKI 393

RESULT 4
 Q9JK61 PRELIMINARY; PRT; 807 AA.
 AC Q9JK61
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Ca2+-independent phospholipase A2 long form (Pla2g6 protein).
 GN Name:Pla2g6;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NH/Swiss;
 RA Chiu C.-H., Jackowski S.;
 RU Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Tomshyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.O., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Prange C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
 RA Strausberg R.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF259401; AAF72651.1; -
 DR EMBL; BC057209; AAH57209.1; -
 DR HSSP; Q60778; IOY3.
 DR MGD; MG1:1859152; Pla2g6.
 DR GO; GO:0003824; F: catabolic activity; IEA.
 DR GO; GO:0045735; F: nutrient reservoir activity; IEA.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR002641; Patacin.
 DR Pfam; PF00023; ANK; 6.
 DR Pfam; PF01734; Patacin; 1.
 DR PRINTS; PR01415; ANKYRIN.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 KM ANK repeat.
 SQ SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match 88.4%; Score 1842; DB 2; Length 807;
 Best Local Similarity 87.8%; Pred. No. 5e-143;
 Matches 345; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSQVNTLFSNPRFVKEVAADYTSDDRVREBQGLILFQNTPRNTDVCVLY 60
 DB 1 MOFGRLVNTLSSVTNLFSPNPRFVKEVSLTDYVSSRRVREBQGLILQVNSRNTDVCVLY 60
 QY 61 NPNRSGSGRLFOLELEADALVNFHOYSQQLPFYSSFOVLTETVLOHITLDIRHPSW 120
 DB 61 SPNPSQSGRLFOLESEADALVNFQFSSQLPFYESSVOVLTETVLOHITLDIRHPSW 120
 QY 121 SYAHLAVEIGIRCEFHHSRIISCAEENBEGTPLHLCKRGDGHIVELVOYCHTOMD 180
 DB 121 TYTHLAVEIGIRCEFHHSRIISCAEENBEGTPLHLCKRGDGHIVELVOYCHTOMD 180
 QY 181 VTDYKGETVFNVAQDQNSQVLTQLGRNVAAGVNNQGLTPHLACQIGKQEWVRL 240
 DB 181 VTDNKGETAFHVAQDQNPVLTQLGKNSAGVNNQGLTPHLACQIGKQEWVRL 240
 QY 241 LCNARCNINGPNQYPIHSAKESQKCAEMTISMSQIHSKDPHYGASPLHWAKAENA 300
 DB 241 LCNARCNINGPNQYPIHSAKESQKCAEMTISMSQIHSKDPHYGASPLHWAKAENA 300

Db 241 LCNARCINMGPGGPIHTAMKFSQKCAEMIIISMSDSQIHSKDPKRYGASPLHAKNAEMA 300

Qy 301 RMLIKGCGVNSSTSSAGNTALHYGNRNRPDCALVLTTHGANDARGEHNTPLHLSMSK 360

Db 301 RMLIKGCGVDSTSSSGNTALHYAVNRNRPDCVWLITTYGANGARGEHNTPLHLSMSK 360

Qy 361 DNEMIKALIVFGAEVDPNDPFGETPTFLASKI 393

Db 361 DNEMIKALIVFGAEVDPNDPFGETPTFLASKI 393

RESULT 5

AAH57209 PRELIMINARY; PRT; 807 AA.

AC AAH57209; (T-EMBLrel. 27, Created)

DT 02-MAR-2004 (T-EMBLrel. 27, last sequence update)

DT 02-MAR-2004 (T-EMBLrel. 27, last sequence update)

DE Plaz26 protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RC STRAIN=NMRI; TISSUE=Mammary tumor;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

SEQUENCE FROM N.A.

RC STRAIN=NMRI; TISSUE=Mammary tumor;

RA Strausberg R.;

RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC057209; AAH57209.1; -

SO SEQUENCE 807 AA; 89559 MW; 3838889731100294 CRC64;

Query Match 88.4%; Score 1842; DB 2; Length 807;

Best Local Similarity 87.8%; Pred. No. 5, Se-143;

Matches 345; Conservative 20; Mismatches 28; Indels 0; Gaps 0;

Qy 1 MOPFGLVNTFSGVTNLFNSPFRKVEYAVADYSSDPVREEGOLIFONTPNRTWPCV 60

Db 1 MOPFGLVNTLSSVTNLFNSPFRKVEYSLTDYSSSEVREGOLILQVNSRTWCV 60

Qy 61 NPNNSQGFRLPQLELEADLVNPHOYSSQLPPESSPOLVTEVQLHLLTDLIRNPSW 120

Db 61 SPNPSQGFRLPQLESEADLVNPHOYSSQLPPESSPOLVTEVQLHLLTDLIRNPSW 120

Qy 121 SVNHLAVELGIRCFPHSRITISNCANENEGCTPLHARKKDGRLVLYVOYCHQMD 180

Db 121 TVNHLAVELGIRCFPHSRITISNCANSTENEGCTPLHARKKDGRLVLYVOYCHQMD 180

Qy 181 VTDYKELTVHYAVOGDNPQVQLQKGNASAGLQVNNQGLTPLHLACRKKQEMVAVLL 240

Db 181 VTDNKGETAHYAVOGDNPQVQLQKGNASAGLQVNNQGLTPLHLACRKKQEMVAVLL 240

Qy 241 LCNARCINMGPGGPIHTAMKFSQKCAEMIIISMSDSQIHSKDPKRYGASPLHAKNAEMA 300

Db 241 LCNARCINMGPGGPIHTAMKFSQKCAEMIIISMSDSQIHSKDPKRYGASPLHAKNAEMA 300

Qy 301 RMLIKGCGVNSSTSSAGNTALHYGNRNRPDCALVLTTHGANDARGEHNTPLHLSMSK 360

Db 301 RMLIKGCGVDSTSSSGNTALHYAVNRNRPDCVWLITTYGANGARGEHNTPLHLSMSK 360

Qy 361 DNEMIKALIVFGAEVDPNDPFGETPTFLASKI 393

Db 361 DNEMIKALIVFGAEVDPNDPFGETPTFLASKI 393

RESULT 6

07TPX2 PRELIMINARY; PRT; 752 AA.

AC 07TPX2; (T-EMBLrel. 25, Created)

DT 01-OCT-2003 (T-EMBLrel. 25, last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, last annotation update)

DE Phospholipase A2, group VI.

GN Name=Plaz26;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RC STRAIN=C3H/He; TISSUE=Osteoblast;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ueda T.B., Toshyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human RT and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

SEQUENCE FROM N.A.

RC STRAIN=C3H/He; TISSUE=Osteoblast;

RA Strausberg R.;

RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC052845; AAH52845.1; -

DR GO; GO:0003824; P: catalytic activity; IEA.

DR GO; GO:0045735; P: nutrient reservoir activity; IEA.

DR InterPro; IPR002110; ANK.

DR InterPro; IPR002641; Patactin.

DR Pfam; PF00023; Anki 6.

DR Pfam; PF01734; Patactin 1.

DR SMART; SM00248; ANK; 6.

DR PROSITE; PSS0088; ANK_REPEAT; 4.

DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.

Qy ANK repeat. 752 AA; 83717 MW; DAC3347B0E14A4FC CRC64;

SO SEQUENCE 752 AA; 83717 MW; DAC3347B0E14A4FC CRC64;

Query Match 87.9%; Score 1832; DB 2; Length 752;

Best Local Similarity 87.5%; Pred. No. 3, 4e-142;

Matches 344; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

CC
 QY 1 MOFGRLVNTFSGVTNLFSNPFPRKEVAVADYTSDBREBQGLIFONTNRTWCCLV 60
 DB 1 MOFGRLVNTFSGVTNLFSNPFPRKEVAVADYTSDBREBQGLIFONTNRTWCCLV 60
 QY 61 NPNRNSGGRFLFQLELEADLVNPHOYSSQLPPEYSSPOVLTETVLQHTLDIRNHPM 120
 DB 61 NPNRNSGGRFLFQLELEADLVNPHOYSSQLPPEYSSPOVLTETVLQHTLDIRNHPM 120
 QY 121 SVNHLAVEIGIRCFPHSRITISCANCAENEBEGCTPLHLAKRGDSILVELVOYCHTOMD 180
 DB 121 SVNHLAVEIGIRCFPHSRITISCANCAENEBEGCTPLHLAKRGDSILVELVOYCHTOMD 180
 QY 121 TVNHLAVEIGIRCFPHSRITISCANCAENEBEGCTPLHLAKRGDSILVELVOYCHTOMD 180
 DB 121 TVNHLAVEIGIRCFPHSRITISCANCAENEBEGCTPLHLAKRGDSILVELVOYCHTOMD 180
 QY 181 VTDYKGETVPHYAVQGDNSQVQLLGRNNAVAGINOVNQGILTPHLACQYKQEMRVLL 240
 DB 181 VTDYKGETVPHYAVQGDNSQVQLLGRNNAVAGINOVNQGILTPHLACQYKQEMRVLL 240
 QY 241 LCNARCNINGPNGYPIHSAMKFSQKCAEMITISMSQIHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCNINGPNGYPIHSAMKFSQKCAEMITISMSQIHSKDPYRGASPLHAKNAEMA 300
 QY 301 RMLKRGCVNNTSSAGNTALHYGVNRNRPDCAIVLLTGHGANDARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCVNNTSSAGNTALHYGVNRNRPDCAIVLLTGHGANDARGEHNTPLHLAMSK 360
 QY 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKI 393
 DB 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKI 393
 RESULT 7
 PA26 RAT STANDARD; PRT; 751 AA.
 AC P97570;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE 85 KDa calcium-independent phospholipase A2 (EC 3.1.1.4) (PLA2) (Cat-PLA2) (Group VI phospholipase A2) (GVI PLA2).
 GN Name=PLA296;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Pancreatic Islets;
 RX MEDLINE=97289008; PubMed=9111008;
 RA Ma Z., Ramachandram S., Kempe K., Chi X.S., Ladenson J., Turk J.;
 RT "Pancreatic Islets express a Ca2+-independent phospholipase A2 enzyme that contains a repeated structural homologue to the integral membrane protein binding domain of ankyrin.";
 RL J. Biol. Chem. 272:11118-11127(1997).
 CC -1- FUNCTION: Catalyzes the release of fatty acids from phospholipids. It has been implicated in normal phospholipid remodeling, nitric oxide-induced or vasopressin-induced arachidonic acid release and in leukotriene and prostaglandin production. May participate in cas mediated apoptosis and in regulating transmembrane ion flux in glucose-stimulated B-cells.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a carboxylate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Found in brain, lung, spleen, kidney, liver, heart and skeletal muscle.
 CC -1- SIMILARITY: Contains 7 ANK repeats.
 CC -----
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CC
 DR EMBL; U51898; AAC3136.1; -
 DR HSSP; Q60778; IOY3.
 DR RGD; 628867; pla2g6.
 DR InterPro; IPR002110; ANK.
 DR Pfam; PF000023; Ank; 6.
 DR PRINTS; PR01415; ANKTRIN.
 DR SMART; SM00248; ANK; 6.
 DR PROSITE; PS50297; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REPEAT; 1.
 KW ANK repeat; Hydrolase; Lipid degradation; Repeat.
 FT REPEAT 150 180 ANK 1.
 FT REPEAT 184 214 ANK 2.
 FT REPEAT 218 247 ANK 3.
 FT REPEAT 250 280 ANK 4.
 FT REPEAT 285 311 ANK 5.
 FT REPEAT 315 344 ANK 6.
 FT REPEAT 348 377 ANK 7.
 FT ACT_SITE 464 464 ANK 7.
 SQ SEQUENCE 751 AA; 83582 MW; 393BBADAVFC99B CRC64;
 Query Match 86.8%; Score 1808.5; DB 1; Length 751;
 Best Local Similarity 86.8%; Pred. No. 2,9e-140;
 Matches 341; Conservative 20; Mismatches 31; Indels 1; Gaps 1;
 QY 1 MOFGRLVNTFSGVTNLFSNPFPRKEVAVADYTSDBREBQGLIFONTNRTWCCLV 60
 DB 1 MOFGRLVNTFSGVTNLFSNPFPRKEVAVADYTSDBREBQGLIFONTNRTWCCLV 60
 QY 61 NPNRNSGGRFLFQLELEADLVNPHOYSSQLPPEYSSPOVLTETVLQHTLDIRNHPM 120
 DB 61 NPNRNSGGRFLFQLELEADLVNPHOYSSQLPPEYSSPOVLTETVLQHTLDIRNHPM 119
 QY 121 SVNHLAVEIGIRCFPHSRITISCANCAENEBEGCTPLHLAKRGDSILVELVOYCHTOMD 180
 DB 121 SVNHLAVEIGIRCFPHSRITISCANCAENEBEGCTPLHLAKRGDSILVELVOYCHTOMD 179
 QY 181 VTDYKGETVPHYAVQGDNSQVQLLGRNNAVAGINOVNQGILTPHLACQYKQEMRVLL 240
 DB 181 VTDYKGETVPHYAVQGDNSQVQLLGRNNAVAGINOVNQGILTPHLACQYKQEMRVLL 239
 QY 241 LCNARCNINGPNGYPIHSAMKFSQKCAEMITISMSQIHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCNINGPNGYPIHSAMKFSQKCAEMITISMSQIHSKDPYRGASPLHAKNAEMA 299
 QY 301 RMLKRGCVNNTSSAGNTALHYGVNRNRPDCAIVLLTGHGANDARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCVNNTSSAGNTALHYGVNRNRPDCAIVLLTGHGANDARGEHNTPLHLAMSK 359
 QY 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKI 393
 DB 361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKI 392
 RESULT 8
 Q6DDK0 PRELIMINARY; PRT; 756 AA.
 ID Q6DDK0;
 AC Q6DDK0;
 DT 01-OCT-2004 (TReMBLrel. 28, Created)
 DT 01-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DE Hypothetical protein.
 DE Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 RN SEQUENCE FROM N.A.
 RP TISSUE=Eye;
 RX MEDLINE=22341132; PubMed=12454917;
 RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RT Dev. Dyn. 225:384-391(2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Klein S., Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RW EMBL: BC077558; AAH77558.1; -.
KW Hypothetical protein.
SQ SEQUENCE 756 AA; 84303 MW; C0278741C5A52A71 CRC64;

Query Match 56.4%; Score 1176; DB 2; Length 756;
Best Local Similarity 54.3%; Pred. No. 4.3e-88;
Matches 213; Conservative 86; Mismatches 93; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFGSVTLPSNPFRKVEAVADYTSRVRREBQGLLFONTNRTMDCVY 60
DB 1 MDLFGRIPTVSAVTLPSNPFRKVEAVADYTSRVRREBQGLLFONTNRTMDCVY 60
QY 61 NPNSQSGRFLPQLELEADLVNPHQYSSQLPFYESSPOVLTETVQLTDLIRNHPM 120
DB 61 NPSSPQNAVRLPQLESEPEALCRFOEYAVLPRPYESSRGLCTLTQQLTDLIRSHPM 120
QY 121 SVNLAVELGIRBCFHHSRIISCANCAENEGCTPLHACRKGDELIVELYOYCHTMD 180
DB 121 SLNLAVELGIRBCFHHSRIISCANCAENEGCTPLHACRKGDELIVELYOYCHTMD 180
QY 181 VTDYKGETVFHYAVQDNGSOVLQGLGRNAVAGLNVNNGQLTPHLACQGLKQEMRVYL 240
DB 181 IDQNGETVYHHAQONNPRVIELCSVPISGVNHNKSNNETPLHYACRLGKTEVLALL 240
QY 241 LCNARCNINPNCYPIHSAKPFQKGCAMETISMSQIHSKPPRGASPLHAKRAENA 300
DB 241 RCHARDIIGKDDYPIHTAKYQKCEVETLIDVSAASQALHAEDPRYQATPIHAKRAENA 300
QY 301 RMLLKGCNVNSTRSSAGNTALHGVNMRPDCALVLTGHCNADARGHENTPLHAKMSK 360
DB 301 RLIIERGCNVNSTRSKLDTPLHIVKRDREALMVLITVADNVNKGHENTPLHAKMSK 360
QY 361 DNEMIKALIVGAEVDTPNDFSETPTFLASK 392
DB 361 DQLELIKALMVFGADVQHNDFETPTGLIAR 392

RESULT 9
Q6NMWYO PRELIMINARY; PRT; 818 AA.
ID Q6NMWYO
AC Q6NMWYO;

DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Zgc:77476.
GN Name=zgc:77476;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxId=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RW EMBL: BC067375; AAH67375.1; -.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ANK_6.
DR Pfam; PF01734; Patatin; 1.
DR PRINTS; PR01415; ANKTRIN.
DR SMART; SM00248; ANK_6.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS02937; ANK_REPEAT_REGION; 1.
KW ANK repeat.
SQ SEQUENCE 818 AA; 90691 MW; C7B5CD45401F8EA9 CRC64;

Query Match 49.8%; Score 1037.5; DB 2; Length 818;
Best Local Similarity 48.7%; Pred. No. 1.2e-76;
Matches 191; Conservative 87; Mismatches 113; Indels 1; Gaps 1;

QY 1 MOFGRLVNTFGSVTLPSNPFRKVEAVADYTSRVRREBQGLLFONTNRTMDCVY 60
DB 1 MDLFGRIPTVSAVTLPSNPFRKVEAVADYTSRVRREBQGLLFONTNRTMDCVY 60
QY 61 NPNSQSGRFLPQLELEADLVNPHQYSSQLPFYESSPOVLTETVQLTDLIRNHPM 120
DB 61 NPSSPQNAVRLPQLESEPEALCRFOEYAVLPRPYESSRGLCTLTQQLTDLIRSHPM 120
QY 121 SVNLAVELGIRBCFHHSRIISCANCAENEGCTPLHACRKGDELIVELYOYCHTMD 180
DB 121 SLNLAVELGIRBCFHHSRIISCANCAENEGCTPLHACRKGDELIVELYOYCHTMD 180
QY 181 VTDYKGETVFHYAVQDNGSOVLQGLGRNAVAGLNVNNGQLTPHLACQGLKQEMRVYL 240
DB 181 IDQNGETVYHHAQONNPRVIELCSVPISGVNHNKSNNETPLHYACRLGKTEVLALL 240
QY 241 LCNARCNINPNCYPIHSAKPFQKGCAMETISMSQIHSKPPRGASPLHAKRAENA 300
DB 241 RCHARDIIGKDDYPIHTAKYQKCEVETLIDVSAASQALHAEDPRYQATPIHAKRAENA 300
QY 301 RMLLKGCNVNSTRSSAGNTALHGVNMRPDCALVLTGHCNADARGHENTPLHAKMSK 360
DB 301 RLIIERGCNVNSTRSKLDTPLHIVKRDREALMVLITVADNVNKGHENTPLHAKMSK 360
QY 361 DNEMIKALIVGAEVDTPNDFSETPTFLASK 392
DB 361 DQLELIKALMVFGADVQHNDFETPTGLIAR 392

QY 241 LCNARCNINPNCYPIHSAKPFQKGCAMETISMSQIHSKPPRGASPLHAKRAENA 300
DB 241 RCHARDIIGKDDYPIHTAKYQKCEVETLIDVSAASQALHAEDPRYQATPIHAKRAENA 300

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Db      240 AGGACRCDINGNNGPFPIHTAMKFEKSCAEAILSSPNQLADDPYGGTGPLHMAKTAEMS 299
QY      301 RMLLKGCNVNSTSSAGNTALTGVNKRNPDCAIYVLTTHGANADARGEHNTPLHLAMSK 360
Db      300 RLLDRCNCVNVYLSKSGESPLHLITKRGFEAAAMTLTTHGADANIRGQDGNATLHLMKL 359
QY      361 DNVEMIKALIVGAEDVTPNDFGERTPTFLASK 392
Db      360 DNMDLIKALMVFAGADVEVHNDVGETPTGLIAR 391

RESULT 10
AAH67375 PRELIMINARY; PRT; 818 AA.
AC AAH67375;
DT 24-MAY-2004 (T-EMBLrel. 27, Created)
DT 24-MAY-2004 (T-EMBLrel. 27, Last sequence update)
DT 24-MAY-2004 (T-EMBLrel. 27, Last annotation update)
DE Zgc:77476.
GN Zgc:77476.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Deje J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.U., Bedn T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richarde S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Holton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywiński M.I., Skalka U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Merra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067375; AAH67375.1; -
SQ SEQUENCE 818 AA; 90691 MW; C7BSCD45401FBEA9 CRC64;

Query Match 49.8%; Score 1037.5; DB 2; Length 818;
Best Local Similarity 48.7%; Pred. No. 1.2e-76;
Matches 191; Conservative 87; Mismatches 113; Indels 1; Gaps 1;

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QY      181 VTDYKGEIVFHYAVQDQNSQVLIQLGRNAVAGLNOVNGLTPLHLACQLGQEMVRVLL 240
Db      180 VQDKNETBPHCAAKQDSSALITIEVLCACQCAVEINNAAGETPMHIACTLGRVEVVKGLL 239
QY      241 LCNARCNINPGVPRHSAAMKFSQKCAEMIISSMSOSHSDPRGASPLHMAKTAEMA 300
Db      240 AGGACRCDINGNNGPFPIHTAMKFEKSCAEAILSSPNQLADDPYGGTGPLHMAKTAEMS 299
QY      301 RMLLKGCNVNSTSSAGNTALTGVNKRNPDCAIYVLTTHGANADARGEHNTPLHLAMSK 360
Db      300 RLLDRCNCVNVYLSKSGESPLHLITKRGFEAAAMTLTTHGADANIRGQDGNATLHLMKL 359
QY      361 DNVEMIKALIVGAEDVTPNDFGERTPTFLASK 392
Db      360 DNMDLIKALMVFAGADVEVHNDVGETPTGLIAR 391

RESULT 11
Q7Q2U1 PRELIMINARY; PRT; 879 AA.
AC Q7Q2U1;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE BdiF359 (Fragment).
GN Name=ebiG3359; ORFNames=ENSANG0000002638;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008968; EAA13225.1; -
DR GO; GO:0003824; F.catalytic activity; IEA.
DR GO; GO:0045735; F.nutrient reservoir activity; IEA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000560; H1Ac_pheptee.
DR InterPro; IPR002641; H1Ac_pheptee.
DR Pfam; PF00023; ANK; 6.
DR Pfam; PF01734; Patactin; 1.
DR PRINTS; PR01415; ANKYRIN.
DR PROSITE; PS50086; ANK_REPEAT; 3.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN_1.
KW ANK repeat.
FT NON_TER 1 1
FT NON_TER 879 879
SQ SEQUENCE 879 AA; 96484 MW; 3491E003CF637188 CRC64;

Query Match 24.6%; Score 512; DB 2; Length 879;
Best Local Similarity 29.8%; Pred. No. 3e-33;
Matches 113; Conservative 81; Mismatches 175; Indels 10; Gaps 5;

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| | | | |
|-----------|---|---|---------|
| Db | 191 | A-STFKEMINMLTAKSTSNLHNCNTDGYTPPLHLACIADPDCVAKALLAGADTNKMA-BG | 248 |
| Qy | 254 | YPIHSAKMFSGQCGAEMITISMSSQSHSDOPRYGASPLIFWAKAAEWAPRLIKRGCVANST | 313 |
| Db | 249 | AGTSYSKSIPISSNVADFLVS-PPNKLFTQDMKGGCTPRLHSSSRFLNSLIERGCVNLV | 307 |
| Qy | 314 | SSAGTATLHVGMRRRFPDCAIVLTITGNAADARAGEGNTPLPLHAMSNDVEMKALIVFG | 373 |
| Db | 308 | NFNGGTPLHVMVARDLSECVALLAHDAEITDVYDMSGNTPLHIAVEKKLIPIVQCLIVFG | 367 |
| Qy | 374 | AEVDTPNDPFGETPTPLASK 392 | |
| Db | 368 | ADFNKKNDDGKTPTPLHVGK 386 | |
| RESULT 12 | | | |
| Q9VT60 | | | |
| Q9VT60 | PRELIMINARY; | PRT; | 877 AA. |
| Q9VT60 | | | |
| DT | 01-MAY-2000 | (TREMBLrel. 13, Created) | |
| DT | 01-OCT-2002 | (TREMBLrel. 22, Last sequence update) | |
| DT | 01-MAR-2004 | (TREMBLrel. 26, Last annotation update) | |
| DE | CG6718-PA. | | |
| GN | ORFNames=CG6718; | | |
| OS | Drosophila melanogaster (Fruit fly). | | |
| OC | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; | | |
| OC | Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; | | |
| OC | Ephydroidea; Drosophilidae; Drosophila. | | |
| OX | NCBI_TaxId=7227; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=20196006; PubMed=10731132; | | |
| RA | Adams M.D., Gelinkner S.E., Holt R.A., Evans C.A., Gocayne J.D., | | |
| RA | Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., | | |
| RA | George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., | | |
| RA | Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X., | | |
| RA | Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., | | |
| RA | Abri1 J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., | | |
| RA | Ballew R.M., Basu A.J., Baxendale J., Bayraktaroglu L., Beasley E.M., | | |
| RA | Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S., | | |
| RA | Borkova D., Botchan M.R., Bouck J., Brokerlein P., Brotlier P., | | |
| RA | Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I., | | |
| RA | Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., | | |
| RA | de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., | | |
| RA | Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., | | |
| RA | Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., | | |
| RA | Foster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K., | | |
| RA | Glodesk A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M., | | |
| RA | Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., | | |
| RA | Hoeftin D., Houston K.A., Howland T.J., Wei M.H., Ibbegam C., | | |
| RA | Jajalali M., Kalush F., Kapen G.H., Ke Z., Kemison J.A., Keichum K.A., | | |
| RA | Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., | | |
| RA | Laoko P., Lei Y., Levitcky A.A., Li J., Li Z., Liang Y., Lin X., | | |
| RA | Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., | | |
| RA | Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshireit A., | | |
| RA | Mount S.M., Moy M., Murphy B., Murphy K., Muzny D.M., Nelson D.L., | | |
| RA | Nelson D.R., Nelson K.A., Nixon K., Nusserkern D.R., Pacleb J.M., | | |
| RA | Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., | | |
| RA | Rehner K., Remington K., Saunders R.D., Scheeler F., Shen H., | | |
| RA | Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., | | |
| RA | Spieler E., Spirding A.C., Stapleton M., Strong R., Sun B., | | |
| RA | Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., | | |
| RA | Wang Z.Y., Massaman D.A., Weinstein G.M., Weissenbach J., | | |
| RA | Williams S.M., Woodgett W., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., | | |
| RA | Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., | | |
| RA | Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., | | |
| RA | Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., | | |
| RT | "The genome sequence of <i>Drosophila melanogaster</i> ." | | |
| RL | Science 287:2185-2195(2000). | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=22426065; PubMed=12537568; | | |

| | | |
|--|--|--|
| | RA | Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frishe E., Hodson A., George R.A., Hoeklin R.A., Lavery T., Muzny D.M., Nelson C.R., Paclik J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svatek R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weissbrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., RT "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence." |
| RL | Genome Biol. | 3:RESEARCH0079-RESEARCH0079(2002). |
| RN | [3] | |
| RN | SEQUENCE FROM N.A. | |
| RP | MEDLINE=22426070; PubMed=12537573; | |
| RX | Medline=22426070; PubMed=12537573; | |
| RA | Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svatek R., Patel S., Frishe E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; | |
| RT | "The transposable elements of the Drosophila melanogaster euchromatic genome perspective." | |
| RL | Genome Biol. | 3:RESEARCH0084-RESEARCH0084(2002). |
| RN | [4] | |
| RN | SEQUENCE FROM N.A. | |
| RP | MEDLINE=22426069; PubMed=12537572; | |
| RX | Medline=22426069; PubMed=12537572; | |
| RA | Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hrdceky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu I., Bernan B.P., Betancourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.; | |
| RT | "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review." | |
| RL | Genome Biol. | 3:RESEARCH0083-RESEARCH0083(2002). |
| RN | [5] | |
| RN | SEQUENCE FROM N.A. | |
| RP | FLYBASE; | |
| RL | Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases. | |
| RN | [6] | |
| RP | SEQUENCE FROM N.A. | |
| RL | Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases. | |
| DR | EMBL; AE003550; AAF50194.3; - | |
| DR | HSSP; Q60778; IOY3. | |
| DR | FLYBase; FBgn0036053; CG6718. | |
| DR | GO; GO:0003824; F:catalytic activity; IEA. | |
| DR | GO; GO:0045735; F:nutrient reservoir activity; IEA. | |
| DR | InterPro; IPRO02110; ANK. | |
| DR | InterPro; IPRO02641; Patatin. | |
| DR | Pfam; PF00023; Ank_5. | |
| DR | Pfam; PF01734; Patatin; 1. | |
| DR | PRINTS; PRO1415; ANKYRIN. | |
| DR | SMART; SM00248; ANK_6. | |
| DR | PROSITE; PS50088; ANK_REPEAT; 3. | |
| DR | PROSITE; PS50297; ANK_REP_REGION; 1. | |
| KW | ANK repeat. | |
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| Query Match | 23.7%; Score 494.5; DB 2; Length 877; | |
| Best Local Similarity | 29.2%; Pred. No. 8.2e-32; | |
| Matches 108; Conservative 81; Mismatches 154; Indels 27; Gaps 5; | | |
| QY | 17 LFSPNPKKEVAVADVTSDDVREBGILLFQNTPNRWDCVLVNPRNSOGGRLLFOEL | 76 |
| DB | 40 LFAPPF-----NSSNKRAVVEYLILORPTSD-----SNTTFSILRSVP | 78 |
| QY | 77 EADLVNHFQSSQLLPYEESPVLHTEVLOHTDLIRNHPSSVAHLAVELGIRECFH | 136 |
| DB | 79 QGBABERNPAFLQRLPVFVSIVKEYVNVNGIQKACDALADNPSTLSLIAVFNLDVIS | 138 |
| QY | 137 HSRIISCAENEGCTPLHLACKRGDEGLVELVOYCHTMQMDVTYKGSTVFHYAVQG | 196 |
| DB | 139 NPKMLQCVDQAATATMSPFQALIKQHMEVWKALLPL--SKLEHIDINSNVFYHA-S | 195 |
| QY | 197 DNSOVLQLGGNAVAGLNQVNNQGITPLHLACQLCKQMVRVLLLCNARCIMGNQPI | 256 |

DB 196 TTKEIINLIIDKSTVNLHNSDGYTPPLHVACLAADKEENYKALLAGANVNL--NAKDI 252
 QY 257 HSAMKFSQKCAEMITISMDSSQIHSKDPYRGASPLHWAKNAEMARMLTKRGCVNNTSSA 316
 DB 253 RKYYKTSAPTTVSSFLRTVNSKLYTQDMKYGTPPLHMCSSRETLHALINEGCVNATNFD 312
 QY 317 GNTALHVGWNRNPFDCALVLLTHGANADARGEHNTPLHLANSKDNVEMIKALIVGAEV 376
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 QY 377 DTNPNGERTP 386
 DB 373 NLKNKDKTTP 382
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 ID AAF50194 PRELIMINARY; PRT; 877 AA.
 AC AAF50194;
 DT 01-APR-2004 (TEMBLrel. 27, Created)
 DT 01-APR-2004 (TEMBLrel. 27, Last sequence update)
 DT 01-APR-2004 (TEMBLrel. 27, Last annotation update)
 DE CG6718-PA.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP MEDLINE=20196006; PubMed=10731132;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutcliffe G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abri J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballow R.Y., Basu P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadelis E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W.,
 RA Folsler K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Jaiswal M., Kalish J., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Jimalal B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matvei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry R., Morris J., Moshireit A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacble J.M.,
 RA Palazotto M., Plittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodard J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacble J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
 RA RT "finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537572;
 RA Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminck J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,
 RA Scapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminck J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomic perspective";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003550; AAF50194.3; -
 DR FLYBASE; FBgn0036053; CG6718.
 SO SEQUENCE 877 AA; 96863 MW; C9DC2CD6C2828698 CR664;
 Query Match 23.7%; Score 494.5; DB 2; Length 877;
 Best Local Similarity 29.2%; Pred. No. 8, 2e-32;
 Matches 108; Conservative 81; Mismatches 154; Indels 27; Gaps 5;
 QY 17 LFSNPRVXEVAVADYTSDDRRBESQILPQTPKRTKTDVYNPNSQSGFRLEQLEL 76
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 QY 77 EADALVNFHYQSSQLPFPFESSPOVLTREVLQHTLDLINHPMSVLAVALGIRECFH 136
 DB 79 QCEAERFRFAFLORLPVPFYSIKEYYNVNGLOKACDALADNSWTLSHLIAFNLVDIYS 138
 QY 137 HSRITSCANCAENBEGCTPLHACRKGDEILVELVQYCHTOMDYVTKGTFVHYAVOG 196
 DB 139 NPKMLQCVQADAAATLMSFPQALIKQGHMEWYKALLPL--SKLEHLDINSNVFHYAA-S 195
 QY 197 DNSQVQLGGRNAVAGLNVNNOGLTPLHLAQLQKQEWVRVLLCNARCNLMGNGVYI 256
 DB 196 TTKEIINLIIDKSTVNLHNSDGYTPPLHVACLAADKEENYKALLAGANVNL--NAKDI 252
 QY 257 HSAMKFSQKCAEMITISMDSSQIHSKDPYRGASPLHWAKNAEMARMLTKRGCVNNTSSA 316
 DB 253 RKYYKTSAPTTVSSFLRTVNSKLYTQDMKYGTPPLHMCSSRETLHALINEGCVNATNFD 312
 QY 317 GNTALHVGWNRNPFDCALVLLTHGANADARGEHNTPLHLANSKDNVEMIKALIVGAEV 376
 DB 313 GRTALHVGWNRNPFECVUTLLAHDAEIDVLDKDGNAALHIAIEKKVLPYVQCLVVGCDI 372
 QY 377 DTNPNGERTP 386

DB 373 NLNKGKTP 382

RESULT 14

ID 07KUD4 PRELIMINARY; PRT; 887 AA.

DT 05-JUL-2004 (TEMBLrel. 27, Created)

DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)

DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)

GN ORFNames=CG6718;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;

OC Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha;

OC Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxId=7227;

[1]

RP MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.H., Blazer R.G., Champagne M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,

RA Adair J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,

RA Burris J.M., Busam D.A., Butler H., Cadiot E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fodor C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibbegan C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paule V., Reese M.G.,

RA Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Sinden-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodgett, Morley K.C., Wu D., Yang S., Yao O.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT The genome sequence of Drosophila melanogaster.

RL Science 287:2185-2195(2000).

RN [2]

RP MEDLINE=22426065; PubMed=12537556;

RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Pfeiffer J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: release 3 of the Drosophila

melanogaster euchromatic genome sequence."

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RP MEDLINE=22426070; PubMed=12537573;

RA Kaminiker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.,

RT "The transposable elements of the Drosophila melanogaster euchromatin:

a genomics perspective."

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN [4]

RP MEDLINE=22426069; PubMed=12537572;

RA Maira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochnik S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Belencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter U., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [5]

RP MEDLINE=22426069; PubMed=12537572;

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RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochnik S.E.,

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RN [5]

RP MEDLINE=22426069; PubMed=12537572;

RA Maira S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochnik S.E.,

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,

RA Belencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter U., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.E.,

RT "Annotation of the Drosophila melanogaster euchromatic genome: a

systematic review."

RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [5]

RP MEDLINE=22426069; PubMed=12537572;

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RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

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RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).

RN [5]

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RA Belencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 12:51:45 ; Search time 79.7757 Seconds
(without alignments)
1771.710 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084
Sequence: 1 MGFERRLVNTPSGVTNLFPSN.....EVDTRNDGERTPLASKIG 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_238sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 2084 | 100.0 | 394 | 2 | AAW17845 |
| 2 | 2084 | 100.0 | 394 | 5 | ABBS2229 |
| 3 | 2084 | 100.0 | 687 | 2 | AAW17847 |
| 4 | 2084 | 100.0 | 687 | 5 | ABBS2231 |
| 5 | 2084 | 100.0 | 688 | 2 | AAW17848 |
| 6 | 2084 | 100.0 | 688 | 5 | ABBS2232 |
| 7 | 2078 | 99.7 | 784 | 7 | ADDP3407 |
| 8 | 2078 | 99.7 | 806 | 5 | AAE23968 |
| 9 | 2078 | 99.7 | 806 | 8 | AD019776 |
| 10 | 1837 | 88.1 | 752 | 2 | AAAR3018 |
| 11 | 1837 | 88.1 | 752 | 2 | AAW01479 |
| 12 | 1837 | 88.1 | 752 | 2 | AAW13163 |
| 13 | 1837 | 88.1 | 752 | 2 | AAW17849 |
| 14 | 1837 | 88.1 | 752 | 2 | AAW1825 |
| 15 | 1837 | 88.1 | 752 | 5 | ABBS2215 |
| 16 | 1808.5 | 86.8 | 751 | 7 | ADDE6244 |
| 17 | 1808.5 | 86.8 | 751 | 7 | ADDE6052 |
| 18 | 1808.5 | 86.8 | 751 | 7 | ADDE6053 |
| 19 | 1808.5 | 86.8 | 751 | 7 | ADDE6053 |
| 20 | 1234.5 | 59.2 | 667 | 7 | ADMO5093 |
| 21 | 836 | 40.1 | 401 | 4 | AAAB9281 |
| 22 | 494.5 | 23.7 | 877 | 4 | ABBS2624 |
| 23 | 338 | 16.2 | 843 | 7 | ADDE27861 |
| 24 | 332 | 15.9 | 1839 | 7 | ADDE27862 |
| 25 | 332 | 15.9 | 1872 | 4 | AAW79160 |

| | | | | | | |
|----|-------|------|------|---|----------|---------------------|
| 26 | 324 | 15.5 | 1330 | 7 | ADM04552 | Adm04552 Human pro |
| 27 | 313.5 | 15.0 | 1549 | 4 | ABBS7412 | ABBS7412 Drosophila |
| 28 | 313.5 | 15.0 | 1549 | 4 | ABBS8328 | ABBS8328 Drosophila |
| 29 | 305.5 | 14.7 | 1745 | 2 | AAW76776 | AAW76776 D. immitis |
| 30 | 305.5 | 14.7 | 1745 | 2 | AAW70608 | AAW70608 Full leng |
| 31 | 305.5 | 14.7 | 1745 | 3 | AAW11589 | AAW11589 D. immitis |
| 32 | 305.5 | 14.7 | 1745 | 5 | AAO21368 | AAO21368 Ankyrin P |
| 33 | 302.5 | 14.5 | 2443 | 5 | ABBS0521 | ABBS0521 Drosophila |
| 34 | 301 | 14.4 | 763 | 3 | AAW79154 | AAW79154 Mouse pro |
| 35 | 301 | 14.4 | 786 | 3 | AAW69163 | AAW69163 Amino aci |
| 36 | 301 | 14.4 | 786 | 6 | ABBS8149 | ABBS8149 Mouse dea |
| 37 | 301 | 14.4 | 786 | 7 | ABW02414 | ABW02414 Mouse pro |
| 38 | 301 | 14.4 | 786 | 7 | ABW02422 | ABW02422 Human PKK |
| 39 | 301 | 14.4 | 786 | 7 | ABW02423 | ABW02423 Human PKK |
| 40 | 301 | 14.4 | 786 | 7 | ABW02424 | ABW02424 Human PKK |
| 41 | 301 | 14.4 | 787 | 3 | AAW76079 | AAW76079 Murine pr |
| 42 | 301 | 14.4 | 787 | 4 | ABBS6018 | ABBS6018 Skin cell |
| 43 | 301 | 14.4 | 787 | 5 | ABBS7218 | ABBS7218 Murine pr |
| 44 | 300.5 | 14.4 | 347 | 7 | ABW02421 | ABW02421 Human PKK |
| 45 | 300.5 | 14.4 | 1724 | 5 | AAO20513 | AAO20513 Protein o |

ALIGNMENTS

RESULT 1
ID AAW17845
AAW17845 standard; protein, 394 AA.

XX
XX
AC AAW17845;
XX
DT 07-AUG-1997 (first entry)
XX
DE Cytosolic phospholipase A2/B (clone 19a product).
XX
XX Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
KM inflammation; inhibitor; antiinflammatory.
XX
XX Homo sapiens.
OS
PN WO9717448-A2.
XX
PD 15-MAY-1997.
XX
PF 07-NOV-1996; 96WO-US017794.
XX
PR 08-NOV-1995; 95US-00555568.
XX
PA (GENE) GENETICS INST INC.
XX
PI Jones S, Tang J;
XX WPI; 1997-281037/25.
XX DR N-PSDB; AAT68823.
XX
PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
PT mammalian subject.
PS
PS Claim 12; Page 43-44; 74pp; English.

A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17845) is characterized by activity in the absence of calcium, by activity in a mixed micelle assay with 1-palmitoyl-2-(14C)- arachidonyl- phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a lack of stimulation by ATP, and by including in its sequence at least one of the amino acid sequences given in AAW17839- 44). It is encoded by a partial cDNA clone 19a (AAT68823), derived from Burkitt's lymphoma Raji (ATCC CRL86) cells. Other PLA2/B enzymes (AAW17846-48) have also been identified. sPLA2/B enzymes are thought to be involved in the release of arachidonic acid in specific tissues. Recombinant sPLA2/B polypeptides produced in transformed host cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory drugs which inhibit the arachidonic acid cascade

XX Sequence 394 AA;
SQ

100.0%; Score 2084; DB 2; Length 394;

Best Local Similarity 100.0%; P-Seq. NO. 2.66-219;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|---|------|
| Qy | 1 | MOFEIRLVNTSGVNTLFSNPRVKEVAADYTSISRVAEEGLIFONTPNKTCVLY | 60 |
| Db | 1 | MOFEIRLVNTSGVNTLFSNPRVKEVAVADYTSISRVAEEGLIFONTPNKTCVLY | 60 |
| Qy | 61 | NPRNSQSGRFLQLELEADALVNFHOYSQQLPFYSSSQVLTAEVLQHTDLIRNHPSW | 120 |
| Db | 61 | NPRNSQSGRFLQLELEADALVNFHOYSQQLPFYSSSQVLTAEVLQHTDLIRNHPSW | 120 |
| Qy | 121 | SVAHIAVBLGRRECEHSHRSISCANCAKEEGCTPLHLA CRKDGEIIVELVGYCHTQMD | 180 |
| Db | 121 | SVAHIAVBLGRRECEHSHRSISCANCAKEEGCTPLHLA CRKDGEIIVELVGYCHTQMD | 180 |
| Qy | 181 | VTDYGEYVFIHYAVOGDNSQVQLQLGRNAVAGLVNNGQLPTLHLACQLGKQEMRVLL | 240 |
| Db | 181 | VTDYGEYVFIHYAVOGDNSQVQLQLGRNAVAGLVNNGQLPTLHLACQLGKQEMRVLL | 240 |
| Qy | 241 | LCNARCNIMGPNGYPIHSAMKPSQKCAEMII SMDSQIHSKDPRYGASPLHWAKNAEMA | 3000 |
| Db | 241 | LCNARCNIMGPNGYPIHSAMKPSQKCAEMII SMDSQIHSKDPRYGASPLHWAKNAEMA | 3000 |
| Qy | 301 | RMLRKGCNVNSTSSAGNTALHVGWNRNFPDCAIYLLTIGANADARGEHNTPLHLAMSK | 360 |
| Db | 301 | RMLRKGCNVNSTSSAGNTALHVGWNRNFPDCAIYLLTIGANADARGEHNTPLHLAMSK | 360 |
| Qy | 361 | DNVEMIKALIVGAEVDTPNDGEPPTFLASKIG | 394 |
| Db | 361 | DNVEMIKALIVGAEVDTPNDGEPPTFLASKIG | 394 |

RESULT 2

ABB82229 standard; protein; 394 AA.

XX
AC
XX

ABB82229;

DT 08-JAN-2003 (first entry)

Calcium independent phospholipase A2/B (cPLA2/B) (clone 19a).

KM Calcium independent phospholipase A₂/B; cPLA₂/B; phospholipase; enzyme; catalytic mechanism; substrate; inhibition; phosphorylation; activation

KW antiasthmatic; human.

XX
OS
XY

Homo sapiens.

XX
PN
XX
US2002106364-

AA PD 08-AUG-2002.

09-AUG-2001; 2001US-00927180.

| | | |
|----|--------------|----------------|
| AA | 27-JUL-1994; | 94US-00281193. |
| PR | 14-APR-1995. | 95US-00422105 |
| DP | | |

| | | |
|----|--------------|----------------|
| PR | 14-APR-1995; | 95US-00422420. |
| PR | 26-JUN-1995 | 95WO-TIS008059 |

| | | |
|----|--------------|----------------|
| EX | 08-DEC-1999; | 95NO-00000005 |
| PR | 08-NOV-1995; | 95US-00555568. |
| PR | 08-SEP-1998 | 98US-00149908 |

06-MAR-2000; 2000US-00519223.

(GEMY) GENETICS INST INC.

Jones S, Tang J;

WPI; 2002-739923/80.
N-PSDB. ABV73009

DN N-ESDB; ADV/3000.
XX

PE Claim 6, Page 18-19, 41pd; English.
 PT Novel composition comprising purified mammalian calcium independent
 PT phospholipase enzyme, useful for the screening of inhibitors of
 PT phospholipase activity, is active in the absence of calcium.
 XX

XX The invention relates to a purified mammalian calcium independent

CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is characterized by activity in the absence of calcium and has a molecular

CC weight of 86 kD on SDS-PAGE. A composition (1) comprising a purified
CC calcium independent phospholipase enzyme is useful for identifying and

CC inhibitor of phospholipase activity which involves consuming (1),
CC phospholipid and candidate inhibitor compound, and observing whether the
CC enzyme cleaves the phospholipid and releases fatty acid from it. A
CC pharmaceutical composition (PC) comprising a therapeutically effective
CC amount of the inhibitor is useful for reducing inflammation and for
CC treating inflammatory conditions including rheumatoid arthritis,
CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC by increased levels of prostaglandins, leukotriene or platelet activating
CC factor. A composition comprising an antibody which binds to (I) is useful
CC as research and diagnostic tool, and is also useful in the study of
CC phospholipase A2 activity and inflammatory conditions. The present
CC sequence represents a human cPLA2/β enzyme (clone 19a)

XX Sequence 394 AA;
SQ

| Query Match | Score | DB 5 | Length |
|-------------|-------|------|--------|
| 100.0% | 2084 | | 394 |

Best Local Similarity 100.0%; P-vec. NO. 2.9e-219;
Matches 394; Conservative 0; Mismatches 0; Indels 0
Gaps 0

| | | | |
|----|-----|--|-----|
| QY | 1 | MOFGRLVNTSSGVTNLESNFPRVXEVAVADYTSDDRREBQOLLPONTPRMTDCVLV | 60 |
| Db | 1 | MOFGRLVNTSSGVTNLESNFPRVXEVAVADYTSDDRREBQOLLPONTPRMTDCVLV | 60 |
| QY | 61 | NPRNSQSGFRLFOLELEADALVNFHOXSQQLPYRESSPOVLHTEVLQHLTDLINHPBW | 120 |
| Db | 61 | NPRNSQSGFRLFOLELEADALVNFHOXSQQLPYRESSPOVLHTEVLQHLTDLINHPBW | 120 |
| QY | 121 | SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDGELLVELVQYCHTQMD | 180 |
| Db | 121 | SVAHLAVELGIRECFHHSRIISCANCAENEBGCTPLHLACRKGDGELLVELVQYCHTQMD | 180 |
| QY | 181 | VTDYKGFVEFHYAVOGDNDQVQLQLGRNAVAGLNVNNQGLTPLHLACQLGQENVRVL | 240 |
| Db | 181 | VTDYKGFVEFHYAVOGDNDQVQLQLGRNAVAGLNVNNQGLTPLHLACQLGQENVRVL | 240 |
| QY | 241 | LCNARCNTMGNGVPIHSAKFQSKCAEMTISMDSSQIHSKDPFYGASPLHWANAEMA | 300 |
| Db | 241 | LCNARCNTMGNGVPIHSAKFQSKCAEMTISMDSSQIHSKDPFYGASPLHWANAEMA | 300 |
| QY | 301 | RMLLKRCGNVSTSAGNTALHVGVMNRFDCAVLLTHGANADARGEHNTPLHLAMSK | 360 |
| Db | 301 | RMLLKRCGNVSTSAGNTALHVGVMNRFDCAVLLTHGANADARGEHNTPLHLAMSK | 360 |
| QY | 361 | DNVEIKALIVFGAEVDTPNDPGEFPTPLASTIG | 394 |
| Db | 361 | DNVEIKALIVFGAEVDTPNDPGEFPTPLASTIG | 394 |

RESULT 3

AAW17847 standard; protein; 687 AA.

XX
AC
AAW17847

DT 07-AUG-1997 (First entry)

XX DE Cytosolic phospholipase A2/B (alternatively spliced clone 19a).

XX Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade.
KM

KW inflammation; inhibitor; antiinflammatory.
XX

OS Homo sapiens

XX MO9717448-A2.
XX 15-MAY-1997.
XX 07-NOV-1996; 96WO-US017794.
XX 08-NOV-1995; 95US-00555568.
XX (GENY) GENETICS INST INC.
XX Jones S, Tang J;
XX WPI, 1997-281037/25.
XX N-PSDB; AAT68825.
XX Calcium independent phospholipase A2/B - used to reduce inflammation in a
XX mammalian subject.
XX Claim 12; Page 49-51; 74pp; English.
XX A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AAW17847) is
XX characterized by activity in the absence of calcium, by activity in a
XX mixed micelle assay with 1-palmitoyl-2-(14C) - arachidonyl-
XX phosphatidylcholine of about 1-20 umol/min.mg, by a pH optimum of 6, a
XX lack of stimulation by ATP, and by including in its sequence at least one
XX of the amino acid sequences given in AAW17839-44). It is an
XX alternatively spliced variant of another isolated polypeptide (AAW17845)
XX and is encoded by an isolated cDNA (AAT68825). Other PLA2/B enzymes are
XX thought to be involved in the release of arachidonic acid in specific
XX tissues. Recombinant sPLA2/B polypeptides produced in transformed host
XX cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
XX drugs which inhibit the arachidonic acid cascade

Sequence 687 AA;

Query Match 100.0%; Score 2084; DB 2; Length 687;

Best Local Similarity 100.0%; Pred. No. 6.5e-219; Indels 0; Gaps 0;
Matches 394; Conservative 0; Mismatches 0;

QY 1 MOFGRLVNTFSGVTLFNSNPRVKEVAADYTSRVRVEEGQLIFONTNRTMPCVLY 60
DB 1 MOFGRLVNTFSGVTLFNSNPRVKEVAADYTSRVRVEEGQLIFONTNRTMPCVLY 60
QY 61 NPNNSGGRFLFQLELEADALVNFHQSQQLPFYESSPQVLTTEVLOHLTDLIRNHPSW 120
DB 61 NPNNSGGRFLFQLELEADALVNFHQSQQLPFYESSPQVLTTEVLOHLTDLIRNHPSW 120
QY 121 SVANLAVEIGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEITVELVOYCHTQMD 180
DB 121 SVANLAVEIGIRECFHHSRIISCANCAENEGCTPLHLACRKGDEITVELVOYCHTQMD 180
QY 181 VVDYKERTVHYAVQGDNSQVQLLGNNAVAGLNQVNNQGLTPLHLACQKGRKEMRVLL 240
DB 181 VVDYKERTVHYAVQGDNSQVQLLGNNAVAGLNQVNNQGLTPLHLACQKGRKEMRVLL 240
QY 241 LCNARCNINGPNGYPIHSAKFQKCAEMIISMDSQIHSKOPRYGASPLHAKNAEMA 300
DB 241 LCNARCNINGPNGYPIHSAKFQKCAEMIISMDSQIHSKOPRYGASPLHAKNAEMA 300
QY 301 RMLKRGCVNVTSSAGNTALAVGMNRNPDCAIVLLTHGANADARGHGNTPLHLSMSK 360
DB 301 RMLKRGCVNVTSSAGNTALAVGMNRNPDCAIVLLTHGANADARGHGNTPLHLSMSK 360
QY 361 DNVEMLKALVPGAEVDTPNDFGTFPLASKIG 394
DB 361 DNVEMLKALVPGAEVDTPNDFGTFPLASKIG 394

RESULT 4
ABB82231
ID ABB82231 standard; protein; 687 AA.

XX ABB82231;
XX 08-JAN-2003 (first entry)
XX Human cPLA2/B splice variant (clone 19a).
XX Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
XX antiinflammatory; antirheumatic; antipsoriatic; antineumatic; cytosolic;
XX antisthmatic; human.
XX Homo sapiens.
XX US2002106364-A1.
XX 08-AUG-2002.
XX 09-AUG-2001; 2001US-00927180.
XX 27-JUL-1994; 94US-00281193.
XX 14-APR-1995; 95US-00422106.
XX 14-APR-1995; 95US-00422420.
XX 26-JUN-1995; 95WO-US008069.
XX 08-NOV-1995; 95US-00555568.
XX 09-SRP-1998; 98US-00149988.
XX 06-MAR-2000; 2000US-00519223.
XX (GENY) GENETICS INST INC.
XX Jones S, Tang J;
XX WPI, 2002-739923/80.
XX N-PSDB; ABV73010.
XX Novel composition comprising purified mammalian calcium independent
XX phospholipase enzyme, useful for the screening of inhibitors of
XX phospholipase activity, is active in the absence of calcium.
XX Claim 6; Page 23-25; 41pp; English.

The invention relates to a purified mammalian calcium independent
cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
characterized by activity in the absence of calcium and has a molecular
weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
calcium independent phospholipase enzyme is useful for identifying an
inhibitor of phospholipase activity which involves combining (I),
phospholipid and candidate inhibitor compound, and observing whether the
enzyme cleaves the phospholipid and releases fatty acid from it. A
pharmaceutical composition (PC) comprising a therapeutically effective
amount of the inhibitor is useful for reducing inflammation and for
treating inflammatory conditions including rheumatoid arthritis,
asthma, inflammatory bowel disease and other diseases mediated
by increased levels of prostaglandins, leukotriene or platelet activating
factor. A composition comprising an antibody which binds to (I) is useful
as research and diagnostic tool, and is also useful in the study of
phospholipase A2 activity and inflammatory conditions. The present
sequence represents a human cPLA2/B enzyme longer splice variant (clone
19a)

Query Match 100.0%; Score 2084; DB 5; Length 687;
Best Local Similarity 100.0%; Pred. No. 6.5e-219; Indels 0; Gaps 0;
Matches 394; Conservative 0; Mismatches 0;

QY 1 MOFGRLVNTFSGVTLFNSNPRVKEVAADYTSRVRVEEGQLIFONTNRTMPCVLY 60
DB 1 MOFGRLVNTFSGVTLFNSNPRVKEVAADYTSRVRVEEGQLIFONTNRTMPCVLY 60
QY 61 NPNNSGGRFLFQLELEADALVNFHQSQQLPFYESSPQVLTTEVLOHLTDLIRNHPSW 120
DB 61 NPNNSGGRFLFQLELEADALVNFHQSQQLPFYESSPQVLTTEVLOHLTDLIRNHPSW 120

```

QY 121 SVANHLAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
DB 121 SVANHLAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
QY 181 VTDYKGETVPHYAVOGDNGVQLLGRNAVAGLVNNOGCLTPLHLACQLGKQKEMVRVLL 240
DB 181 VTDYKGETVPHYAVOGDNGVQLLGRNAVAGLVNNOGCLTPLHLACQLGKQKEMVRVLL 240
QY 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLKRGCVNSTSSAGNTALHVGWRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNSTSSAGNTALHVGWRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVGAEDVTPNDPGETPTPLASKIG 394
DB 361 DNVEIMKALIVGAEDVTPNDPGETPTPLASKIG 394

RESULT 5
AA17848
ID AA17848 standard; protein, 688 AA.
XX
AC AA17848;
XX
DT 07-AUG-1997 (first entry)
XX
DE Cytosolic phospholipase A2/B (alternatively spliced clone 19b).
XX
KW Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade;
XX inflammation; inhibitor; antiinflammatory.
XX
OS Homo sapiens.
XX
PN WO9717448-A2.
XX
PD 15-MAY-1997.
XX
PF 07-NOV-1996; 96WO-US017794.
XX
PR 08-NOV-1995; 95US-00555568.
XX
PA (GEMV ) GENETICS INST INC.
XX
PI Jones S, Tang J;
XX
DR WPI, 1997-281037/25.
XX
DR N-PSDB; AAT68826.
XX
PT Calcium independent phospholipase A2/B - used to reduce inflammation in a
XX mammalian subject.
XX
PS Claim 12; Page 54-56; 74pp; English.
XX
XX
CC A novel human cytosolic phospholipase A2/B (sPLA2/B) enzyme (AA17848) is
CC characterized by activity in the absence of calcium, by activity in a
CC mixed micelle assay with 1-palmitoyl-2-(14C)-arachidonyl-
CC phosphatidylcholine by ATP, and by including in its sequence at least one
CC lack of stimulation by ATP, and by including in its sequence at least one
CC of the amino acid sequences given in AA17839-44). It is an
CC alternatively spliced variant of another isolated polypeptide (AA17846)
CC and is encoded by an isolated cDNA (AAT68826). Other PLA2/B enzymes
CC (AA17845, AA17847) have also been identified. sPLA2/B enzymes are
CC thought to be involved in the release of arachidonic acid in specific
CC tissues. Recombinant sPLA2/B polypeptides produced in transformed host
CC cells can be used to screen for sPLA2/B inhibitors, i.e. antiinflammatory
CC drugs which inhibit the arachidonic acid cascade
XX
SQ Sequence 688 AA;

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```

QY 1 MOFGRLVNTFSGVTLFNSNPRVKEVAVADTSSDRVVEEGQLIFONTPNRTMPCVLV 60
DB 1 MOFGRLVNTFSGVTLFNSNPRVKEVAVADTSSDRVVEEGQLIFONTPNRTMPCVLV 60
QY 61 NPNRSQSGFRLQLELEADALVNFQYSQQLPFYESSPOVLHTEVLOHITDLIRNHPGM 120
DB 61 NPNRSQSGFRLQLELEADALVNFQYSQQLPFYESSPOVLHTEVLOHITDLIRNHPGM 120
QY 121 SVANHLAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
DB 121 SVANHLAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
QY 181 VTDYKGETVPHYAVOGDNGVQLLGRNAVAGLVNNOGCLTPLHLACQLGKQKEMVRVLL 240
DB 181 VTDYKGETVPHYAVOGDNGVQLLGRNAVAGLVNNOGCLTPLHLACQLGKQKEMVRVLL 240
QY 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
DB 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
QY 301 RMLKRGCVNSTSSAGNTALHVGWRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNSTSSAGNTALHVGWRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVGAEDVTPNDPGETPTPLASKIG 394
DB 361 DNVEIMKALIVGAEDVTPNDPGETPTPLASKIG 394

RESULT 6
ABB82232
ID ABB82232 standard; protein, 688 AA.
XX
AC ABB82232;
XX
DT 08-JAN-2003 (first entry)
XX
DE Human cPLA2/B splice variant (clone 19b).
XX
KW Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
XX antiinflammatory; antidiarrhetic; antipsoxiatic; antirheumatic; cytosolic;
XX antiaesthetic; human.
XX
OS Homo sapiens.
XX
PN US2002106364-A1.
XX
PD 08-AUG-2002.
XX
PF 09-AUG-2001; 2001US-00927180.
XX
PR 27-UTL-1994; 94US-00281193.
XX
PR 14-APR-1995; 95US-00422106.
XX
PR 14-APR-1995; 95US-00422420.
XX
PR 26-JUN-1995; 95WO-US008069.
XX
PR 08-NOV-1995; 95US-00555568.
XX
PR 09-SEP-1998; 98US-00149988.
XX
PR 06-MAR-2000; 2000US-00519223.
XX
PA (GEMV ) GENETICS INST INC.
XX
PI Jones S, Tang J;
XX
DR WPI, 2002-739923/80.
XX
DR N-PSDB; ABV73011.
XX
PT Novel composition comprising purified mammalian calcium independent
XX phospholipase enzyme, useful for the screening of inhibitors of
XX phospholipase activity, is active in the absence of calcium.
XX

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Query Match 100.0%; Score 2084; DB 2; Length 688;

PS Claim 6; Page 28-30; 41pp; English.

XX The invention relates to a purified mammalian calcium independent
 CC cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
 CC characterized by activity in the absence of calcium and has a molecular
 CC weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
 CC calcium independent phospholipase enzyme is useful for identifying an
 CC inhibitor of phospholipase activity which involves combining (II),
 CC phospholipid and candidate inhibitor compound, and observing whether the
 CC enzyme cleaves the phospholipid and releases fatty acid from it. A
 CC pharmaceutical composition (PC) comprising a therapeutically effective
 CC amount of the inhibitor is useful for reducing inflammation and for
 CC treating inflammatory conditions including rheumatoid arthritis,
 CC psoriasis, asthma, inflammatory bowel disease and other diseases mediated
 CC by increased levels of prostaglandins, leukotriene or platelet activating
 CC factor. A composition comprising an antibody which binds to (I) is useful
 CC as research and diagnostic tool, and is also useful in the study of
 CC phospholipase A2 activity and inflammatory conditions. The present
 CC sequence represents a human cPLA2/B enzyme longer splice variant (clone
 CC 19b)

XX Sequence 668 AA;

Query Match 100.0%; Score 2084; DB 5; Length 688;
 Best Local Similarity 100.0%; Pred. No. 6.5e-219;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSGVTNLFSPNPRVKEVAADYTSRVRBEGQLIFONTNRTMDCVLY 60
 DB 1 MOFGRLVNTFSGVTNLFSPNPRVKEVAADYTSRVRBEGQLIFONTNRTMDCVLY 60
 QY 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSQVLAHTVLAHTLDIRNHPBW 120
 DB 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSQVLAHTVLAHTLDIRNHPBW 120
 QY 121 SVAHLAVERIGRBCFHSRIISCANCAENBEGCTPLHLACRKGDSILVELVOYCHTQND 180
 DB 121 SVAHLAVERIGRBCFHSRIISCANCAENBEGCTPLHLACRKGDSILVELVOYCHTQND 180
 QY 181 VTDYKGETVPHYAVQDNSQVTLQGRNNAVAGINQVNNQGLTPPLHLACQLGKQEMVRVLL 240
 DB 181 VTDYKGETVPHYAVQDNSQVTLQGRNNAVAGINQVNNQGLTPPLHLACQLGKQEMVRVLL 240
 QY 241 LCNARININGPNYPIHSAKFSQKCAEMTISMDSSQHSKDPKRYGASPLHAKNAEMA 300
 DB 241 LCNARININGPNYPIHSAKFSQKCAEMTISMDSSQHSKDPKRYGASPLHAKNAEMA 300
 QY 301 RMLLKRCGVNSTSSAGNTALHGVWRNRPDCAIVLLTGANADARGHGNTPLHLAMSK 360
 DB 301 RMLLKRCGVNSTSSAGNTALHGVWRNRPDCAIVLLTGANADARGHGNTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDTNDFGSETPTFLASKIG 394
 DB 361 DNVEMIKALIVFGAEVDTNDFGSETPTFLASKIG 394

RESULT 7
 ID ADD93407 standard; protein; 784 AA.
 AC ADD93407;

XX 29-JUN-2004 (first entry)

XX Human lipid-associated molecule LIPAM-14 polypeptide.

KM Human, lipid-associated molecule; LIPAM-14; neuroprotective; relaxant;
 KM antihypertensive; antidiabetic; cytostatic; dermatologic; immunosuppressive;
 KM antiinflammatory; chrysotherapeutic; antiallergic; cerebroprotective;
 KM gastrointestinal; hepatotropic; nephroprotective; anticonvulsant;
 KM antiparkinsonian; antibacterial; antiparasitic; fungicide; protozoacide;
 KM vtrucide; uteroblastic; antirheumatic; cardiac; cardiovascular; anti-HIV;
 KM nootropic.

XX Homo sapiens.

XX WO2003083081-A2.

XX 09-OCT-2003.

XX 27-MAR-2003; 2003WO-US0009755.

XX 29-MAR-2002; 2002US-0368722P.

XX 03-MAY-2002; 2002US-037576P.

XX 05-JUL-2002; 2002US-0393934P.

XX 27-SEP-2002; 2002US-0414269P.

XX (INCYTE) INCYTE CORP.

XX Emerling BM, Margulis JP, Chawla NK, Lee SY, Duggan BM, Warren BA,
 PI Baughn MR, Lee EA, Griffin JA, Kabie AE, Elliott VS, Chang H,
 PI Lee S, Ramkumar J, Bulloch SA, Hafalia Avb, Khare R, Jiang X,
 PI Jackson AA;

XX WPI, 2003-788347/74.

XX N-PSDB; ADD93426.

XX New LIPAM polypeptides, useful for diagnosing, preventing, and treating
 PT disorders associated with abnormal expression or activity of LIPAM, e.g.
 PT neuromuscular, immunological, cardiovascular disorders, cancer and/or
 PT infections.

XX Claim 69; Page 206-207; 238pp; English.

XX The present sequence is the protein sequence of human lipid-associated
 CC molecule LIPAM-14 (Incyte polypeptide 7512662CD), a protein that shows
 CC homology to human Ca2+-independent phospholipase A2 short isoform. This
 CC is one of 19 LIPAM polypeptides of the invention. The invention relates
 CC to these novel LIPAMs and the nucleic acids encoding them, and to the use
 CC of nucleic acids and proteins in the diagnosis, treatment and prevention
 CC of disorders associated with abnormal expression or activity of LIPAM
 CC such as neurodegenerative disorders (e.g. Parkinson's disease,
 CC Alzheimer's disease), muscular disorders (e.g. myotonic dystrophy,
 CC catatonias), endocrine disorders (e.g. diabetes, Grave's disease), cancers
 CC (e.g. leukemia, cervical or breast cancers), immunological disorders
 CC (e.g. scleroderma, systemic lupus erythematosus, allergies),
 CC gastrointestinal disorders (e.g. Crohn's disease), renal disorders (e.g.
 CC Goodpasture's syndrome), infections (e.g. viral, bacterial, fungal,
 CC parasitic, protozoal, helminthic), cardiovascular disorders (e.g.
 CC atherosclerosis), or hepatic diseases (e.g. cirrhosis). The invention
 CC also relates to the assessment of the effects of exogenous compounds on
 CC the expression of nucleic acids and LIPAMs. The invention provides
 CC expression vectors, host cells, antibodies, agonists and antagonists,
 CC transgenic organisms, and arrays and microarrays of the polynucleotides.

XX Sequence 784 AA;

Query Match 99.7%; Score 2078; DB 7; Length 784;
 Best Local Similarity 99.7%; Pred. No. 3.6e-218;
 Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSGVTNLFSPNPRVKEVAADYTSRVRBEGQLIFONTNRTMDCVLY 60
 DB 33 MOFGRLVNTFSGVTNLFSPNPRVKEVAADYTSRVRBEGQLIFONTNRTMDCVLY 92
 QY 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSQVLAHTVLAHTLDIRNHPBW 120
 DB 93 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSQVLAHTVLAHTLDIRNHPBW 152
 QY 121 SVAHLAVERIGRBCFHSRIISCANCAENBEGCTPLHLACRKGDSILVELVOYCHTQND 180
 DB 153 SVAHLAVERIGRBCFHSRIISCANCAENBEGCTPLHLACRKGDSILVELVOYCHTQND 212
 QY 181 VTDYKGETVPHYAVQDNSQVTLQGRNNAVAGINQVNNQGLTPPLHLACQLGKQEMVRVLL 240
 DB 213 VTDYKGETVPHYAVQDNSQVTLQGRNNAVAGINQVNNQGLTPPLHLACQLGKQEMVRVLL 272

QY 241 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQIHSKDPXYGASPLHWAKNAENA 300
 DB 273 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQIHSKDPXYGASPLHWAKNAENA 332
 QY 301 RMLKRGCVNSTSSAGNTALHVGVMRNPDCAIYVLTTHGANADARGEHNTPLHLAMSK 360
 DB 333 RMLKRGCVNSTSSAGNTALHVGVMRNPDCAIYVLTTHGANADARGEHNTPLHLAMSK 392
 QY 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
 DB 393 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 426

RESULT 8
 AAE25968
 ID AAE25968 standard; protein; 806 AA.
 XX AAE25968;
 AC
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human PLA2 group VI (Ca2+-independent) protein.
 XX
 KW Human; antisense; phospholipase A2; infection; inflammation; tumour;
 KW antisense therapy; PLA2 protein.
 XX
 OS Homo sapiens.
 XX
 PN US6410325-B1.
 PD 25-JUN-2002.
 XX
 PF 09-MAY-2001; 2001US-00851896.
 XX
 PR 09-MAY-2001; 2001US-00851896.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Freiler SM, Watt AT;
 XX
 DR WPI; 2002-616513/66.
 DR N-PSDB; AAD42941.
 XX
 PT Novel antisense compounds useful for inhibiting gene expression of human
 PT phospholipase A2, group VI and for treating diseases associated with
 PT expression of phospholipase A2, group VI.
 XX
 PS Disclosure; Col 109-116; 72pp; English.
 XX
 CC The present invention relates to novel antisense compounds which inhibit
 CC the expression of phospholipase A2 (PLA2), group VI (Ca2+-independent).
 CC The invention is useful for inhibiting the expression of PLA2, group VI
 CC (Ca2+-independent) in human cells or tissues and for treating an animal,
 CC particularly a human suspected of having or being prone to a disease or
 CC condition associated with expression of human PLA2, group VI (Ca2+-
 CC independent). It is useful for diagnosis, therapeutics and as research
 CC reagent, e.g. prophylactically to prevent or delay infection, tumour
 CC formation or inflammation. The present sequence is human PLA2 group VI
 CC (Ca2+-independent) protein
 CC
 XX
 SQ Sequence 806 AA;

Query Match 99.7%; Score 2078; DB 5; Length 806;
 Best Local Similarity 99.7%; Pred. No. 3 8e-218;
 Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQFGRLVNTFGSVTLFSPNPRFVKEVAVADYSSDRVREBQGLIFONTPRMTDCLV 60
 DB 1 MQFGRLVNTFGSVTLFSPNPRFVKEVAVADYSSDRVREBQGLIFONTPRMTDCLV 60
 QY 61 NPNRNSQSGRLTQLEADALVNFHOYSQQLPFYSSQVLTTEVLQHLTDLIRNHPW 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 61 NPNRNSQSGRLTQLEADALVNFHOYSQQLPFYSSQVLTTEVLQHLTDLIRNHPW 120
 QY 121 SVAAHLAVELGIEPCFHSRIISCANCAENEBGCTPLHLACRGDEILVELVQYCHTQMD 180
 DB 121 SVAAHLAVELGIEPCFHSRIISCANCAENEBGCTPLHLACRGDEILVELVQYCHTQMD 180
 QY 181 VTDYKGETVFHYAVQDNSQVLTQLGRNAVAGLNQVNNQGLTPLHLACQLGQENVRVLL 240
 DB 181 VTDYKGETVFHYAVQDNSQVLTQLGRNAVAGLNQVNNQGLTPLHLACQLGQENVRVLL 240
 QY 241 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQIHSKDPXYGASPLHWAKNAENA 300
 DB 241 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQIHSKDPXYGASPLHWAKNAENA 300
 QY 301 RMLKRGCVNSTSSAGNTALHVGVMRNPDCAIYVLTTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCVNSTSSAGNTALHVGVMRNPDCAIYVLTTHGANADARGEHNTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394
 DB 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394

RESULT 9
 ADO19776
 ID ADO19776 standard; protein; 806 AA.
 XX ADO19776;
 AC
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human PRO polypeptide #350.
 XX
 KW Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX
 OS Homo sapiens.
 XX
 PN WO2004043361-A2.
 XX
 PD 27-MAY-2004.
 XX
 PF 06-NOV-2003; 2003WO-US035268.
 XX
 PR 08-NOV-2002; 2002US-0425235P.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 XX
 DR WPI; 2004-420067/39.
 DR N-PSDB; ADO19775.
 XX
 PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthritis.
 XX
 PS Claim 7, SEQ ID NO 700; 1731pp; English.
 XX
 CC The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune

CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.

XX Sequence 806 AA;

Query Match 99.7%; Score 2078; DB 8; Length 806;
 Best Local Similarity 99.7%; Pred. No. 3.8e-218;
 Matches 333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAADYTSDDRVREBGLIFONTPNRTMDCVLY 60
 DB 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAADYTSDDRVREBGLIFONTPNRTMDCVLY 60
 QY 61 NPNNSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLTHTVLOHITDILRNHPSW 120
 DB 61 NPNNSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLTHTVLOHITDILRNHPSW 120
 QY 121 SVNHLAVEIGIRCEPHHSRIISCANCAENEBGCTPLHLACRKDGSEIIVELVOYCHTQMD 180
 DB 121 SVNHLAVEIGIRCEPHHSRIISCANCAENEBGCTPLHLACRKDGSEIIVELVOYCHTQMD 180
 QY 181 VTDYKGETVPHVAVOGDSQVQLLGRNAVAGLNQVNNQGLTPHLACQIGKQEMRVLL 240
 DB 181 VTDYKGETVPHVAVOGDSQVQLLGRNAVAGLNQVNNQGLTPHLACQIGKQEMRVLL 240
 QY 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
 DB 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
 QY 301 RMLKRGCVNVSSTSSAGNTALHVGVMNRPFDCALVLTGADADARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCVNVSSTSSAGNTALHVGVMNRPFDCALVLTGADADARGEHNTPLHLAMSK 360
 QY 361 DNEMIKALIVFGAVDTPNDPGETPTFLASKIG 394
 DB 361 DNEMIKALIVFGAVDTPNDPGETPTFLASKIG 394

RESULT 10

AAR83018 standard; protein; 752 AA.

AC AAR83018;

DT 15-JUN-1996 (first entry)

DB Calcium-independent cytosolic phospholipase-A2/B enzyme.

XX CHO; calcium-independent cytosolic phospholipase-A2/B; enzyme;
 KW phospholipase-A2; phospholipase-B; drug screening; antiinflammatory;
 KM antibody.

OS Cricetus griseus.

PN US546595-A.

PD 14-NOV-1995.

PF 27-JUL-1994; 94US-00281193.

PR 27-JUL-1994; 94US-00281193.

XX (GEMV) GENETICS INST INC.

PI Tang J, Jones S;

XX WPI; 1996-009526/01.

DR N-PSDB; AAT05842.

PT Isolated polynucleotide encoding cytosolic phospholipase A2/8 - for
 PT producing enzyme for use in screening anti-inflammatory agents and prodn.
 PT of antibodies.

XX Claim 5; Col 15-22; 24pp; English.

CC The enzyme may be produced recombinantly in host cells such as animal
 CC cells, insect cells, eukaryotes, prokaryotes, etc. The protein may also
 CC be expressed in transgenic animals (e.g. milk of transgenic cow). The
 CC protein is used to screen for agents which inhibit phospholipase activity
 CC for use as antiinflammatory agents. These agents can be used to treat
 CC e.g. rheumatoid arthritis, psoriasis, asthma, inflammatory bowel disease
 CC and other disease mediated by increased levels of prostaglandins,
 CC leukotriene or platelet activating factor. The enzyme can also be used
 CC for the production of antibodies for use as research or diagnostic tools

XX Sequence 752 AA;

Query Match 88.1%; Score 1837; DB 2; Length 752;
 Best Local Similarity 87.3%; Pred. No. 1e-191;
 Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAADYTSDDRVREBGLIFONTPNRTMDCVLY 60
 DB 1 MOFFGLVNTFSGVTNLFSPNPRVKEVAADYTSDDRVREBGLIFONTPNRTMDCVLY 60
 QY 61 NPNNSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLTHTVLOHITDILRNHPSW 120
 DB 61 NPNNSQSGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLTHTVLOHITDILRNHPSW 120
 QY 121 SVNHLAVEIGIRCEPHHSRIISCANCAENEBGCTPLHLACRKDGSEIIVELVOYCHTQMD 180
 DB 121 SVNHLAVEIGIRCEPHHSRIISCANCAENEBGCTPLHLACRKDGSEIIVELVOYCHTQMD 180
 QY 181 VTDYKGETVPHVAVOGDSQVQLLGRNAVAGLNQVNNQGLTPHLACQIGKQEMRVLL 240
 DB 181 VTDYKGETVPHVAVOGDSQVQLLGRNAVAGLNQVNNQGLTPHLACQIGKQEMRVLL 240
 QY 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
 DB 241 LCNARCNIMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPRYGASPLHAKNAEMA 300
 QY 301 RMLKRGCVNVSSTSSAGNTALHVGVMNRPFDCALVLTGADADARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCVNVSSTSSAGNTALHVGVMNRPFDCALVLTGADADARGEHNTPLHLAMSK 360
 QY 361 DNEMIKALIVFGAVDTPNDPGETPTFLASKI 393
 DB 361 DNEMIKALIVFGAVDTPNDPGETPTFLASKI 393

RESULT 11

AAW01479 standard; protein; 752 AA.

AC AAW01479;

DT 25-MAR-2003 (revised)

DT 12-FEB-1997 (first entry)

DB Calcium-independent cytosolic phospholipase A2/B.

XX cPLA2/B; calcium-independent cytosolic phospholipase A2/B;
 KW arachidonic acid; 1-palmitoyl-2-[14C]-arachidonyl-phosphatidylcholine;
 KM anti-inflammatory; screen; rheumatoid arthritis.

OS Synthetic.

PN US5554511-A.

PD 10-SEP-1996.

PF 14-APR-1995; 95US-00422420.

Db 301 RMLKRGCDVSTSAAGNTALHVAWRNFDCCMVLITGANAAGTGEHNTPLHLAIISK 360

Qy 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKI 393
Db 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKI 393

RESULT 13

AAW17849 standard; protein; 752 AA.

AAW17849;

DT 27-AUG-2003 (revised)
DT 07-AUG-1997 (first entry)

DE Hamster cytosolic phospholipase A2/B.

KM Cytosolic phospholipase A2/B; sPLA2/B; arachidonic acid cascade; inflammation; inhibitor; antiinflammatory; CHO.

OS Cricetus.

Key Location/Qualifiers
Active-site 465 /note="mutagenesis of Ser-465 results in loss of activity"

WO9717448-A2.

PD 15-MAY-1997.

PF 07-NOV-1996; 96WO-US017794.

PR 08-NOV-1995; 95US-00555568.

PA (GENY) GENETICS INST INC.

PI Jones S, Tang J;

DR WPI; 1997-281037/25.

DR N-PSDB; AAT68827.

PT Calcium independent phospholipase A2/B - used to reduce inflammation in a mammalian subject.

Example 4; Page 33-36; 74pp; English.

CC A novel hamster cytosolic phospholipase A2/B (sPLA2/B) (AAW17849) is thought to be involved in the arachidonic acid cascade. Its amino acid sequence was deduced from a cDNA clone (AAT68827) obtd. from a CHO-DUX cDNA library. The recombinant enzyme has been expressed in CHO and COS host cells. Human sPLA2/B polypeptides (see also AAW17845-48) have also been isolated. These can be used to screen for inhibitors useful as antiinflammatory agents that block the arachidonic acid cascade in mammals. (Updated on 27-AUG-2003 to correct OS field.)

CC mammals. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 752 AA;

Query Match 88.1%; Score 1837; DB 2; Length 752; Best Local Similarity 87.3%; Pred. No. 1e-191; Indels 0; Gaps 0; Matches 343; Conservative 23; Mismatches 27;

Qy 1 MOFFGLVNTFSGVTNLFSNPFVKVAVADYSSDRVREBGLIFONTPTMTDCVLY 60

Db 1 MOFFGLVNTFSGVTNLFSNPFVKVAVADYSSDRVREBGLIFONTPTMTDCVLY 60

Qy 61 NPNSGSGRRLPQLEADALVNFHOYSSQLPFYESSPOVLAHTEVLAQHLTLIRNHP 120

Db 61 SPNPSGSGRRLPQLEADALVNFHOYSSQLPFYESSPOVLAHTEVLAQHLTLIRNHP 120

Qy 121 SVNHLAVELGIRCFHRSRIISCANCAENEGCTPLHLACRKGDELIVELVQYCHTQMD 180

Db 121 TVTHLAVELGIRCFHRSRIISCANCAENEGCTPLHLACRKGDELIVELVQYCHTQMD 180

Qy 181 VTDYKGEIVFHYAVOGDNSQVLIQGRNAVAGLNVNNGLTPLHLACQLGQEMRVTL 240
Db 181 VTDNKGTEFHYAVOGDNSQVLIQGRNAVAGLNVNNGLTPLHLACQLGQEMRVTL 240

Qy 241 LCNARCNMGPNQYPIHSAMKFSQKGCAMIIISMSOIHSDKDPYASPLHMAKXAEWA 300
Db 241 LCNARCNMGPNQYPIHSAMKFSQKGCAMIIISMSOIHSDKDPYASPLHMAKXAEWA 300

Qy 301 RMLKRGCDVSTSAAGNTALHVAWRNFDCCMVLITGANAAGTGEHNTPLHLAIISK 360

Db 301 RMLKRGCDVSTSAAGNTALHVAWRNFDCCMVLITGANAAGTGEHNTPLHLAIISK 360

Qy 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKI 393
Db 361 DNVEMIKALIVFGAEVDTPNDFGETPTFLASKI 393

RESULT 14

AAW81825 standard; protein; 752 AA.

AAW81825;

DT 02-FEB-1999 (first entry)

DE Chinese hamster calcium independent cPLA2/B protein.

KM Calcium independent; cytosolic phospholipase A2/B; cPLA2/B; screening; anti-inflammatory; arachidonic acid cascade; chinese hamster.

OS Cricetus griseus.

PN US840511-A.

PD 24-NOV-1998.

PF 23-OCT-1996; 96US-00735716.

PR 27-JUL-1994; 94US-00281193.

PR 14-APR-1995; 95US-00422106.

PA (GENY) GENETICS INST INC.

PI Tang J, Jones S;

DR WPI; 1999-034032/03.

DR N-PSDB; AAV64840.

PT Screening assay for phospholipase inhibitors - using specified phospholipase polypeptide.

PS Claim 1b; Col 21-24; 24pp; English.

CC This sequence represents a novel calcium independent cytosolic phospholipase A2/B enzyme isolated from chinese hamster ovary cells. This protein can be used for screening unknown compounds for anti-inflammatory activity mediated by the arachidonic acid cascade

CC activity mediated by the arachidonic acid cascade

XX Sequence 752 AA;

Query Match 88.1%; Score 1837; DB 2; Length 752; Best Local Similarity 87.3%; Pred. No. 1e-191; Indels 0; Gaps 0; Matches 343; Conservative 23; Mismatches 27;

Qy 1 MOFFGLVNTFSGVTNLFSNPFVKVAVADYSSDRVREBGLIFONTPTMTDCVLY 60

Db 1 MOFFGLVNTFSGVTNLFSNPFVKVAVADYSSDRVREBGLIFONTPTMTDCVLY 60

Qy 61 NPNSGSGRRLPQLEADALVNFHOYSSQLPFYESSPOVLAHTEVLAQHLTLIRNHP 120

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Db      61 SPKPHSGFRLFQLESEADALVNFQSSQLPPFYESSVQVLAHEVLAQHLSDLIRHPSM 120
Qy      121 SYAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
Db      121 TVTHLAVALGIRECFHSHRIISCANSTENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
Qy      181 VTDYKGETVFAHYAVQGDNSQVQLLGRNAVAGLQVNNQGLTPHLACQLGKQEMVRVLL 240
Db      181 VTDNKGETAFAHYAVQGDNSQVQLLGRNAVAGLQVNNQGLTPHLACQLGKQEMVRVLL 240
Qy      241 LCNARCNMGPGVPIHSAAMKPSQKCAEMIISMDSQHSKDPRYGASPLHMAKKAEMA 300
Db      241 LCNARCNMGPGVPIHSAAMKPSQKCAEMIISMDSQHSKDPRYGASPLHMAKKAEMA 300
Qy      301 RMLLRKGCNVNSTSSAGNTALHVGVRNRFDCAVILTLTGANADARGEHNTPLHLAMSK 360
Db      301 RMLLRKGCNVNSTSSAGNTALHVGVRNRFDCAVILTLTGANADARGEHNTPLHLAMSK 360
Qy      361 DNVEMIKALIVFGAEVDTPNDFGETPTPLASKI 393
Db      361 DNVEMIKALIVFGAEVDTPNDFGETPTPLASKI 393

RESULT 15
AB882215
ID      AB882215 standard; protein; 752 AA.
AC      AB882215;
XX      08-JAN-2003 (first entry)
DE      Calcium independent phospholipase A2/B (cPLA2/B) (clone 9).
XX      Calcium independent phospholipase A2/B; cPLA2/B; phospholipase; enzyme;
XX      antiinflammatory; antiarthritic; antipsoriatic; antirheumatic; cytotoxic;
XX      antiaesthetic.
XX      Unidentified.
XX      US2002106364-A1.
XX      08-AUG-2002.
PD      08-AUG-2002.
XX      09-AUG-2001; 2001US-00927180.
XX      27-JUL-1994; 94US-00281193.
XX      14-APR-1995; 95US-00422106.
XX      14-APR-1995; 95US-00422420.
XX      26-JUN-1995; 95WO-US008069.
XX      08-NOV-1995; 95US-00555568.
XX      09-SEP-1998; 98US-00149988.
XX      06-MAR-2000; 2000US-00519223.
XX      (GENY ) GENETICS INST INC.
XX      Jones S, Tang J;
XX      PI
XX      WPI: 2002-739923/80.
XX      N-PSDB; ABV73007.
XX      Novel composition comprising purified mammalian calcium independent
XX      phospholipase enzyme, useful for the screening of inhibitors of
XX      phospholipase activity, is active in the absence of calcium.
XX      Example 4; Page 10-12; 41pp; English.
XX      The invention relates to a purified mammalian calcium independent
XX      cytosolic phospholipase A2/B (cPLA2/B) enzyme. The cPLA2/B enzyme is
XX      characterized by activity in the absence of calcium and has a molecular
XX      weight of 86 kD on SDS-PAGE. A composition (I) comprising a purified
XX      calcium independent phospholipase enzyme is useful for identifying an
XX      inhibitor of phospholipase activity which involves combining (I),
XX      phospholipid and candidate inhibitor compound, and observing whether the

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CC      enzyme cleaves the phospholipid and releases fatty acid from it. A
CC      pharmaceutical composition (PC) comprising a therapeutically effective
CC      amount of the inhibitor is useful for reducing inflammation and for
CC      treating inflammatory conditions including rheumatoid arthritis,
CC      psoriasis, asthma, inflammatory bowel disease and other diseases mediated
CC      by increased levels of prostaglandins, leukotriene or platelet activating
CC      factor. A composition comprising an antibody which binds to (I) is useful
CC      as research and diagnostic tool, and is also useful in the study of
CC      phospholipase A2 activity and inflammatory conditions. The present
CC      sequence represents a cPLA2/B enzyme (clone 9)
XX      Sequence 752 AA:
SQ      Query Match      88.1%; Score 1837; DB 5; Length 752;
        Best Local Similarity 87.3%; Pred. No. 16-191;
        Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;
Qy      1 MOPFGRVLTNTSEGVNTNLFENPPRYKEVAVADYTTSSDRVAREEQGLIFONTPTMDCVLV 60
Db      1 MOPFGRVLTNTLSSVNTNLFENPPRYKEISVADYTSHERVAREEQGLIFONASNRPTDCILV 60
Qy      61 SPKPHSGFRLFQLESEADALVNFQSSQLPPFYESSVQVLAHEVLAQHLSDLIRHPSM 120
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Qy      121 SYAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
Db      121 TVTHLAVALGIRECFHSHRIISCANSTENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
Qy      181 VTDYKGETVFAHYAVQGDNSQVQLLGRNAVAGLQVNNQGLTPHLACQLGKQEMVRVLL 240
Db      181 VTDNKGETAFAHYAVQGDNSQVQLLGRNAVAGLQVNNQGLTPHLACQLGKQEMVRVLL 240
Qy      241 LCNARCNMGPGVPIHSAAMKPSQKCAEMIISMDSQHSKDPRYGASPLHMAKKAEMA 300
Db      241 LCNARCNMGPGVPIHSAAMKPSQKCAEMIISMDSQHSKDPRYGASPLHMAKKAEMA 300
Qy      301 RMLLRKGCNVNSTSSAGNTALHVGVRNRFDCAVILTLTGANADARGEHNTPLHLAMSK 360
Db      301 RMLLRKGCNVNSTSSAGNTALHVGVRNRFDCAVILTLTGANADARGEHNTPLHLAMSK 360
Qy      361 DNVEMIKALIVFGAEVDTPNDFGETPTPLASKI 393
Db      361 DNVEMIKALIVFGAEVDTPNDFGETPTPLASKI 393

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Search completed: December 15, 2004, 13:08:03
 Job time : 82.7757 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 15, 2004, 13:01:00 ; Search time 20.0874 Seconds
(Without alignments)
1300.780 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084
Sequence: 1 MOPFGLVNTFSGVTNLFSN.....EVDTPNDFGTPLASKIG 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapect 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/aa/5A_COMB.pep:*
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5: /cgn2_6/prodata/1/aa/5A_COMB.pep:*
6: /cgn2_6/prodata/1/aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------|
| 1 | 2084 | 100.0 | 394 | 2 | US-08-555-568B-17 |
| 2 | 2084 | 100.0 | 394 | 3 | US-09-519-223-17 |
| 3 | 2084 | 100.0 | 394 | 4 | US-09-927-180-17 |
| 4 | 2084 | 100.0 | 687 | 2 | US-08-555-568B-21 |
| 5 | 2084 | 100.0 | 687 | 3 | US-09-519-223-21 |
| 6 | 2084 | 100.0 | 687 | 4 | US-09-927-180-21 |
| 7 | 2084 | 100.0 | 688 | 2 | US-08-555-568B-23 |
| 8 | 2084 | 100.0 | 688 | 3 | US-09-519-223-23 |
| 9 | 2084 | 100.0 | 688 | 4 | US-09-927-180-23 |
| 10 | 1837 | 88.1 | 752 | 1 | US-08-281-193-2 |
| 11 | 1837 | 88.1 | 752 | 1 | US-08-422-106-2 |
| 12 | 1837 | 88.1 | 752 | 2 | US-08-735-716-2 |
| 13 | 1837 | 88.1 | 752 | 2 | US-08-555-568B-2 |
| 14 | 1837 | 88.1 | 752 | 3 | US-09-519-223-2 |
| 15 | 1837 | 88.1 | 752 | 3 | US-09-927-180-2 |
| 16 | 1837 | 88.1 | 752 | 5 | PCT-US95-08069-2 |
| 17 | 494.5 | 17.3 | 896 | 4 | US-09-270-767-46130 |
| 18 | 359.5 | 12.7 | 545 | 4 | US-09-270-767-61684 |
| 19 | 338 | 16.2 | 843 | 2 | US-09-172-977-3 |
| 20 | 338 | 16.2 | 843 | 4 | US-09-404-108-3 |
| 21 | 332 | 15.9 | 1839 | 2 | US-09-172-977-4 |
| 22 | 332 | 15.9 | 1839 | 4 | US-09-404-108-4 |
| 23 | 332 | 15.9 | 1839 | 4 | US-09-538-092-1246 |
| 24 | 305.5 | 14.7 | 1745 | 2 | US-09-031-485-33 |
| 25 | 305.5 | 14.7 | 1745 | 2 | US-08-847-429A-33 |
| 26 | 305.5 | 14.7 | 1745 | 3 | US-09-065-474-33 |
| 27 | 305.5 | 14.7 | 1745 | 3 | US-09-557-034-33 |

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|----|-------|------|------|---|--------------------|-------------------|
| 28 | 301 | 14.4 | 786 | 4 | US-09-509-802-2 | Sequence 2, App1 |
| 29 | 301 | 14.4 | 787 | 4 | US-09-188-930-334 | Sequence 334, App |
| 30 | 301 | 14.4 | 787 | 4 | US-09-312-283C-334 | Sequence 334, App |
| 31 | 296 | 14.2 | 1088 | 3 | US-09-082-059-2 | Sequence 2, App1 |
| 32 | 282.5 | 13.6 | 303 | 2 | US-09-031-485-23 | Sequence 23, App1 |
| 33 | 282.5 | 13.6 | 303 | 2 | US-08-847-429A-23 | Sequence 23, App1 |
| 34 | 282.5 | 13.6 | 303 | 3 | US-09-065-474-23 | Sequence 23, App1 |
| 35 | 282.5 | 13.6 | 303 | 3 | US-09-557-034-23 | Sequence 23, App1 |
| 36 | 281.5 | 13.5 | 784 | 4 | US-09-781-882-2 | Sequence 2, App1 |
| 37 | 272 | 13.1 | 994 | 4 | US-10-164-595-38 | Sequence 38, App1 |
| 38 | 271 | 13.0 | 352 | 3 | US-09-065-474-139 | Sequence 139, App |
| 39 | 271 | 13.0 | 352 | 3 | US-09-557-034-139 | Sequence 139, App |
| 40 | 270.5 | 13.0 | 302 | 2 | US-09-031-485-38 | Sequence 38, App1 |
| 41 | 270.5 | 13.0 | 302 | 2 | US-08-847-429A-38 | Sequence 38, App1 |
| 42 | 270.5 | 13.0 | 302 | 3 | US-09-065-474-38 | Sequence 38, App1 |
| 43 | 270.5 | 13.0 | 302 | 3 | US-09-557-034-38 | Sequence 38, App1 |
| 44 | 253.5 | 12.2 | 1619 | 4 | US-09-392-812A-4 | Sequence 4, App1 |
| 45 | 252.5 | 12.1 | 348 | 2 | US-09-031-485-28 | Sequence 28, App1 |

ALIGNMENTS

RESULT 1
US-08-555-568B-17
Sequence 17, Application US/08555568B
Patent No. 597854
GENERAL INFORMATION:
APPLICANT: Jones, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.,
STREET: 87 Cambridgepark Drive
City: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 496-5851
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-555-568B-17
Query Match 100.0%; Score 2084; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 4,4e-223; Indels 0; Gaps 0;
Matches 394; Conservative 0; Mismatches 0;

QY 1 MOPFGLVNTFSGVTNLFSNPPRVKVAADYSSDRVBEGLIFONTPTNPTMCVY 60
DB 1 MOPFGLVNTFSGVTNLFSNPPRVKVAADYSSDRVBEGLIFONTPTNPTMCVY 60
QY 61 NPNSGSGRLPQLEADALVNFHOYSQSLPFYSSPQVLTTEVLOHLTDIRNHPN 120
DB 61 NPNSGSGRLPQLEADALVNFHOYSQSLPFYSSPQVLTTEVLOHLTDIRNHPN 120

QY 121 SVANLAVELGIRCEPHHSRIISCANCAENEBEGCTPLHLACRKGDELIVELVOYCHTOMD 180
DB 121 SVANLAVELGIRCEPHHSRIISCANCAENEBEGCTPLHLACRKGDELIVELVOYCHTOMD 180
QY 181 VTDYKGETVPHYAVQGDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVPHYAVQGDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNINGPNQYPIHSAMKFSQKGCAMETISMDSSQHSKDPKRYGASPLHWAKAEMA 300
DB 241 LCNARCNINGPNQYPIHSAMKFSQKGCAMETISMDSSQHSKDPKRYGASPLHWAKAEMA 300
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DB 301 RMLKRGCVNSTSSAGNTALHGVWRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNEMIKALIVGAEVDTPNDFGETPTFLASKIG 394
DB 361 DNEMIKALIVGAEVDTPNDFGETPTFLASKIG 394

RESULT 2

US-09-519-223-17
; Sequence 17, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (PPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-519-223-17

Query Match 100.0%; Score 2084; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 4.4e-223;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSQVTLFNSNPRFKEVAVADYTSRVRBEGQLIFONTPNRTMPCVLY 60
DB 1 MOFGRLVNTFSQVTLFNSNPRFKEVAVADYTSRVRBEGQLIFONTPNRTMPCVLY 60
QY 61 NPNSSQGRFLFQLEADALVNFHOYSQQLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120

DB 61 NPNSSQGRFLFQLEADALVNFHOYSQQLPFYESSPOVLHTEVLQHLTDLIRNHPSW 120
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DB 181 VTDYKGETVPHYAVQGDNSQVLLQGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
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DB 241 LCNARCNINGPNQYPIHSAMKFSQKGCAMETISMDSSQHSKDPKRYGASPLHWAKAEMA 300
QY 301 RMLKRGCVNSTSSAGNTALHGVWRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
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DB 361 DNEMIKALIVGAEVDTPNDFGETPTFLASKIG 394

RESULT 3

US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (PPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
; US-09-927-180-17

Query Match 100.0%; Score 2084; DB 4; Length 394;
Best Local Similarity 100.0%; Pred. No. 4.4e-223;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSQVTLFNSNPRFKEVAVADYTSRVRBEGQLIFONTPNRTMPCVLY 60

Db 1 MGFGLVNTFSGVTNLFSNPFRVKEVAVADYTSRDRVREBGLILFQNTPNRTMDCVLV 60
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 Db 61 NPNRSGGRLFLQLELEADALVNFHOYSQQLPFYESSPOVLATEYLQHLTDLIRNHPM 120
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 Db 121 SVAHLAVELGIRECFHSHRIISCANCAENEBECTPLHLACRKGDEILVELVOYCHTQMD 180
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 Db 361 DNVEMIKALIVFGAEVDTNPDPGETPTFLASKIG 394

RESULT 4

US-08-555-568B-21
 ; Sequence 21, Application US/08555568B
 ; Patent No. 5976854
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 687 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-555-568B-21

Query Match 100.0%; Score 2084; DB 2; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1,1e-222;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGFGLVNTFSGVTNLFSNPFRVKEVAVADYTSRDRVREBGLILFQNTPNRTMDCVLV 60
 Db 1 MGFGLVNTFSGVTNLFSNPFRVKEVAVADYTSRDRVREBGLILFQNTPNRTMDCVLV 60

QY 61 NPNRSGGRLFLQLELEADALVNFHOYSQQLPFYESSPOVLATEYLQHLTDLIRNHPM 120
 Db 61 NPNRSGGRLFLQLELEADALVNFHOYSQQLPFYESSPOVLATEYLQHLTDLIRNHPM 120
 QY 121 SVAHLAVELGIRECFHSHRIISCANCAENEBECTPLHLACRKGDEILVELVOYCHTQMD 180
 Db 121 SVAHLAVELGIRECFHSHRIISCANCAENEBECTPLHLACRKGDEILVELVOYCHTQMD 180
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 Db 181 VTDYKGETVFFHYAVOGDNSQVLLQGRNAVAGLNQVNNQGLTPHLACQLGKQEWVRVLL 240
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 Db 241 LCNARCNIMGPNPGYPIHSAKMFQKCAEMITSMDSQHSKDPYRGASPLHMAKNAEVA 300
 QY 301 RMLLRKGCNVNSTSSAGNTALHGVNRNRPDCAIYLTHGANADARGHGNTPLHLAMSK 360
 Db 301 RMLLRKGCNVNSTSSAGNTALHGVNRNRPDCAIYLTHGANADARGHGNTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDTNPDPGETPTFLASKIG 394
 Db 361 DNVEMIKALIVFGAEVDTNPDPGETPTFLASKIG 394

RESULT 5

US-09-519-223-21
 ; Sequence 21, Application US/09519223
 ; Patent No. 6274140
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/519,223
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 687 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-519-223-21

Query Match 100.0%; Score 2084; DB 3; Length 687;
 Best Local Similarity 100.0%; Pred. No. 1,1e-222;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGFGLVNTFSGVTNLFSNPFRVKEVAVADYTSRDRVREBGLILFQNTPNRTMDCVLV 60
 Db 1 MGFGLVNTFSGVTNLFSNPFRVKEVAVADYTSRDRVREBGLILFQNTPNRTMDCVLV 60

Db 1 MOFGRLVNTFSGVTNLFNSNPFVKYAVADYSSDRVREBQILFQNTPNRTWDCVLV 60
Qy 61 NPNRSQGFRLFOLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLTDLIRNHPW 120
Db 61 NPNRSQGFRLFOLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLTDLIRNHPW 120
Qy 121 SVAHAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
Db 121 SVAHAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
Qy 181 VTDYKGETVHYAVQGNQSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVHYAVQGNQSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
Qy 241 LCNARCINMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHMAKNAEMA 300
Db 241 LCNARCINMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHMAKNAEMA 300
Qy 301 RMLLRKGCNVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCNVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Qy 361 DNVEMIKALIVFGAEVDTPNDFGPTFLASKIG 394
Db 361 DNVEMIKALIVFGAEVDTPNDFGPTFLASKIG 394

RESULT 6
US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. 6645736

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 687 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Query Match 100.0%; Score 2084; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MOFGRLVNTFSGVTNLFNSNPFVKYAVADYSSDRVREBQILFQNTPNRTWDCVLV 60
Db 1 MOFGRLVNTFSGVTNLFNSNPFVKYAVADYSSDRVREBQILFQNTPNRTWDCVLV 60
Qy 61 NPNRSQGFRLFOLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLTDLIRNHPW 120
Db 61 NPNRSQGFRLFOLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLTDLIRNHPW 120
Qy 121 SVAHAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
Db 121 SVAHAVEIGIRECFHHSRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHTOMD 180
Qy 181 VTDYKGETVHYAVQGNQSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVHYAVQGNQSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
Qy 241 LCNARCINMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHMAKNAEMA 300
Db 241 LCNARCINMGPNQYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHMAKNAEMA 300
Qy 301 RMLLRKGCNVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLRKGCNVNSTSSAGNTALHVGWNRFPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Qy 361 DNVEMIKALIVFGAEVDTPNDFGPTFLASKIG 394
Db 361 DNVEMIKALIVFGAEVDTPNDFGPTFLASKIG 394

RESULT 7
US-08-555-568B-23
; Sequence 23, Application US/08555568B
; Patent No. 5976854

GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/555,568B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 688 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 100.0%; Score 2084; DB 2; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFGRLVNTFSGVNTLFSNPPRVKAVAVADYTSDDRVREBQQLILFONTPNRMDCVLV 60
DB 1 MOFGRLVNTFSGVNTLFSNPPRVKAVAVADYTSDDRVREBQQLILFONTPNRMDCVLV 60
QY 61 NPNRSOSGRLPOLLEADALVNFHOYSQQLPFYESSQVLTTEVLQHLTDLIRNHPM 120
DB 61 NPNRSOSGRLPOLLEADALVNFHOYSQQLPFYESSQVLTTEVLQHLTDLIRNHPM 120
QY 121 SVAHLAVEIGIRECFHSHRIISCANCAENEBECPPLHLACRKGDEILVELVOYCHTQMD 180
DB 121 SVAHLAVEIGIRECFHSHRIISCANCAENEBECPPLHLACRKGDEILVELVOYCHTQMD 180
QY 181 VTDYGEVTFHYAVOGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
DB 181 VTDYGEVTFHYAVOGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQHSKDPYRGASPLHMAKNAEMA 300
DB 241 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQHSKDPYRGASPLHMAKNAEMA 300
QY 301 RMLLRGCVNSTSSAGNTALHVGVRNRFDCALVLLTGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCVNSTSSAGNTALHVGVRNRFDCALVLLTGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVGAEDVTPNDPFGETPTFLASKIG 394
DB 361 DNVEMIKALIVGAEDVTPNDPFGETPTFLASKIG 394

RESULT 8

US-09-519-223-23
Sequence 23, Application US/09519223
Patent No. 6274140

GENERAL INFORMATION:
APPLICANT: Jones, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/519,223
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-519-223-23

Query Match 100.0%; Score 2084; DB 3; Length 688;

Best Local Similarity 100.0%; Pred. No. 1,1e-222;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MOFGRLVNTFSGVNTLFSNPPRVKAVAVADYTSDDRVREBQQLILFONTPNRMDCVLV 60
DB 1 MOFGRLVNTFSGVNTLFSNPPRVKAVAVADYTSDDRVREBQQLILFONTPNRMDCVLV 60
QY 61 NPNRSOSGRLPOLLEADALVNFHOYSQQLPFYESSQVLTTEVLQHLTDLIRNHPM 120
DB 61 NPNRSOSGRLPOLLEADALVNFHOYSQQLPFYESSQVLTTEVLQHLTDLIRNHPM 120
QY 121 SVAHLAVEIGIRECFHSHRIISCANCAENEBECPPLHLACRKGDEILVELVOYCHTQMD 180
DB 121 SVAHLAVEIGIRECFHSHRIISCANCAENEBECPPLHLACRKGDEILVELVOYCHTQMD 180
QY 181 VTDYGEVTFHYAVOGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
DB 181 VTDYGEVTFHYAVOGDNSQVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQHSKDPYRGASPLHMAKNAEMA 300
DB 241 LCNARCNIMGPGYPIHSAMKFSQKCAEMIISMDSQHSKDPYRGASPLHMAKNAEMA 300
QY 301 RMLLRGCVNSTSSAGNTALHVGVRNRFDCALVLLTGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRGCVNSTSSAGNTALHVGVRNRFDCALVLLTGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVGAEDVTPNDPFGETPTFLASKIG 394
DB 361 DNVEMIKALIVGAEDVTPNDPFGETPTFLASKIG 394

RESULT 9

US-09-927-180-23
Sequence 23, Application US/09927180
Patent No. 6645736

GENERAL INFORMATION:
APPLICANT: Jones, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23;

US-09-927-180-23

Query Match 100.0%; Score 2084; DB 4; Length 688;
 Best Local Similarity 100.0%; Pred. No. 1,1e-222;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGLVNTFSGVTNLFSPNFRVKEVAVADYSSDRVREEGQLIFQNTPNRTWCVLV 60
 DB 1 MOFFGLVNTFSGVTNLFSPNFRVKEVAVADYSSDRVREEGQLIFQNTPNRTWCVLV 60
 QY 61 NPNNSGGRFLFQLEADALVNFHOYSSQLPFYESSPOVLHTEVLOHLDLIRNHP 120
 DB 61 NPNNSGGRFLFQLEADALVNFHOYSSQLPFYESSPOVLHTEVLOHLDLIRNHP 120
 QY 121 SVNHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELVELVQYCHTQMD 180
 DB 121 SVNHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELVELVQYCHTQMD 180
 QY 121 VTDYKGETVFHYAVQDNGSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 DB 121 VTDYKGETVFHYAVQDNGSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 QY 181 VTDYKGETVFHYAVQDNGSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 DB 181 VTDYKGETVFHYAVQDNGSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 QY 241 LCNARCNINGPNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCNINGPNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 QY 301 RMLKRGCVNNTSSAGNTALHYGVNRNRPDCALVLLTGANADARGENGTPLHLAMSK 360
 DB 301 RMLKRGCVNNTSSAGNTALHYGVNRNRPDCALVLLTGANADARGENGTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDTNPDPFGETPTFLASKIG 394
 DB 361 DNVEMIKALIVFGAEVDTNPDPFGETPTFLASKIG 394

RESULT 10
 US-08-281-193-2
 ; Sequence 2, Application US/08281193
 ; Patent No. 5466595
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 15
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/281,193
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-281-193-2

Query Match 88.1%; Score 1837; DB 1; Length 752;
 Best Local Similarity 87.3%; Pred. No. 3.9e-195;
 Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGLVNTFSGVTNLFSPNFRVKEVAVADYSSDRVREEGQLIFQNTPNRTWCVLV 60
 DB 1 MOFFGLVNTFSGVTNLFSPNFRVKEVAVADYSSDRVREEGQLIFQNTPNRTWCVLV 60
 QY 61 NPNNSGGRFLFQLEADALVNFHOYSSQLPFYESSPOVLHTEVLOHLDLIRNHP 120
 DB 61 NPNNSGGRFLFQLEADALVNFHOYSSQLPFYESSPOVLHTEVLOHLDLIRNHP 120

QY 121 SVNHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELVELVQYCHTQMD 180
 DB 121 TVTHLAVELGIRCFHHSRIISCANSTENEGCTPLHLACRKDGSELVELVQYCHTQMD 180
 QY 181 VTDYKGETVFHYAVQDNGSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 DB 181 VTDYKGETVFHYAVQDNGSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 QY 241 LCNARCNINGPNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCNINGPNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 QY 301 RMLKRGCVNNTSSAGNTALHYGVNRNRPDCALVLLTGANADARGENGTPLHLAMSK 360
 DB 301 RMLKRGCVNNTSSAGNTALHYGVNRNRPDCALVLLTGANADARGENGTPLHLAMSK 360
 QY 361 DNVEMIKALIVFGAEVDTNPDPFGETPTFLASKI 393
 DB 361 DNVEMIKALIVFGAEVDTNPDPFGETPTFLASKI 393

RESULT 11
 US-08-422-106-2
 ; Sequence 2, Application US/08422106
 ; Patent No. 5589170
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 15
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/422,106
 ; FILING DATE: 14-APR-1995
 ; CLASSIFICATION: 435
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-422-106-2

Query Match 88.1%; Score 1837; DB 1; Length 752;
 Best Local Similarity 87.3%; Pred. No. 3.9e-195;
 Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOFFGLVNTFSGVTNLFSPNFRVKEVAVADYSSDRVREEGQLIFQNTPNRTWCVLV 60
 DB 1 MOFFGLVNTFSGVTNLFSPNFRVKEVAVADYSSDRVREEGQLIFQNTPNRTWCVLV 60
 QY 61 NPNNSGGRFLFQLEADALVNFHOYSSQLPFYESSPOVLHTEVLOHLDLIRNHP 120
 DB 61 NPNNSGGRFLFQLEADALVNFHOYSSQLPFYESSPOVLHTEVLOHLDLIRNHP 120
 QY 121 SVNHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELVELVQYCHTQMD 180
 DB 121 TVTHLAVELGIRCFHHSRIISCANSTENEGCTPLHLACRKDGSELVELVQYCHTQMD 180
 QY 181 VTDYKGETVFHYAVQDNGSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 DB 181 VTDYKGETVFHYAVQDNGSVQLLGRNAVAGLNQVNNQGLTPHLACQLGKQEMRVLL 240
 QY 241 LCNARCNINGPNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
 DB 241 LCNARCNINGPNGYPPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300

QY 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRPDCAIYLTHGANADARGEHTPLHAKM 360
 DB 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRPDCAIYLTHGANADARGEHTPLHAKM 360
 QY 361 DNEMIKALIVFGAEVDTPNDFGETPFAASKI 393
 DB 361 DNEMIKALIVFGAEVDTPNDFGETPFAASKI 393

RESULT 12

US-08-735-716-2
 ; Sequence 2, Application US/08735716
 ; Patent No. 5840511
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 15
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/735,716
 ; FILING DATE: 23-OCT-1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/261,193
 ; FILING DATE: 27-JUL-1994
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-735-716-2

Query Match 88.1%; Score 1837; DB 2; Length 752;
 Best Local Similarity 87.3%; Pred. No. 3.9e-195;
 Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOPFGRLVNTFSGVNTLFSNPRKVEAVADYTSRDRVEEGQLIFONTPRRTMDCVLY 60
 DB 1 MOPFGRLVNTLSSVNTLFSNPRKVEAVADYTSRDRVEEGQLIFONTPRRTMDCVLY 60
 QY 61 NPNRSQSGRFLQLELEADALVNFHQSOLLPFYESSPOVLATTEVLOHLDLIRNHP 120
 DB 61 NPNRSQSGRFLQLELEADALVNFHQSOLLPFYESSPOVLATTEVLOHLDLIRNHP 120
 QY 121 SVAAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHT 180
 DB 121 SVAAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHT 180
 QY 121 TVTHLAVELGIRECFHSHRIISCANSTENEBEGCTPLHLACRKGDEILVELVOYCHT 180
 DB 121 TVTHLAVELGIRECFHSHRIISCANSTENEBEGCTPLHLACRKGDEILVELVOYCHT 180
 QY 181 VTDYKGETVFNHVAVOGDSNQVLOLGRNAVAGLNQVNNQGLTPHLACOLGKGRMVRVLL 240
 DB 181 VTDYKGETVFNHVAVOGDSNQVLOLGRNAVAGLNQVNNQGLTPHLACOLGKGRMVRVLL 240
 QY 181 VTDYKGETVFNHVAVOGDSNQVLOLGRNAVAGLNQVNNQGLTPHLACOLGKGRMVRVLL 240
 DB 181 VTDYKGETVFNHVAVOGDSNQVLOLGRNAVAGLNQVNNQGLTPHLACOLGKGRMVRVLL 240
 QY 241 LCNARCNINPNNGYPPIHSMKFSQKCAEMIISMDSQHSKDPKRYGASPLHAKNAEMA 300
 DB 241 LCNARCNINPNNGYPPIHSMKFSQKCAEMIISMDSQHSKDPKRYGASPLHAKNAEMA 300
 QY 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRPDCAIYLTHGANADARGEHTPLHAKM 360
 DB 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRPDCAIYLTHGANADARGEHTPLHAKM 360
 QY 361 DNEMIKALIVFGAEVDTPNDFGETPFAASKI 393
 DB 361 DNEMIKALIVFGAEVDTPNDFGETPFAASKI 393

RESULT 13

US-08-555-568B-2
 ; Sequence 2, Application US/08555568B
 ; Patent No. 5976854
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; APPLICANT: Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568B
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A. 32,724
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-555-568B-2

Query Match 88.1%; Score 1837; DB 2; Length 752;
 Best Local Similarity 87.3%; Pred. No. 3.9e-195;
 Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 1 MOPFGRLVNTFSGVNTLFSNPRKVEAVADYTSRDRVEEGQLIFONTPRRTMDCVLY 60
 DB 1 MOPFGRLVNTLSSVNTLFSNPRKVEAVADYTSRDRVEEGQLIFONTPRRTMDCVLY 60
 QY 61 NPNRSQSGRFLQLELEADALVNFHQSOLLPFYESSPOVLATTEVLOHLDLIRNHP 120
 DB 61 NPNRSQSGRFLQLELEADALVNFHQSOLLPFYESSPOVLATTEVLOHLDLIRNHP 120
 QY 121 SVAAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHT 180
 DB 121 SVAAHLAVELGIRECFHSHRIISCANCAENEBEGCTPLHLACRKGDEILVELVOYCHT 180
 QY 121 TVTHLAVELGIRECFHSHRIISCANSTENEBEGCTPLHLACRKGDEILVELVOYCHT 180
 DB 121 TVTHLAVELGIRECFHSHRIISCANSTENEBEGCTPLHLACRKGDEILVELVOYCHT 180
 QY 181 VTDYKGETVFNHVAVOGDSNQVLOLGRNAVAGLNQVNNQGLTPHLACOLGKGRMVRVLL 240
 DB 181 VTDYKGETVFNHVAVOGDSNQVLOLGRNAVAGLNQVNNQGLTPHLACOLGKGRMVRVLL 240
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 QY 241 LCNARCNINPNNGYPPIHSMKFSQKCAEMIISMDSQHSKDPKRYGASPLHAKNAEMA 300
 DB 241 LCNARCNINPNNGYPPIHSMKFSQKCAEMIISMDSQHSKDPKRYGASPLHAKNAEMA 300
 QY 301 RMLLRKGCNVNSTSSAGNTALHVGVRNRPDCAIYLTHGANADARGEHTPLHAKM 360
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 QY 361 DNEMIKALIVFGAEVDTPNDFGETPFAASKI 393
 DB 361 DNEMIKALIVFGAEVDTPNDFGETPFAASKI 393

RESULT 14

US-09-519-223-2

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; Sequence 2, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-519-223-2

Query Match      88.1%; Score 1837; DB 3; Length 752;
Best Local Similarity 87.3%; Pred. No. 3.9e-195;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

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RESULT 15
US-09-927-180-2
; Sequence 2, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2

Query Match      88.1%; Score 1837; DB 4; Length 752;
Best Local Similarity 87.3%; Pred. No. 3.9e-195;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

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' Thu Dec 16 19:13:23 2004

us-10-612-668-17.ra1

Page 9

Db 361 DNMEMIKALIVFGAEVDTPNDFGSTPPAFMASKI 393

Search completed: December 15, 2004, 13:15:31
Job time : 21.0874 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: December 15, 2004, 13:13:21 ; Search time 69.158 Seconds
(without alignments)
2034.879 Million cell updates/sec

Title: US-10-612-668-17

Perfect score: 2084
Sequence: 1 MGFPRGLVNTFGSVTLFNSN.....EVDTPNDPGETPPLSKITG 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Listing first 45 summaries

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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 2084 | 100.0 | 394 | 9 US-09-927-180-17 | Sequence 17, Appl |
| 2 | 2084 | 100.0 | 687 | 9 US-09-927-180-21 | Sequence 21, Appl |
| 3 | 2084 | 100.0 | 688 | 9 US-09-927-180-23 | Sequence 23, Appl |
| 4 | 1837 | 88.1 | 752 | 9 US-09-927-180-2 | Sequence 2, Appl |
| 5 | 1234.5 | 59.2 | 667 | 15 US-10-108-260A-3778 | Sequence 3237, Ap |
| 6 | 324 | 15.5 | 1330 | 15 US-10-108-260A-3237 | Sequence 3237, Ap |
| 7 | 301 | 14.4 | 786 | 14 US-10-164-080-2 | Sequence 2, Appl |
| 8 | 301 | 14.4 | 786 | 14 US-10-299-327-2 | Sequence 2, Appl |
| 9 | 301 | 14.4 | 786 | 14 US-10-128-174-13 | Sequence 13, Appl |
| 10 | 301 | 14.4 | 786 | 14 US-10-128-174-31 | Sequence 31, Appl |
| 11 | 301 | 14.4 | 786 | 14 US-10-128-174-32 | Sequence 32, Appl |
| 12 | 301 | 14.4 | 786 | 14 US-10-128-174-33 | Sequence 33, Appl |
| 13 | 301 | 14.4 | 787 | 10 US-09-866-050A-334 | Sequence 334, Appl |

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| 14 | 300.5 | 14.4 | 347 | 14 US-10-128-174-30 | Sequence 30, Appl |
| 15 | 300.5 | 14.4 | 1724 | 9 US-09-964-899-43 | Sequence 43, Appl |
| 16 | 286 | 14.2 | 3913 | 15 US-10-334-143-45 | Sequence 45, Appl |
| 17 | 288 | 13.8 | 1762 | 14 US-10-205-194-117 | Sequence 117, Appl |
| 18 | 283.5 | 13.6 | 784 | 14 US-10-164-080-7 | Sequence 7, Appl |
| 19 | 283.5 | 13.6 | 784 | 14 US-10-256-951-70 | Sequence 70, Appl |
| 20 | 281.5 | 13.5 | 784 | 14 US-10-354-358-38 | Sequence 38, Appl |
| 21 | 281.5 | 13.5 | 784 | 14 US-10-128-174-12 | Sequence 12, Appl |
| 22 | 281.5 | 13.5 | 784 | 15 US-10-658-904-2 | Sequence 2, Appl |
| 23 | 280.5 | 13.5 | 720 | 15 US-10-433-794-20 | Sequence 20, Appl |
| 24 | 280.5 | 13.5 | 765 | 14 US-10-128-174-3 | Sequence 3, Appl |
| 25 | 280.5 | 13.5 | 765 | 14 US-10-128-174-34 | Sequence 34, Appl |
| 26 | 280.5 | 13.5 | 765 | 14 US-10-128-174-35 | Sequence 35, Appl |
| 27 | 280.5 | 13.5 | 765 | 14 US-10-128-174-36 | Sequence 36, Appl |
| 28 | 280.5 | 13.5 | 765 | 14 US-10-128-174-37 | Sequence 37, Appl |
| 29 | 280.5 | 13.5 | 765 | 14 US-10-128-174-38 | Sequence 38, Appl |
| 30 | 280.5 | 13.5 | 765 | 14 US-10-128-174-39 | Sequence 39, Appl |
| 31 | 280.5 | 13.5 | 765 | 14 US-10-128-174-40 | Sequence 40, Appl |
| 32 | 280.5 | 13.5 | 765 | 14 US-10-128-174-41 | Sequence 41, Appl |
| 33 | 280.5 | 13.5 | 765 | 14 US-10-128-174-42 | Sequence 42, Appl |
| 34 | 280.5 | 13.5 | 765 | 14 US-10-128-174-43 | Sequence 43, Appl |
| 35 | 280.5 | 13.5 | 765 | 14 US-10-128-174-44 | Sequence 44, Appl |
| 36 | 280.5 | 13.5 | 765 | 14 US-10-182-243-56 | Sequence 56, Appl |
| 37 | 278.5 | 13.4 | 784 | 16 US-10-648-593-153 | Sequence 153, Appl |
| 38 | 272 | 13.1 | 367 | 15 US-10-250-613-6 | Sequence 6, Appl |
| 39 | 271.5 | 13.0 | 1053 | 14 US-10-291-172-343 | Sequence 343, Appl |
| 40 | 271.5 | 13.0 | 1053 | 15 US-10-221-278-343 | Sequence 4122, Appl |
| 41 | 267.5 | 12.8 | 919 | 15 US-10-108-260A-4122 | Sequence 6689, Appl |
| 42 | 258 | 12.4 | 1023 | 14 US-10-369-493-6689 | Sequence 6690, Appl |
| 43 | 258 | 12.4 | 1023 | 14 US-10-369-493-6690 | Sequence 4, Appl |
| 44 | 253.5 | 12.2 | 1619 | 14 US-10-369-978-4 | Sequence 2, Appl |
| 45 | 253 | 12.0 | 1704 | 14 US-10-369-978-2 | |

ALIGNMENTS

RESULT 1
US-09-927-180-17
Sequence 17, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:

LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17

Query Match 100.0%; Score 2084; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.4e-190;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLDLIRNHPSM 120
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DB 121 SVAHLAVELGIRCEFHHSRIISCANCAENEGCTPLHLACRKGDELVELVOYCHTQMD 180
QY 181 VTDYKGETVFNHVAOQDNGSQLGLGRNAVAGLNQVNOGLTPHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFNHVAOQDNGSQLGLGRNAVAGLNQVNOGLTPHLACQLGKQEMVRVLL 240
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DB 241 LCNARCNINMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKAENA 300
QY 301 RMLKRGCVNVSSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNVSSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEMIKALIVFGAEVDTNPDPGERTPTFLASKIG 394
DB 361 DNVEMIKALIVFGAEVDTNPDPGERTPTFLASKIG 394

RESULT 2
US-09-927-180-21

Sequence 21, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02140

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 33,724

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 2084; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGFGLVNTFSGVTNLFSPNFRVKEVAADYTSDDRVREEGQLIFONTPNRTMDCVLY 60
QY 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLDLIRNHPSM 120
DB 61 NPNNSGGRFLFQLEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLDLIRNHPSM 120
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DB 121 SVAHLAVELGIRCEFHHSRIISCANCAENEGCTPLHLACRKGDELVELVOYCHTQMD 180
QY 181 VTDYKGETVFNHVAOQDNGSQLGLGRNAVAGLNQVNOGLTPHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFNHVAOQDNGSQLGLGRNAVAGLNQVNOGLTPHLACQLGKQEMVRVLL 240
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DB 241 LCNARCNINMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPRYGASPLHWAKAENA 300
QY 301 RMLKRGCVNVSSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLKRGCVNVSSTSSAGNTALHVGWNRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
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DB 361 DNVEMIKALIVFGAEVDTNPDPGERTPTFLASKIG 394

RESULT 3
US-09-927-180-23

Sequence 23, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/927,180

FILING DATE: 09-Aug-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 100.0%; Score 2084; DB 9; Length 688;
Best Local Similarity 100.0%; Pred. No. 1.2e-189;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-927-180-2
Sequence 2, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:
APPLICANT: Jones, Simon
Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION NUMBER: US/09/927,180
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-927-180-2

Query Match 88.1%; Score 1837; DB 9; Length 752;
Best Local Similarity 87.3%; Pred. No. 5e-166;
Matches 343; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

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61 NPNRNSGGRFLFQLELEADALVNFHOYSQQLPFYESSPOVLHTEVLOHLTDLIRNHP 120
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121 SVAHLAVELGIRECFHRSRIISCANCAENEBCGTPHLACRKDGELIVELVQYCHTQND 180
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361 DNEMIKALIVFGAEVDTPNDFGETPTFLASKIG 393

RESULT 5
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Sequence 3778, Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3778
LENGTH: 667
TYPE: PRT
ORGANISM: Homo sapiens
US-10-108-260A-3778

Query Match 59.2%; Score 1234.5; DB 15; Length 667;
Best Local Similarity 64.0%; Pred. No. 1.3e-108;
Matches 252; Conservative 1; Mismatches 2; Indels 139; Gaps 1;

1 MOFFGLVNTFGSVTLFSPNPRVKEVAADYSSDRVREBQQLIFONTPTNTWCILV 60
1 MOFFGLVNTFGSVTLFSPNPRVKEVAADYSSDRVREBQQLIFONTPTNTWCILV 60

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Db      1 MOFFGLVNTFSGVTNLFSPNPFVKEVAVADYTS SDRVREEGQLIFONTPNRTWDCVLV 60
Qy      61 NPNRSOSGRFLFQLEADALVNFHOYSQQLPFYESSQVLTHTVLTDLIRNHPWS 120
Db      61 YPNRSOSGRFLFQLEADALVNFHOYS----- 89
Qy      121 SVAHLAVELGIRBCFHHSRILISCANCAENEGCTPLHLACRKGDELVELVOYCHTQMD 180
Db      90 ----- 89
Qy      181 VNDYKGETVPHYAVQGDNSQVQLLGRNNAVAGLNQVNNQGLTPLHLACQKQEMRVLL 240
Db      90 ----- 101
Qy      241 LCNARCNINGPNGYPIHSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 300
Db      102 LCNARCNINGPNGYPIYSAMKFSQKCAEMIISMDSQIHSKDPYRGASPLHAKNAEMA 161
Qy      301 RMLLKGCNVNSTSSAGNTALHVGMRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db      162 RMLLKGCNVNSTSSAGNTALHVGMRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 221
Qy      361 DNVEMIKALIVGAEVDTPNDEGETPFLASKIG 394
Db      222 DNVEMIKALIVGAEVDTPNDEGETPFLASKIG 255

```

RESULT 6

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US-10-108-260A-3237
; Sequence 3237, Application US/10108260A
; Publication No. US2004005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US2004005560A1el full length cdna
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3237
; LENGTH: 1330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3237

```

```

Query Match      15.5%; Score 324; DB 15; Length 1330;
Best Local Similarity 27.0%; Pred. No. 2.8e-21;
Matches 99; Conservative 62; Mismatches 128; Indels 77; Gaps 9;

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Qy      103 HTEVLQHTD-----LIRNHPWSVAHLAVELGIRCEFH-----SRII 141
Db      290 HQGVVELLERGAPLARTKNGSLPLHMAQGDHVECVKLLQHKAPVDDVTLDYLTALH 349
Qy      142 SCANC-----AENEGCTPLHLACRKGDELVELVOY----- 174
Db      350 VAHCHGYRVTKLLDKRANPNARALNGFTPLHIACKKRIKYMELLVKKGASIOAITES 409
Qy      175 -----CH-----TQMDVTDYKGETVPHYAVQGDNSQVQLLGRNNAVAG 212
Db      410 GLTPPIVAAPMGHNLVLLQLNGASPDVTNIRGETPLHMAARAGOVVRCILRRNG-AL 468
Qy      213 LNVQVNNQGLTPLHLACQKQEMRVLLLCNARCNINGPNGY-PIHSAMKFSQKCAEMI 271
Db      469 VDBARABEQPHIASHRTKTEIVQLLQHMABDAAITRYPPLHISAEGVDVAVSL 528
Qy      272 ISMDSQIHSKDPYRGASPLHMAK--NAEMAMLLKGCNVNSTSSAGNTALHVGMRN 328
Db      529 --LEAANAASLTKKGTPLHVAKYGSLDVAKLLQRRAAADSAGKNGLTPHVAHYD 586
Qy      329 RPDCAIVLLTHGANADARGEHNTPLHLAMSNDNEMIKALIVGAEVDTPNDEGETPFL 368
Db      587 NQKVALLLEKGSAPHATKAGYTPPLHIAKKKQMOIASTLLNLYGAEITNIVTQGVTPHL 646

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Qy      389 LASKIG 394
Db      647 LASQEG 652

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RESULT 7

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US-10-164-080-2
; Sequence 2, Application US/10164080
; Publication No. US2003008741A1
; GENERAL INFORMATION:
; APPLICANT: BIRD, Timothy, A.
; APPLICANT: HOLLAND, Pamela, M.
; APPLICANT: PESCHON, Jacques, J.
; APPLICANT: VIRCA, George, D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS (DAKAR)
; FILE REFERENCE: 3280-B
; CURRENT APPLICATION NUMBER: US/10/164,080
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/295,959
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/334,362
; PRIOR FILING DATE: 2001-11-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 786
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-164-080-2

```

```

Query Match      14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 2.1e-19;
Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

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Qy      112 DLIRNHPWSVAHLAVELGIRCEFHHSRIISCANCAENEGCTPPLHLAC-RKDGSELIVE 170
Db      434 DLVLD--SSASLHLAAVEAQOECVKWLLNNANPNLTNRKSTPLHMAVERKRG--IYE 490
Qy      171 LVQCHTQMDVTDYKGETVPHYAVQ--GDNSQVQLLGRNNAVAGLNQVNNQGLTPLHLACQ 229
Db      491 LILAKRTSVNADDEDDQWTLHPAONGDEASTLLLEK--ASVNEVDEGRTPHVAQCQ 548
Qy      230 LQKQEMRVLLLCNARCNINGPNGY-PIHSAMKFSQKCAEMIISMDSQIHSKDPYRG 288
Db      549 HGGENIVRTLRGVDVGLQGDAMPLPHYAAWQGLPIVLLAKQPGVSVNAQ--TLDR 607
Qy      289 SPLHMAK--NAEMAMLLKGCNVNSTSSAGNTALHVGMRNRPDCAIVLLTHGANADA 345
Db      608 TPLHLAQRGHYRVARILIDLCSDVNICSLOQTPHVAEETGHTSTARLLHKGAKEA 667
Qy      346 RGEHNTPLHLAMSNDNEMIKALIVGAEVDTPNDEGETPFLASKIG 394
Db      668 LTSEGTALHLAONGHLATVKLLIEKADVWARGPLNGTALHLAARG 716

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RESULT 8

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US-10-299-327-2
; Sequence 2, Application US/10299327
; Publication No. US20030104482A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corp.
; APPLICANT: BIRD, Timothy
; APPLICANT: VIRCA, G.D.
; TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS
; FILE REFERENCE: 2889-US
; CURRENT APPLICATION NUMBER: US/10/299,327
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US/09/509,802
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0

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Qy      112 DLIRNHPWSVAHLAVELGIRCEFHHSRIISCANCAENEGCTPPLHLAC-RKDGSELIVE 170
Db      434 DLVLD--SSASLHLAAVEAQOECVKWLLNNANPNLTNRKSTPLHMAVERKRG--IYE 490
Qy      171 LVQCHTQMDVTDYKGETVPHYAVQ--GDNSQVQLLGRNNAVAGLNQVNNQGLTPLHLACQ 229
Db      491 LILAKRTSVNADDEDDQWTLHPAONGDEASTLLLEK--ASVNEVDEGRTPHVAQCQ 548
Qy      230 LQKQEMRVLLLCNARCNINGPNGY-PIHSAMKFSQKCAEMIISMDSQIHSKDPYRG 288
Db      549 HGGENIVRTLRGVDVGLQGDAMPLPHYAAWQGLPIVLLAKQPGVSVNAQ--TLDR 607
Qy      289 SPLHMAK--NAEMAMLLKGCNVNSTSSAGNTALHVGMRNRPDCAIVLLTHGANADA 345
Db      608 TPLHLAQRGHYRVARILIDLCSDVNICSLOQTPHVAEETGHTSTARLLHKGAKEA 667
Qy      346 RGEHNTPLHLAMSNDNEMIKALIVGAEVDTPNDEGETPFLASKIG 394
Db      668 LTSEGTALHLAONGHLATVKLLIEKADVWARGPLNGTALHLAARG 716

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SEQ ID NO 2
LENGTH: 786
TYPE: PRT
ORGANISM: Mus sp.
US-10-299-327-2

Query Match 14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 2.1e-19;

Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

112 DLIRNPSVAVLAVALGIRECFHHSRIISCANCAENEGCTPLHLAC-RKGDGELIVE 170

434 DLVLD-SSASLHLAVALGAGEECVKWLLNNANPNLTNRKGSTPLHMAVERKRG--IVE 490

171 LVQYCHTQMDVTDYKGETVPHYAVQ-GDNSQVQLQLGRNAVAGLNQVNNQGLTPHLACQ 229

491 LLIAKRTSVNAKDEQWTALHFAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548

230 LKQKEMVRVLLCNARCNINMGNGY-PHSAKMFSGKCAEMTISMSQIHSKDPHYGA 288

549 HGOENIVRTLRRGVVGLQKDMPLHYAAMOGHLPYKLLAKOPGVSVNAQ-TLDGR 607

289 SPLHMAK--NAEMARMLKRGCVNSTSSAGNTALHVGWRRKFCATVLLTHGANADA 345

608 TPLHAAQRGHYRVARILIDLCSDVNICSLQAOPTPLHVAETGHTSTARLLHHRGAGKEA 667

346 RGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394

668 LTSEGYTALHAAQNGHLATVKKLIEBKADVMARGPLNQTALHLLAAARG 716

RESULT 9

US-10-128-174-13

Sequence 13; Application US/10128174

Publication No. US20030199462A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohito

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

FILE REFERENCE: UM-06967

CURRENT APPLICATION NUMBER: US/10/128,174

CURRENT FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 13

LENGTH: 786

TYPE: PRT

ORGANISM: Mus musculus

US-10-128-174-13

Query Match 14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 2.1e-19;

Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

112 DLIRNPSVAVLAVALGIRECFHHSRIISCANCAENEGCTPLHLAC-RKGDGELIVE 170

434 DLVLD-SSASLHLAVALGAGEECVKWLLNNANPNLTNRKGSTPLHMAVERKRG--IVE 490

171 LVQYCHTQMDVTDYKGETVPHYAVQ-GDNSQVQLQLGRNAVAGLNQVNNQGLTPHLACQ 229

491 LLIAKRTSVNAKDEQWTALHFAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548

230 LKQKEMVRVLLCNARCNINMGNGY-PHSAKMFSGKCAEMTISMSQIHSKDPHYGA 288

549 HGOENIVRTLRRGVVGLQKDMPLHYAAMOGHLPYKLLAKOPGVSVNAQ-TLDGR 607

289 SPLHMAK--NAEMARMLKRGCVNSTSSAGNTALHVGWRRKFCATVLLTHGANADA 345

608 TPLHAAQRGHYRVARILIDLCSDVNICSLQAOPTPLHVAETGHTSTARLLHHRGAGKEA 667

346 RGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394

668 LTSEGYTALHAAQNGHLATVKKLIEBKADVMARGPLNQTALHLLAAARG 716

RESULT 10

US-10-128-174-31

Sequence 31; Application US/10128174

Publication No. US20030199462A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohito

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

FILE REFERENCE: UM-06967

CURRENT APPLICATION NUMBER: US/10/128,174

CURRENT FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 31

LENGTH: 786

TYPE: PRT

ORGANISM: Mus musculus

US-10-128-174-31

Query Match 14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 2.1e-19;

Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

112 DLIRNPSVAVLAVALGIRECFHHSRIISCANCAENEGCTPLHLAC-RKGDGELIVE 170

434 DLVLD-SSASLHLAVALGAGEECVKWLLNNANPNLTNRKGSTPLHMAVERKRG--IVE 490

171 LVQYCHTQMDVTDYKGETVPHYAVQ-GDNSQVQLQLGRNAVAGLNQVNNQGLTPHLACQ 229

491 LLIAKRTSVNAKDEQWTALHFAQNGDEASTRLLEKN--ASVNEVDPEGRTPMHVACQ 548

230 LKQKEMVRVLLCNARCNINMGNGY-PHSAKMFSGKCAEMTISMSQIHSKDPHYGA 288

549 HGOENIVRTLRRGVVGLQKDMPLHYAAMOGHLPYKLLAKOPGVSVNAQ-TLDGR 607

289 SPLHMAK--MEMARMLKRGCVNSTSSAGNTALHVGWRRKFCATVLLTHGANADA 345

608 TPLHAAQRGHYRVARILIDLCSDVNICSLQAOPTPLHVAETGHTSTARLLHHRGAGKEA 667

346 RGEHNTPLHLAMSKDNVEMIKALIVFGAEVDTPNDFGETPTFLASKIG 394

668 LTSEGYTALHAAQNGHLATVKKLIEBKADVMARGPLNQTALHLLAAARG 716

RESULT 11

US-10-128-174-32

Sequence 32; Application US/10128174

Publication No. US20030199462A1

GENERAL INFORMATION:

APPLICANT: Nunez, Gabriel

APPLICANT: Inohara, Naohito

TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling

FILE REFERENCE: UM-06967

CURRENT APPLICATION NUMBER: US/10/128,174

CURRENT FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PatentIn version 3.1

SEQ ID NO 32

LENGTH: 786

TYPE: PRT

ORGANISM: Mus musculus

US-10-128-174-32

Query Match 14.4%; Score 301; DB 14; Length 786;
Best Local Similarity 31.8%; Pred. No. 2.1e-19;

Matches 92; Conservative 48; Mismatches 137; Indels 12; Gaps 8;

112 DLIRNPSVAVLAVALGIRECFHHSRIISCANCAENEGCTPLHLAC-RKGDGELIVE 170

434 DLVLD-SSASLHLAVALGAGEECVKWLLNNANPNLTNRKGSTPLHMAVERKRG--IVE 490

Db 176 QRGHYVAVARLILDLCSVDNLCISLAQOTPLHVAAEHTGHTSTARILLIRGAGKEALTSEGT 235
 QY 353 PHLIAMSNDVENIKALIVFGAEVDPNDGEPFLASKIG 394
 Db 236 ALHLAONGHLATVVKLLIEKADVMARGPLNQTAHLAAARG 277

RESULT 15

US-09-964-899-43
 ; Sequence 43, Application US/09964899
 ; Patent No. US2002017446A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Dalia et al.
 ; TITLE OF INVENTION: Identification of Genes Involved in
 ; FILE REFERENCE: 4-31612 A
 ; CURRENT APPLICATION NUMBER: US/09/964,899
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: 60/236,893
 ; PRIOR FILING DATE: 2000-09-29
 ; PRIOR APPLICATION NUMBER: 60/298,309
 ; NUMBER OF SEQ ID NOS: 53
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 43
 ; LENGTH: 1724
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-09-964-899-43

Query Match 14.4%; Score 300.5; DB 9; Length 1724;
 Best Local Similarity 28.4%; Pred. No. 7e-19;
 Matches 85; Conservative 71; Mismatches 120; Indels 23; Gaps 10;
 QY 106 VLOH--LTFDLINHPMSVAHLAVELGIRECFHH--SRIISCANCAENE--GCTPLH 157
 Db 315 LLOHNPVDDVTNDY--LTFALHVA--HCHYKVAKVLDDKANPNKALNGFTPLH 367
 QY 158 LACRKGDEILVELVOYCHTQMDVTDYKGETVFHYAVQDGNQOYLQLRNNAVAGLNQVN 217
 Db 368 IACKKRIKVMELLLKHGASIQAVTE-RGETALHMAARSGQAEVVRVYLDG-AQVEAKA 425
 QY 218 NQGLTPLHLACQCGKQEMRVLLCNARCINMGNGY-PHSAKBSQKCAEMIISMS 276
 Db 426 KDDQTPHLHSARLGKADIVQQLQCGASPNAAATTSGYTPLHSARBGEHEDVAFLDHGA 485
 QY 277 SQIHSKDPXYGASPLHWA--KNAEMARMLLKRGCVNSTSSAGNTALHYGVNRNRPDCA 333
 Db 486 SL--SITTKSGLTPLHVAHYDNQKVALLLDDGASPHAAAKNGYTPPLHIAKKNQMDIA 543
 QY 334 IVLLTHGANADARGEHGTPLHLAMSNDVENIKALIVFGAEVDPNDGEPFLASK 392
 Db 544 TTLLEYGADANAVTRQGIASVHLAAQGHVDVSLILGRNANVNLNYSKSGLTPLHLAAQ 602

Search completed: December 15, 2004, 13:34:52
 Job time: 70.158 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 16, 2004, 11:36:42 ; Search time 4401 Seconds
(without alignments)
10573.401 Million cell updates/sec

Title: US-10-612-668-18
Perfect score: 1277
Sequence: 1 GAATCTTACGCCCCAGATTC.....CAGACGGCGCGCGGAATTC 1277

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821965908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 854.2 | 66.9 | 2259 | AY421137 | AY421137 Homo sapi |
| 2 | 818.4 | 64.1 | 2259 | AY421138 | AY421138 Pan trogl |
| 3 | 770.8 | 60.4 | 914 | BG751481 | BG751481 602730060 |
| 4 | 763.8 | 59.8 | 776 | BG746419 | BG746419 602703692 |
| 5 | 759.2 | 59.5 | 1042 | BM805376 | BM805376 AGENCOURT |
| 6 | 747.4 | 58.5 | 851 | B1819262 | B1819262 603034691 |
| 7 | 698.6 | 54.7 | 3010 | BC061866 | BC061866 Rattus no |
| 8 | 697.4 | 54.6 | 2259 | AY421139 | AY421139 Mus muscu |
| 9 | 671.6 | 52.6 | 815 | BG328183 | BG328183 602427250 |
| 10 | 653.2 | 51.2 | 910 | CA489815 | CA489815 AGENCOURT |
| 11 | 631.4 | 49.4 | 636 | BG575678 | BG575678 602598744 |
| 12 | 590.2 | 46.2 | 658 | BG752410 | BG752410 602730892 |
| 13 | 577.4 | 45.2 | 940 | BQ423546 | BQ423546 AGENCOURT |
| 14 | 544.8 | 42.7 | 741 | BG576880 | BG576880 602597576 |
| 15 | 526.8 | 41.3 | 980 | BF178544 | BF178544 601807913 |
| 16 | 514.4 | 40.3 | 1868 | BM903742 | BM903742 AGENCOURT |
| 17 | 506 | 39.6 | 1060 | BO899244 | BO899244 AGENCOURT |
| 18 | 505.4 | 39.6 | 516 | B1013478 | B1013478 RCO-ET018 |
| 19 | 505.4 | 39.6 | 732 | CK356848 | CK356848 AGENCOURT |
| 20 | 494.2 | 38.7 | 620 | BM729323 | BM729323 UT-E-EO1 |
| 21 | 493 | 38.6 | 865 | CB204862 | CB204862 AGENCOURT |
| 22 | 482.6 | 37.8 | 615 | BO840333 | BO840333 mah66a10 |
| 23 | 463.2 | 36.3 | 741 | BG576307 | BG576307 602597017 |
| 24 | 450.8 | 35.3 | 604 | AM210136 | AM210136 U151c10.Y |

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|----|-------|------|------|----------|--------------------|
| 25 | 450 | 35.2 | 1080 | BM547662 | BM547662 AGENCOURT |
| 26 | 430.4 | 33.7 | 776 | CB948314 | CB948314 AGENCOURT |
| 27 | 425.6 | 33.3 | 544 | CB612036 | CB612036 AMGNMNC-N |
| 28 | 412 | 32.3 | 528 | BM107521 | BM107521 511770 MA |
| 29 | 393.8 | 30.8 | 600 | BU924627 | BU924627 7094-21 M |
| 30 | 393.4 | 30.8 | 570 | AM753653 | AM753653 CM0-CT027 |
| 31 | 371.2 | 29.1 | 759 | B130667 | B130667 602982618 |
| 32 | 368.2 | 28.8 | 565 | H10676 | H10676 Y199911.X1 |
| 33 | 357.8 | 28.0 | 648 | AM825629 | AM825629 un1907.Y |
| 34 | 356.2 | 27.9 | 530 | EX524262 | EX524262 EX524262 |
| 35 | 352.4 | 27.6 | 361 | CF139617 | CF139617 UT-HF-CBO |
| 36 | 346.8 | 27.2 | 593 | BG917622 | BG917622 602820461 |
| 37 | 344.8 | 27.0 | 540 | BX119788 | BX119788 BX119788 |
| 38 | 343.6 | 26.9 | 566 | AI663704 | AI663704 u647601.Y |
| 39 | 330.4 | 25.9 | 865 | CA488194 | CA488194 AGENCOURT |
| 40 | 323.8 | 25.4 | 612 | BI697743 | BI697743 603346835 |
| 41 | 323.4 | 25.3 | 769 | CO385967 | CO385967 AGENCOURT |
| 42 | 315.8 | 24.7 | 468 | BF930043 | BF930043 MR2-NT013 |
| 43 | 299.4 | 23.4 | 599 | AI568578 | AI568578 tn41a11.X |
| 44 | 291.2 | 22.8 | 682 | BX298130 | BX298130 BX298130 |
| 45 | 288.2 | 22.6 | 747 | BF178956 | BF178956 601808073 |

ALIGNMENTS

RESULT 1
AY421137
LOCUS
DEFINITION Homo sapiens PLA2G6 gene, VIRTUAL TRANSCRIPT, partial sequence,
AY421137 genomic survey sequence.
ACCESSION AY421137 GI:39777094
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2259)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 2259)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence as made by sequencing genomic exons and ordering them
based on alignment.
Location/Qualifiers
1..2259
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..-2259
/gene="PLA2G6"
/locus_tag="HCW7457"
ORIGIN
Query Match 66.9%; Score 854.2; DB 9; Length 2259;
Best Local Similarity 99.7%; Pred. No. 4.7e-196;
Matches 856; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CY 389 CACAGACTACAGATCTCATGCAATCTCACGGGCGGAGACCGGATTCCTGGG 448
|||

| | | | | | |
|----|------|---------------------------------|--------------------------------------|---|--------------------------------|
| Db | 1182 | AAGACAACCTAAGATCTCAATGCAACTCTCA | CGGGCCCGGAAGCCAGGCTTCATCTCGG | 1241 | |
| Qy | 449 | CTCCATGAGGGAACGAGAA | CGCGGACCCAGACCACTGCTGTGCTCTGAT | TGAGAGAGAGT 508 | |
| Db | 1242 | CTCCATGAGGGAACGAGAA | CGCGGACCCAGACCACTGCTGTGCTCTGAT | TGAGAGAGAGT 1301 | |
| Qy | 509 | GAAAGGCTCATCATCATCCAGCT | CTCTCATCGCCATCAGAAAGGCTCGGGTGTGGCCAC | 568 | |
| Db | 1302 | GAAAGGCTCATCATCATCCAGCT | CTCTCATCGCCATCAGAAAGGCTCGGGTGTGGCCAC | 1361 | |
| Qy | 569 | CAGGACCTGTTTGA | CTGSGGTGGGGCACAACGCACTGAGAGCAT | CCTGGCCCTGGCCAT 628 | |
| Db | 1362 | CAGGACCTGTTTGA | CTGSGGTGGGGCACAACGCACTGAGAGCAT | CCTGGCCCTGGCCAT 1421 | |
| Qy | 629 | TCTGCA | CAGTAAGTCCATGAGCTCTA | TAGGCGGGCCATGATCTTTGGCATGAAAGATAGAGT 688 | |
| Db | 1422 | TCTGCA | CAGTAAGTCCATGAGCTCTA | TAGGCGGGCCATGATCTTTGGCATGAAAGATAGAGT 1481 | |
| Qy | 689 | GTTCCGGGGCTTC | CAGGCCCTCA | CGAGTCGGGGCCCTCTGAGAGATGTTCTTGAA | CGCGGAGTT 748 |
| Db | 1482 | GTTCCGGGGCTTC | CAGGCCCTCA | CGAGTCGGGGCCCTCTGAGAGATGTTCTTGAA | CGCGGAGTT 1541 |
| Qy | 749 | TGGGGAGACAC | CCAAAGATGACGACGT | TAGGAAACCAAGGTATGCTGAC | CAGGACACT 808 |
| Db | 1542 | TGGGGAGACAC | CCAAAGATGACGACGT | TAGGAAACCAAGGTATGCTGAC | CAGGACACT 1601 |
| Qy | 809 | GTCGAC | CGGAGCGGGCTGAACT | CTCACTCTTC | CGGAACTACGATGCTCCAGAACTGT 868 |
| Db | 1602 | GTCGAC | CGGAGCGGGCTGAACT | CTCACTCTCTTC | CGGAACTACGATGCTCCAGAACTGT 1661 |
| Qy | 869 | CCGGAGGCTCTGTTTCAA | CACGAA | CGTTAACCTCAGGCTTC | CAGCTCAGACCACCA 928 |
| Db | 1662 | CCGGAGGCTCTGTTTCAA | CACGAA | CGTTAACCTCAGGCTTC | CAGCTCAGACCACCA 1721 |
| Qy | 929 | GCTGTGTGTGGGGGGGGG | CGGACGAGGGGGGAGCTCTCTA | CTTACTTC | TGCGAACCCCAATGG 988 |
| Db | 1722 | GCTGTGTGTGGGGGGGGG | CGGACGAGGGGGGAGCTCTCTA | CTTACTTC | TGCGAACCCCAATGG 1781 |
| Qy | 989 | GCGGCTTC | TCGACGATGGGCTGTGGCCAA | CAACCCACGCTGATGTCAT | GACCGAGAT 1048 |
| Db | 1782 | GCGGCTTC | TCGACGATGGGCTGTGGCCAA | CAACCCACGCTGATGTCAT | GACCGAGAT 1841 |
| Qy | 1049 | CCATGAGTACA | TAACGAACTCTGATTC | CGGAAAGGTACAGCCCA | CAAGGTGAAAGAACTTC 1108 |
| Db | 1842 | CCATGAGTACA | TAACGAACTCTGATTC | CGGAAAGGTACAGCCCA | CAAGGTGAAAGAACTTC 1901 |
| Qy | 1109 | CATGCTGTGTCTCC | CTGGGGGACAGGAGGT | CTCCCAACATGCTGTGAC | CTGTGTGATGT 1168 |
| Db | 1902 | CATGCTGTGTCTCC | CTGGGGGACAGGAGGT | CTCCCAACATGCTGTGAC | CTGTGTGATGT 1961 |
| Qy | 1169 | CTTCCGTC | CCAGCAACCCCTGGGAGCTGGCC | CAAGCTGTTTTTTTGGGG | CCAGAGAACTGGG 1228 |
| Db | 1962 | CTTCCGTC | CCAGCAACCCCTGGGAGCTGGCC | CAAGCTGTTTTTTTGGGG | CCAGAGAACTGGG 2021 |
| Qy | 1229 | CANAGATGTGTGACTGT | 1247 | | |
| Db | 2022 | CANAGATGTGTGACTGT | 2040 | | |

[illegible]

| TITLE | JOURNAL | PUBMED | REFERENCE | AUTHORS |
|-----------------------|---|----------|---------------------|---|
| TITLE | Science 302 (5652), 1960-1963 (2003) | 14671302 | 2 (bases 1 to 2259) | Todd,M.A., Tanenbaum,D.M.,Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. |
| TITLE | Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA | | | Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Keitelwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. |
| COMMENT | This sequence as made by sequencing genomic exons and ordering them based on alignment. | | | |
| FEATURES | Location/Qualifiers | | | |
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| gene | /mol_type="genomic DNA" | | | /db_xref="taxon:9598" |
| | <1..>2259 | | | /gene="PLA2G6" |
| | /locus_tag="HCM7457" | | | |
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| Best Local Similarity | 95.7%; Pred. No. 2,38-187; | | | |
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| Db | 1182 CAGACNNNNNNNNNNNNCTCATGCACTCTCCGCTCCGGAAGCAGGTCATCTCGGG | | | 1241 |
| QY | 449 CTCATAGAGGAGCAGAGAGGAGGACCAAGACACACTGCTGAGCTGTGATGAGAGAGAGT | | | 508 |
| Db | 1242 CNCATATAGGAGATGAGAGGAGGACCCAGACACACTCTGTGCTGTGATGAGAGAGAGT | | | 1301 |
| QY | 509 GAAAGGCTCATCATCATCCAGCTCTCATGCCATCGAAGAGGCTTGGGTGTGGCCAC | | | 568 |
| Db | 1302 GAAAGGCTCATCATCATCCAGCTCTCATGCCATCGAAGAGGCTTGGGTGTGGCCAC | | | 1361 |
| QY | 569 CAAGAGACTCTTTGACATGAGTGGGGGACACAGAGCTGAGAGATCCTGGGCTCGGCCAT | | | 628 |
| Db | 1362 CAAGAGACTCTTTGACATGAGTGGGGGACACAGAGCTGAGAGATCCTGGGCTCGGCCAT | | | 1421 |
| QY | 629 TCTGCACAGTAAAGTCATAGGCTCTACATGCGCGCATGTACTTTCGCATGAAGATGAGT | | | 688 |
| Db | 1422 TCTGCACAGTAAAGTCATAGGCTCTACATGCGCGCATGTACTTTCGCATGAAGATGAGT | | | 1481 |
| QY | 689 GTTCCGGGGCTCCAGGCGCTTACAGATGGGGGCCCTTGAGAGATTTCTTGAAGCGGGAATT | | | 748 |
| Db | 1482 GTTCCGGGGCTCCAGGCGCTTACAGATGGGGGCCCTTGAGAGATTTCTTGAAGCGGGAATT | | | 1541 |
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| Db | 1542 TGGGAGACACACCAAGATGACGAGCGTCAGAGAACCAAGGTGATGTCGACAGGAGCACT | | | 1601 |
| QY | 809 GTCTGACCGGACGCGGCTGAATCTCACTTTTCGGAATACGATGCTCCAGAACTGT | | | 868 |
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| QY | 869 CCGGAGACTCTGTTTCAACAGAACTTTAATCTTACAGCTTCCACTACAGCCTTGAAGCA | | | 928 |
| Db | 1662 CCGGAGACTCTGTTTCAACAGAACTTTAATCTTACAGCTTCCACTACAGCCTTGAAGCA | | | 1721 |
| QY | 929 GCTGTGTGTGGCGGGCGCCGGAAGCAGGGGGAGCTCTTACTTACTTTCGAGCCCAATG | | | 988 |
| Db | 1722 GCTGTGTGTGGCGGGCGCCGGAAGCAGGGGGAGCTCTTACTTACTTTCGAGCCCAATG | | | 1781 |
| QY | 989 GCGCTTCTTGAAGGTGGCTGTTGGCAACACCCAGCTGATGTCATGACCGAGAT | | | 1048 |

Db 1782 GGGCTTCCTGGAGCGTGGGCTGCTGGCAACACCCAGCTGGATCCATGACCGAGAT 1841
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 Qy 1169 CTTCCGTCCTCAGCAACCCCTGGAGAGCTGAGCCAAAGACTGTTTGGGCGCAAGAACTGGG 1228
 Db 1962 CTTCCGTCCTCAGCAACCCCTGGAGAGCTGAGCCAAAGACTGTTTGGGCGCAAGAACTGGG 2021
 Qy 1229 CAAGATGTGTGTGACTGT 1247
 Db 2022 CAAGATGTGTGTGACTGT 2040

RESULT 3
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 LOCUS 602730060F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4873766 5',
 DEFINITION mRNA sequence.

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 VERSION Bg751481
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 914)
 NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LNCMT752 row: 9 column: 15
 High quality sequence stop: 804.
 Location/Qualifiers

FEATURES

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 /note="Organ: eye; Vector: pORF7, Site_1: XhoI, Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library. |"

ORIGIN

Query Match 60.4%; Score 770.8; DB 4; Length 914;
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 Db 63 CAGACAACTACAGGATCTCATGCACTCTCAAGGCGCCGGAAGCCAGGTTTCATCTGGG 122

Qy 449 CTCATGAGGAGACGAGAGCGGACCCACGACCACTGTCTGTGCTGGATGAGAGAGAT 508
 Db 123 CTCATGAGGAGACGAGAGCGGACCCACGACCACTGTCTGTGCTGGATGAGAGAGAT 182
 Qy 509 GAAAGGCTCATCATCATCCAGCTCTCATTCGCAATGAGAAAGGCTCGGCTGTGCGCAC 568
 Db 183 GAAAGGCTCATCATCATCCAGCTCTCATTCGCAATGAGAAAGGCTCGGCTGTGCGCAC 242
 Qy 569 CAAAGACTGTTTGAATCGGCTGCGGACACAGACTGAGAGGCAATCTGGCCCTTGGCCAT 628
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 Qy 629 TCAGCAGTAAAGTCCATGAGCTACATGCGCCGATGTACTTTCCGATAGAGATAGAT 688
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 Qy 689 GTTCCGGGGCTCCAGGCGCCCTACAGATCGGAGCCCTGAGAGATTTCTGAAAGCGGAGTT 748
 Db 363 GTTCCGGGGCTCCAGGCGCCCTACAGATCGGAGCCCTGAGAGATTTCTGAAAGCGGAGTT 422
 Qy 749 TGGGAGACACCAAGATGACGAGCTCAGAGAAACCAAGGTGATGCTGACAGGACACT 808
 Db 423 TGGGAGACACCAAGATGACGAGCTCAGAGAAACCAAGGTGATGCTGACAGGACACT 482
 Qy 809 GTCTGACCGGACCGGCTGAACTCCACCTCTCCGGAATGATGCTCCAGAACTGT 868
 Db 483 GTCTGACCGGACCGGCTGAACTCCACCTCTCCGGAATGATGCTCCAGAACTGT 542
 Qy 869 CCGGAGGCTCGTTTCAACAGAACCTTAACTCAGGCTCCAGCTCAGGCTCAGACCA 928
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 Qy 1228 GCAAGATGTGTG 1239
 Db 898 GCAAGATGTGTG 909

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 LOCUS 602703692F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4856903 5',
 DEFINITION mRNA sequence.

ACCESSION Bg746419 GI:14057072
 VERSION Bg746419
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 776)
 NIH-MGC http://mgi.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999).
 JOURNAL


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Db      121 TTTCGACAGTAAGTCAATGCGCCATGAGCGGCACTTTCGATGAGGATGAGG 180
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Qy      1108 CCAATGCTGTCTCCCTGAGGAGCAAGGAGTCCCAAGATGCTGTGATGCTGTGATG 1167
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Qy      1168 TCTTCCCTCCAGCAACCCCTGAGGAGTGGCCAAAGCTGTTTGGGGCAAGGACTGG 1227
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Db      721 GCAAGATGTGTGTGAGCTGTTGACGAGATCCAGACGGGCGGCGGCTG 765

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VERSION   BI819262.1 GI:15930812
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
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           Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 851)
           NIH-MGC http://mgs.nci.nih.gov/.
           National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished (1999)
           Contact: Robert Strauberg, Ph.D.
           Email: ggaabs-remail.nih.gov
           Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LNL at:
           http://image.llnl.gov
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source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

ORIGIN
Query Match      58.5%; Score 747.4; DB 4; Length 851;
Best local Similarity 98.9%; Pred. No. 3,1e-170;
Matches 784; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

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Db      124 AGCAGTGAAGGAGCTTCGCGCTGCGCATCTGTCAGATGATGATGATGATGATGATG 183
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Db      304 AAACCAAGGTATGCTGACAGGAGCACTGTGACCGGACGCGGCTGCACTC 363
Qy      840 TTCCGGAATACAGTCTCCAGAACTGTCCGGAGCTTCGTTTCAACCAAGAGTTAAC 899
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Qy      900 CTGAGGCTTCAGACTCAGGCTTCAAGACAGTGTGTGTGGGCGGCGGCGGAGAC 959
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Qy      960 GCAAGCTCTTACTTCTCCAGACCAATGAGGCGCTTCCTGAGCGGTGGGCTGTTGGCAAC 1019
Db      484 GCAAGCTCTTACTTCTCCAGACCAATGAGGCGCTTCCTGAGCGGTGGGCTGTTGGCAAC 543
Qy      1020 AACCCACGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1079
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Qy      1080 GGTTCAGGCGCAACAGTGAAGAACTCTCATGTGTGTCTCTCTGGGG-ACAGGAGGTC 1138
Db      604 GGTTCAGGCGCAACAGTGAAGAACTCTCATGTGTGTCTCTCTGGGGACAGGAGGTC 663
Qy      1139 CCACCAAGTGCCTGTGACCGTGTGATGATGATGATGATGATGATGATGATGATGATG 1198
Db      664 CCACCAAGTGCCTGTGACCGTGTGATGATGATGATGATGATGATGATGATGATGATG 723
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Db      724 CAAGACTGTTTGGGGCGC-AGGACTGGCGCAAGATGTGTGTGAGTGTG-AGGACTGGATC 781

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QY 1259 AGACGGCGCGCCG 1271
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 DB 782 AGACGGCGCGCTG 794

RESULT 7
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 VERSION BC061866.1 GI:38511544
 KEYWORDS
 SOURCE HTC.
 ORGANISM Rattus norvegicus (Norway rat)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE
 AUTHORS 1 (bases 1 to 3010)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Umedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loggellano, N.A., Peters, G.J., Abramson, R.D., Mullan, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richardson, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, X., Gibbs, R.A., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Jackson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butler, D., Scher, J., Krzywinski, M.I., Skalska, U., Smalins, D.E., Scheraga, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL MEDLINE 22388257
 PUBMED 12477932
 2 (bases 1 to 3010)
 Strausberg, R.
 Direct Submission
 Submitted (05-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

TITLE NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Jeff Green/Faturnu Kondalah, NCI.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc.mgc@hgrl.nih.gov
 Akher, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakeley, R.W., Bouffard, G.G., Brinton, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaapi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantirpop, S., Thomas, P.J., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

REMARK
 COMMENT
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov
 Series: IRAC Plate: 137 Row: b Column: 23

FEATURES
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ORIGIN

Query Match 54.7%; Score 698.6; DB 3; Length 3010;
 Best Local Similarity 86.2%; Pred. No. 2,7e-158;
 Matches 773; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

376 CTGCTCTGCTCCACAGACTACAGATCTCATGACATCTCAGCGGCCGGAAGCCAG 435
 1340 CTTCAGAGATCAGACAGACGCTTCAGACCTCATGCCCTCCGAGCCGGAAGCCAG 1399
 436 CGTTTCCTCTGAGCTTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495
 1400 CGTTTCCTCTGAGCTTCATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1459
 496 ATGAG 555
 1460 AGGAG 1519
 556 CGGAGTGGCCACAG 615
 1520 CAGGTGGCTACAG 1579
 616 TGCCCTGACCATCTTCAGACAGTACAGTACAGTACAGTACAGTACAGTACAGT 675
 1580 TGCCCTGACCATCTTCAGACAGTACAGTACAGTACAGTACAGTACAGTACAGT 1639
 676 TGAAGATGAGTGTTCGGGGGCTCCAGGCTTCAGAGTCCGGGGGCTTCAGAGTTC 735
 1640 TGAAGATGAGTGTTCGGGGGCTCCAGGCTTCAGAGTTCGGGGGCTTCAGAGTTC 1699
 736 TGAAGCGGAGTTCGGGGGCTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAG 795
 1700 TGAAGCGTATGTTGGGGGCTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAG 1759
 796 TGAAGCGGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAG 855
 1760 TGAAGCGGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAG 1819
 856 CTTCAGAACTGTCCGGGAGCTCTGTTTCAACCAAGCTTAACTCAGAGCTTCAG 915
 1820 CCCCAAGGCGCTTCGGGAGCTCTGTTTCAACCAAGCTTAACTCAGAGCTTCAG 1879
 916 AGCCCTCAGACGAGTGTGTGGGGGCGCCGGAAGAGAGAGAGAGAGAGAGAGAG 975
 1880 AGCTTCAGACGAGTGTGTGGGGGCGCCGGAAGAGAGAGAGAGAGAGAGAGAG 1939
 976 TCCGACCAATGAGGCGCTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAG 1035
 1940 TCCGACCAATGAGGCGCTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAG 1095
 1036 CCAATGACGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAG 1095
 2000 CCAATGACGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAGTTCAGAG 2059
 1096 TGAAGAACTTCATGCTGTGTCTCCCTGGGAGAGAGAGAGAGAGAGAGAGAGAG 1155
 2060 TGAAGAACTTCATGCTGTGTCTCCCTGGGAGAGAGAGAGAGAGAGAGAGAGAG 2119
 1156 CCGTGTGTGATGTCCTTCCTCCAGCAACCTCGGAGAGTTCAGAGTTCAGAGTTC 1215

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Db      2120 CCTGTAGATGCTTTTCCTCCAGCAACCTTGGAGCTGGCCAGACACTGTTTGGAG 2179
Qy      1216 CCAGAGAACTGGGCAAGATGCTGTGATCTGTTGACCGATCCAAGCGGCGCCGG 1272
Db      2180 CCAGAGAACTGGGCAAGATGCTGTGATCTGTTGACCGATCCAAGATGGCGGCGCTG 2236

RESULT 8
AY421139      2259 bp      DNA      linear      GSS 17-DEC-2003
LOCUS      Mus musculus PLA2G6 gene, VIRUTAL TRANSCRIPT, partial sequence,
DEFINITION      AY421139
ACCESSION      AY421139
VERSION      AY421139.1 GI:39777096
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2259)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED      14671302
2 (bases 1 to 2259)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civejlo,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submision
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT      This sequence as made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
source
1..2259
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>2259
/gene="PLA2G6"
/locus_tag="HCM7457"

ORIGIN
Query Match      54.6%; Score 697.4; DB 9; Length 2259;
Best Local Similarity 88.2%; Pred. No. 5e-158;
Matches 758; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy      389 CACAGAACTACAGATCTCATGACATCTCAGCGGCGCCGGAAGCGTTACTCTGGG 448
Db      1182 CAGAGAGCTTCAGAGATCTATGCCCATCTCTCAGCGCCGGAAGCGTTACTCTGAG 1241
Qy      449 CTCATGAGGAGCAGAAAGCGAAGCCACGACCACTCTGCTGCTGANTGAGAGAGAGT 508
Db      1242 CTCATGAGGAGCAGAAAGCGAAGTCACGACCACTCTGCTGCTGAGCGAGGCGT 1301
Qy      509 GAAAGGCTCATCATCATCTCCATCTCCATCGGCATGAGAAAGCCCTGGGTGTGGCAC 568
Db      1302 GAAAGGCTGGTATATTCAGCTTCTCATCTGCGCATGAGAAAGCCCTGGGAGTGGCAC 1361
Qy      569 CAAGAGCTGTGACTGGTGGCGGACACAGACATGAGAGCATCTTGGCCCTGGCCAT 628
Db      1362 CAAGAGCTTTCAGCTGGGTGGCGGACACAGACAGGGGGCATCTTGGCCCTGGCCAT 1421
Qy      629 TCTGCAAGTAAGTCCATGCTTACATGCGCGGCGCATCTTTCGACGTAAGATGAGT 688
Db      1422 TCTGCAAGTAAGTCCATGCTTACATGCTGCTGCTGCTTACTCTCGTATGAAGACGAGT 1481

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Qy      689 GTTCCGGGCTCCAGGCGCTTACAGATCGGGGCCCTCGAGAGATTCTCTGAAGCGGAGTT 748
Db      1482 GTTTCGGGGCTACAGGCGCTTATGATGCTGGGCCCTCGAGAGATTCTCTGAAGCGGAGTT 1541
Qy      749 TGGGAGACACACCAAGATGACGAGCGTCAAGAAACCAAGTATCTGAACAGGACACT 808
Db      1542 TGGGAGACACACCAAGATGACAGATGTCAAAACCAAGTATCTGAACAGGAGACACT 1601
Qy      809 GTCTGACCGGACAGCGGCTGAACTCCACTCTTCCGGAACCTAGATGCTCCGAAACTGT 868
Db      1602 GTCTGACCGGACAGCGGCTGAACTCCACTCTTCCGGAACCTAGATGCTCCGAAACTGT 1661
Qy      869 CGGAGAGCTCGTTTCAACAGAACTTAACCTCAGGCTCCAGCTCAGCGCTCAGACCA 928
Db      1662 TCGAGAGCGGCTCGTTTCAACAGAACTTAACCTCAGGCTCCAGCTCAGCGCTCAGACCA 1721
Qy      929 GCTGATGAGCGGCGGCGCGGCGAAGCAAGCGGCGAGCTCTACTTACTTCGACCAATGG 988
Db      1722 ACTGATGAGCGGCGGCGGCGGCGAAGCAAGCGGCGAGCTCTACTTACTTCGAGCCAAATGG 1781
Qy      989 GCGCTTCTCTGAGAGGTGGGCTGTGGCCAAACCCCAAGCTGAGATGCCATGACGAGAT 1048
Db      1782 ACGCTTCTCTGAGAGGTGGGCTGTGGCCAAACCCCAAGCTGAGATGCCATGAGATGAGAT 1841
Qy      1049 CCATGAGTACATACAGACCTGATCCGCAAGGCTCAGGCAACAGGTGAAGAACTCTC 1108
Db      1842 CCATGAGTACATACAGACCTGATCCGCAAGGCTCAGGCAACAGGTGAAGAACTCTC 1901
Qy      1109 CATCGTGTCTCCCTGGGAGCAGGAGGTGCCCAAGTGCCTGTGACCTGTGTGATGT 1168
Db      1902 CATAGTGTGTCTCTGGGAGCAGGAAAGTCCCTCAAGTGCCTGTGATGATGT 1961
Qy      1169 CTTCCTCTCCAGAACCCCTGGGAGCTGGCCAAAGATGTTTGGGCGCAAGAACTGGG 1228
Db      1962 CTTCCTCTCCAGAACCCCTGGGAGCTGGCCAAAGATGTTTGGGCGCAAGAACTGGG 2021
Qy      1229 CAAGATGTGTGAGTGTG 1247
Db      2022 CAAGATGTGTGAGTGTG 2040

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RESULT 9
BG328183      815 bp      mRNA      linear      EST 27-FEB-2001
LOCUS      602427250P1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:454525 5',
DEFINITION      mRNA sequence.
ACCESSION      BG328183
VERSION      BG328183.1 GI:13134621
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 815)
TITLE      NIH-MGC http://mgs.nci.nih.gov/.
JOURNAL      National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/HLN at:
http://image.llnl.gov
Plate: LHC41233 row: d column: 14
High quality sequence stop: 753.
FEATURES
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1..815
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/mol_type="mRNA"
/db_xref="taxon:9606"

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/clone="IMAGE:4546525"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH MG.C.15"
/notes="Organ: colon; Vector: pOT7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAAGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

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ORIGIN

```

Query Match      52.6%; Score 671.6; DB 4; Length 815;
Best Local Similarity 95.6%; Pred. No. 7.4e-152;
Matches 767; Conservative 0; Mismatches 24; Indels 11; Gaps 7;

QY 473 CCAAGACCACTGCTGCTGCTGATGAGAGAGTAAAGGCTCATCATCCAGCT 532
DB 6 CCAAGACCACTGCTGCTGCTGATGAGAGAGTAAAGGCTCATCATCCAGCT 65
QY 533 CCTCATGCGCATGAGAGAGGCTCGGGTGGCCACCAAGGACCTGTTGACTGGGTGGC 592
DB 66 CCTCATGCGCATGAGAGAGGCTCGGGTGGCCACCAAGGACCTGTTGACTGGGTGGC 125
QY 593 GGGCACCAGCAGCTGAGAGCATCTGAGCCCTGAGCCATTCTGACAGTAACTCAAGGCTTA 652
DB 126 GGGCACCAGCAGCTGAGAGCATCTGAGCCCTGAGCCATTCTGACAGTAACTCAAGGCTTA 165
QY 653 CATGCGGCGCATGATCTTTGCGATGAAGATGAGTGTCCGGGGCTCCAGGCCCTACGA 712
DB 186 CATGCGGCGCATGATCTTTGCGATGAAGATGAGTGTCCGGGGCTCCAGGCCCTACGA 245
QY 713 GTGGGGGGCCCTGGAGAGGTTCTGAGAGCGGGAGTTGGGAGAGACCAAGATGAGGA 772
DB 246 GTGGGGGGCCCTGGAGAGGTTCTGAGAGCGGGAGTTGGGAGAGACCAAGATGAGGA 305
QY 773 CGTCAGAGAAACCAAGGTGATGCTGACAGAGGACACTGTCTGACCGGAGCGGCTGACT 832
DB 306 CGTCAGAGAAACCAAGGTGATGCTGACAGAGGACACTGTCTGACCGGAGCGGCTGACT 365
QY 833 CCAACTCTTCCGGAACCTGATGCTCCAGAACTGTCCGGAGCCTGTTCAACCAAGAA 892
DB 366 CCAACTCTTCCGGAACCTGATGCTCCAGAACTGTCCGGAGCCTGTTCAACCAAGAA 425
QY 893 CGTTAACCTAGGCTCAGCTCAGGCTCAGACCAAGCTGATGAGGGGGCGGCGGAG 952
DB 426 CGTTAACCTAGGCTCAGCTCAGGCTCAGACCAAGCTGATGAGGGGGCGGCGGAG 485
QY 953 CAGCGGGGAGCTCTTACTTACTTCCAGCCCAATGGCGCTTCTGAGCGGTGGCTGTT 1012
DB 486 CAGCGGGGAGCTCTTACTTACTTCCAGCCCAATGGCGCTTCTGAGCGGTGGCTGTT 545
QY 1013 GGGCAACAACCCCAAGCTGATGCTGATGATGATGATGATGATGATGATGATGATGAT 1072
DB 546 GGGC--AACAACAACCCCAAGCTGATGCTGATGATGATGATGATGATGATGATGATGAT 603
QY 1073 CCGCAAGGGGCAAGGCAAGGTAAGAACTCTCATGATGTTGCTCCCGGGGAGCAG 1132
DB 604 CCGCAAGGGGCAAGGCAAGGTAAGAACTCTCATGATGTTGCT--CTTGGGAGCAGG 662
QY 1133 GAGGTCCCAACAAGTGTGATCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 1192
DB 663 GAGGT--CCCAACAAGTGTGATCTGTGTGATGATGATGATGATGATGATGATGATGATGAT 720
QY 1193 GCTGGCCAAACAGTGTGTTGGGGCAAAGAACTGGGCAAGATGGTGTGATCTGTTGAC 1252
DB 721 GCTGGC--AGACTGTTTGGGG--CAAGAACTGGGCAAGATGGTGTG--CGGATGCC 774
QY 1253 GGAATCCAGAGGGGGCGGCGGAA 1274
DB 775 GGTTCAAAAGGGGGCGGTGA 796

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RESULT 10
CA489815
LOCUS
DEFINITION
AGENCOURT_10810716 MABCL Homo sapiens cDNA clone IMAGE:6722303 5',
mRNA sequence.
ACCESSION
CA489815
VERSION
CA489815.1 GI:24952606
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 910)
NIH-MGC http://mgc.nci.nih.gov/.
Natlional Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Straubeberg, Ph.D.
Email: csapbs-remail.nih.gov
Tissue Procurement: Kristi A. Eglund, Ira Pastan
cDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL4284 row: m column: 23
High quality sequence stop: 612.
Location/Qualifiers

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FEATURES

source

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1..910
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/clone="IMAGE:6722303"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
hTERT-HMEL, LNCaP"
/lab_host="EMDH10B"
/clone_1lb="MABCL"
/notes="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Straubeberg,
Bungkok Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

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ORIGIN

```

Query Match      51.2%; Score 653.2; DB 6; Length 910;
Best Local Similarity 99.3%; Pred. No. 2.2e-147;
Matches 677; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 593 GGGCACCAGCAGCTGAGAGGATCTCTGCGCCCTGGGCATTCTGCAAGTAAGTCAAGGCTTA 652
DB 1 GGGCACCAGCAGCTGAGAGGATCTCTGCGCCCTGGGCATTCTGCAAGTAAGTCAAGGCTTA 60
QY 653 CATGCGGCGCATTAATTTGCGATGAGAGTGAAGTGTTCGGGGGCTCCAGGCCCTACGA 712
DB 61 CATGCGGCGCATTAATTTGCGATGAGAGTGAAGTGTTCGGGGGCTCCAGGCCCTACGA 120
QY 713 GTGGGGGGCCCTGGAGAGGTTCTGGAAGCGGAGTTGGGGAGCACCAAGATGACGA 772
DB 121 GTGGGGGGCCCTGGAGAGGTTCTGGAAGCGGAGTTGGGGAGCACCAAGATGACGA 180
QY 773 CGTCAGAGAAACCAAGTGTGATGCTGACAGAGAACTGTCTGACCGGAGCGGCTTAAGCT 832
DB 181 CGTCAGAGAAACCAAGTGTGATGCTGACAGAGAACTGTCTGACCGGAGCGGCTTAAGCT 240
QY 833 CCAACTCTTCCGGAACCTGATGCTCCAGAACTGTCCGGAGCCTGTTCAACCAAGAA 892
DB 241 CCAACTCTTCCGGAACCTGATGCTCCAGAACTGTCCGGAGCCTGTTCAACCAAGAA 300

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| | | | |
|----|------|--|------|
| Qy | 893 | CGTTAACTCAGGCGCTCAGCTCAGCGCTCAGACCGAGCTGGGTGGGGGGCCCGAAG | 952 |
| Db | 301 | CGTTAACTCAGGCGCTCAGCTCAGCGCTCAGACCGAGCTGGGTGGGGGGCCCGAAG | 360 |
| Qy | 953 | CAGCGGGCAGCTCCTACTTACTTCCGACCCMATGGGGCTTCTCGACGGTGGGCTGT | 1012 |
| Db | 361 | CAGCGGGCAGCTCCTACTTACTTCCGACCCMATGGGGCTTCTCGACGGTGGGCTGT | 420 |
| Qy | 1013 | GGCCCAACCCCAAGCTGGATGCCATGACCGAGTTCATGATGATCAATCAGAGCTGAT | 1072 |
| Db | 421 | GGCCCAACCCCAAGCTGGATGCCATGACCGAGTTCATGATGATCAATCAGAGCTGAT | 480 |
| Qy | 1073 | CGCAAGGGTCAGGCGCAACAGGTGAAGAACTCCATCGTGTCTCCCT--GGGGACAG | 1131 |
| Db | 481 | CGCAAGGGTCAGGCGCAACAGGTGAAGAACTCTCCATCGTGTCTCCCTGGGGACAG | 540 |
| Qy | 1132 | GGAAGTCCCAACAAGTGCCTGTGACTGTGTGGATGTCCTTCGTCCAGCAACCCCTGGG | 1191 |
| Db | 541 | GGAAGTCCCAACAAGTGCCTGTGACTGTGTGGATGTCCTTCGTCCAGCAACCCCTGGG | 600 |
| Qy | 1192 | AGCTGGCCAAAGCTGTTTTTTGGGGCCAAAGAACTGG--GCAGATGGTGGTGAATCTGTTGC | 1251 |
| Db | 601 | AGCTGGCCAAAGCTGTTTTTTGGGGCCAAAGAACTGGAGATGGTGGTGAATCTGTTGC | 660 |
| Qy | 1251 | ACGATTCAGACGGGGCGGCGG 1272 | |
| Db | 661 | ACGATTCAGACGGGGCGGCGG 682 | |

| | |
|------------|--|
| RESULT 11 | |
| BG575678 | |
| LOCUS | BG575678 |
| DEFINITION | BG575678 636 bp mRNA linear EST 10-APR-2001 |
| | 602598744.1 NIH_MGC_87 Homo sapiens CDNA clone IMAGE:4707491 5', |
| | mRNA sequence. |

| | | |
|-----------|--------------|-------------|
| ACCESSION | BC575678 | GI:13563331 |
| VERSION | BC575678.1 | |
| KEYWORDS | EST. | |
| SOURCE | Homo sapiens | (human) |
| ORGANISM | Homo sapiens | |

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 636)
NIH-MGC <http://mgc.ncl.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: csapds-rc@mail.nih.gov
Tissue Procurement: DCRD/DRP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
<http://imgc.lnl.gov>
Plate: LNA10577 Row: g Column: 12
High quality sequence start: 2
High quality sequence stop: 631.

| FEATURES | location/Qualifiers |
|----------|---------------------|
| source | 1. .636 |

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/db_xref="taxon:9606"
/clone="IMAGE:4707491"
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/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."

```

ORIGIN

| | | | | |
|---------------------------|-------|--------------------|----------|------------|
| Query Match | 49.4% | Score 631.4 | DB 4 | Length 636 |
| Best Local Similarity | 99.8% | Pred. No. 3.9e-142 | | |
| Matches 632; Conservative | 0 | Mismatches 1 | Indels 0 | Gaps 0 |

401 GGAATTCATGCAATCTCAGGGAGCCGGAGACGTTTCATCTCGGGCTCATGAGGA 460
|||||
1 GGAATTCATGCAATCTCAGGGAGCCGGAGACGTTTCATCTCGGGCTCATGAGGA 60

461 CGAAGACGGACCCAGACCACTCTGTCCTGATGGAAGAGCGTGAAGGCGCTCAT 520
|||||
61 CGAAGACGGACCCAGACCACTCTGTCCTGATGGAAGAGCGTGAAGGCGCTCAT 120

521 CATCATCCAGCTCTCATCGCCATGAGAGGCTCGGGTGTGGCCACCAAGAACTTT 580
|||||
121 CATCATCCAGCTCTCATCGCCATGAGAGGCTCGGGTGTGGCCACCAAGAACTTT 180

581 TGACTGGGTGGCGGGGACCGAGCATTCCTGGCCCTGGCCATTTCGACAAGTAA 640
|||||
181 TGACTGGGTGGCGGGGACCGAGCATTCCTGGCCCTGGCCATTTCGACAAGTAA 240

641 GTCCATGSCCTACATGCGGCGCATGTACTTTGGCATGAAGATGAGGTTCGGGGCTC 700
|||||
241 GTCCATGSCCTACATGCGGCGCATGTACTTTGGCATGAAGATGAGGTTCGGGGCTC 300

701 CAGGCCCTACAGACTCGGGGCCCCCTGGAGGAGTTCCTGAAGCGGGAGTTGGGGAGCACAC 760
|||||
301 CAGGCCCTACAGACTCGGGGCCCCCTGGAGGAGTTCCTGAAGCGGGAGTTGGGGAGCACAC 360

761 CAAGATGACGGACGTCAGGAAACCCAGGTGATGCTGACAGGGACACTGTGTGACCCGCA 820
|||||
361 CAAGATGACGGACGTCAGGAAACCCAGGTGATGCTGACAGGGACACTGTGTGACCCGCA 420

821 GCCGCTGAATCCACTTTCGGAACTACAGATCCTCAGAACTGTCCGGAGCTTCG 880
| | | | |
421 GCGCGTGAACTCACTTTCCGGAACTACAGATCCTCAGAACTGTCCGGAGCTTCG 480

881 TTTCACCGAAGTTAACCTCAGGGCTTCAAGCCCTCAGA CCAAGTGGTGCG 940
481 TTTCACCGAAGTTAACCTCAGGGCTTCAAGCCCTCAGA CCAAGTGGTGCG 940

941 GGGCGCCCGGAGAGCGGGGCAAGCTTCTTACTTCTCGACCCAAATGGAGCGCTTCTTCTGGA 1000

1001 CGGTGGGCTTTGGCCAACACCCACGGTGA 1033
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601 CGGTGGGCTTTGGCCAACACCCACGGTGA 633
|||||||

| | 650 bp | mRNA | linear | EST 15-MAY-2001 |
|---|--------|------|--------|-----------------|
| LOCUS | | | | |
| DEFINITION | | | | |
| 602730892F1 NIH_MGC_43 Homo sapiens CDNA clone IMAGE:4874542 5' | | | | |
| BG572410 | | | | |
| RESULT 12 | | | | |
| GG752410 | | | | |

mRNA sequence.
 BG752410
 BG752410.1 GI:14063063
 EST.

| SOURCE ORGANISM | ORGANISM |
|---|--------------|
| Homo sapiens (human) | Homo sapiens |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | |

REFERENCE
1 (bases 1 to 658)
AUTHORS
TITLE NIH-MGC <http://mgc.nci.nih.gov/>.
NATIONAL Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL

COMMENT Contact: Robert Strausberg, Ph.D.
Email: c9aphs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LNLN),
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:

| | | | |
|----|-----|---|-----|
| QY | 515 | CCTATCATATCCAGGCTTCATATGCCATGAGAAAGGCTCGGGTGTGGCCACAAGA | 574 |
| Db | 481 | CCTCATCATCATCAGCTCTCATATGCCATTCGAAGAGGCTTCGGGTGTGGCCACAAGA | 540 |
| QY | 575 | CCTGTTTGACTGGGTGTGGGGGACCAAGCACTGGAGGCAATCCTGCGCCCTGSCCATTTGCA | 634 |
| Db | 541 | CCTGTTTGACTGGGTGTGGGGGACCAAGCACTGGAGGCAATCCTGCGCCCTGSCCATTTGCA | 600 |
| QY | 635 | CAGTAAGTCCATGCGCTTACATGCGGGGAGATGTACTTTGCGATGAAGATGAGTGTTCG | 694 |
| Db | 601 | CAGTAAGTCCATGCGCTTACATGCGGGGAGATGTACTTTGCGATGAAGATGAGTGTTCG | 660 |
| QY | 695 | GGGCTCCAGGCGCCCTACGAGTCGGGG--CCCTCGAGAGAGTTCTCTGAAGCGGGAG--TTTG | 750 |
| Db | 661 | GGGCTCCAGGCGCTTACGAGTCGGGGCGCCCTCGAGAGAGTCCCTGAAGACGGAGATTGG | 720 |
| QY | 751 | GGGAGCAACCAAGATGA--CGGAGCTCAGGAAACCCAAAGGTATCTCTGACAGGACACTG | 809 |
| Db | 721 | GGGAAACCCCCAAGATGACCGGAGCTTCAGGAAACCCAAAGGAGATGCTTGAACAGGAA | 780 |
| QY | 810 | TCTGACCGGACCGGCTG 828 | |
| Db | 781 | ACTGCTTGAGACCGGAG 799 | |

| | | | | | |
|------------|---|--------|------|--------|-----------------|
| RESULT 14 | | | | | |
| BC576680 | | | | | |
| LOCUS | BC576680 | 741 bp | mRNA | linear | EST 10-APR-2001 |
| DEFINITION | 6025597576r1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4706347 5', | | | | |

| | |
|-----------|-------------|
| ACCESSION | BG576680 |
| VERSION | BG576680.1 |
| | GI:13584333 |

| SOURCE ORGANISM | Homo sapiens (human) |
|-----------------|----------------------|
| | Homo sapiens |

REFERENCE
1 (bases 1 to 741)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT 1
Contact: Robert Strauberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTB/DTP

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
RNA Sequencing by: TruSeq Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

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 Average insert size 1.383 kb. library enriched f

full-length clones and constructed by life technologies
 Note: this is a NIH_MGC Library."

| Query Match | Score | DB 4; | Length |
|-------------|-----------|---------|--------|
| 42.7%; | 544.8; | DB 4; | 741; |
| 87.3%; | Prod No 4 | 1e-121. | |

Matches 647; Conservative 0; Mismatches 3; Indels 91;

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Db 181 TGACTGGGTGGGGGCAACAGACTGGAGGCATCTGGCCCTGGCCATTTCGACAGTAA 24

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DB 241 GTCCATGCGCCACATGCGCGGAGTACTTTCGCAATGAGGATGAGGATGATCCCGGGGCGC 30

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761 CAAGATGACGACGTACGAAACCCA-----78

QY 788 -----GG 78
11

Db 421 GGAGAGAGCCTGTTTGGCGGGATGTGCGGGAGAAAGCCACCTATCCCGAACAGAGGG 48

Db 481 TGATGTCACGGGACACTGTGTGACCGGCA GCGGCTTAACCTCCACTCTTCCGAACT 54

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910 CAGCTCAGCCCTCAGACAGCAGCTGTTGGCCGGCGGCGCGGAGCGACAGCGGCGACTCTTA 98

Db 601 CAGCTAGGCCCTCAGACCAGCTGGTGTGGCGGCGGCCGAGACGCGGGGACGCTTCCTA 66

970 CTTACCTTCCGACCCAAATGGGCGCTTCCGGAAGTATGGCGTGTGGCCAAACCAACCCACAGC 10

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RESULT 15
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DEFINITION 601807933F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4038626 5' mRNA sequence.

ACCESSION BF178544
VERSION 1
KEYWORDS BF178544.1 GI:11056686
EST.

| SOURCE | ORGANISM |
|---|----------|
| Mus musculus (mouse) | |
| Mus musculus | |
| Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi: | |

REFERENCE
AUTHORS
1 (bases 1 to 980)
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

| | |
|----------------------------|--|
| JOURNAL TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) |
| Unpublished (1999) | |
| Contact: Robert Strausberg | Dh D |
| Comment: | |

Email: cgapbs-remail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 and Thomas Rosenblatt, Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9317 row: j column: 03
High quality sequence stop: 647.
Location/Qualifiers

FEATURES

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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

ORIGIN

Query Match 41.3%; Score 526.8; DB 2; Length 980;
Best Local Similarity 84.8%; Pred. No. 1e-116;
Matches 626; Conservative 0; Mismatches 107; Indels 5; Gaps 3;

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Search completed: December 16, 2004, 15:10:00
Job time : 4411 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 15, 2004, 13:01:00 ; Search time 35.0255 Seconds
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Title: US-10-612-668-21

Sequence: 1 MOEFGRLVNTFSGVTNLFNSN.....GAKELGMVVDCTDPDGR 687

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Post-processing: Minimum Match 0%
Maximum Match 100%

Database : Issued Patents AA:*
Listing first 45 summaries

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SUMMARIES

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| 2 | 3620 | 100.0 | 687 | US-09-519-223-21 | Sequence 21, Appl |
| 3 | 3620 | 100.0 | 687 | US-09-927-180-21 | Sequence 21, Appl |
| 4 | 3606.5 | 99.6 | 688 | US-08-555-568B-23 | Sequence 23, Appl |
| 5 | 3606.5 | 99.6 | 688 | US-09-519-223-23 | Sequence 23, Appl |
| 6 | 3606.5 | 99.6 | 688 | US-09-927-180-23 | Sequence 23, Appl |
| 7 | 3302.5 | 91.2 | 752 | US-08-281-193-2 | Sequence 2, Appl |
| 8 | 3302.5 | 91.2 | 752 | US-08-422-106-2 | Sequence 2, Appl |
| 9 | 3302.5 | 91.2 | 752 | US-08-735-716-2 | Sequence 2, Appl |
| 10 | 3302.5 | 91.2 | 752 | US-08-555-568B-2 | Sequence 2, Appl |
| 11 | 3302.5 | 91.2 | 752 | US-09-519-223-2 | Sequence 2, Appl |
| 12 | 3302.5 | 91.2 | 752 | US-09-927-180-2 | Sequence 2, Appl |
| 13 | 3302.5 | 91.2 | 752 | PCT-US95-08069-2 | Sequence 2, Appl |
| 14 | 2084 | 57.6 | 394 | US-08-555-568B-17 | Sequence 17, Appl |
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| 21 | 902.5 | 24.9 | 545 | US-09-270-767-61684 | Sequence 61684, A |
| 22 | 371 | 10.2 | 143 | US-09-172-977-3 | Sequence 33298, A |
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| 42 | 273 | 7.5 | 994 | 4 | US-10-164-595-38 | Sequence 38, Appl |
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ALIGNMENTS

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RESULT 1
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; Sequence 21, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-555-568B-21

Query Match      100.0%; Score 3620; DB 2; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 21, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-21

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Query Match 100.0%; Score 3620; DB 3; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 21, Application US/09927180
; Patent No. 6645736
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25

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CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match      100.0%; Score 3620; DB 4; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MGFGRVLTFTSGVTNLFSNPFVKYKVAADYTSDDVREEGQLIFQNTPNRTWDCVLV 60
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DB 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
QY 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
DB 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
QY 181 VTDYKGETVHYAVQGDNSQVLLQILGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
DB 181 VTDYKGETVHYAVQGDNSQVLLQILGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
QY 241 LCNARCNIMGPNGPIHSAKFKSGKCAEMISMDSSQHSKDPRYGASPLHAKNAEMA 300
DB 241 LCNARCNIMGPNGPIHSAKFKSGKCAEMISMDSSQHSKDPRYGASPLHAKNAEMA 300
QY 301 RMLLKSGCNVNSTSSAGNTALHYGVNMRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKSGCNVNSTSSAGNTALHYGVNMRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTPDFTPTFLASKIGKLODLNHSIPARPAVILGSMRDEKR 420
DB 361 DNVEIMKALIVFGAEVDTPDFTPTFLASKIGKLODLNHSIPARPAVILGSMRDEKR 420
QY 421 THDHLCLDGGGVKGLIIQLLAIERKASGVAATKDLFDWYAGTSTGSLALAIHSKMA 480
DB 421 THDHLCLDGGGVKGLIIQLLAIERKASGVAATKDLFDWYAGTSTGSLALAIHSKMA 480
QY 481 YMGMYFRMKDEVFRGSRPYESGPLEBFLKREFEHTKMTDVARKPKMYLTGTLSDROPAS 540
DB 481 YMGMYFRMKDEVFRGSRPYESGPLEBFLKREFEHTKMTDVARKPKMYLTGTLSDROPAS 540

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QY 541 LHLFRYVDAPEYREBPFRNONVNLAPPAPSDQLVYRAASSGAAPTYRPNGRFLDGL 600
DB 541 LHLFRYVDAPEYREBPFRNONVNLAPPAPSDQLVYRAASSGAAPTYRPNGRFLDGL 600
QY 601 LANPPTLDANTEIHEYNODLIRKQANKYKKSIVSLGTGRSPQVPTCVDFRPSNPW 660
DB 601 LANPPTLDANTEIHEYNODLIRKQANKYKKSIVSLGTGRSPQVPTCVDFRPSNPW 660
QY 661 ELAKTYFGAEKELGRNVVDCCTPDGRP 687
DB 661 ELAKTYFGAEKELGRNVVDCCTPDGRP 687

RESULT 4
US-08-555-568B-23
Sequence 23, Application US/08555568B
Patent No. 5976854
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-555-568B-23

Query Match      99.6%; Score 3606.5; DB 2; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGFGRVLTFTSGVTNLFSNPFVKYKVAADYTSDDVREEGQLIFQNTPNRTWDCVLV 60
DB 1 MGFGRVLTFTSGVTNLFSNPFVKYKVAADYTSDDVREEGQLIFQNTPNRTWDCVLV 60
QY 61 NPNRSOSGFRFLFOLELEADLVNPHOYSSQLLPFYESSPOVLTHTVQLTDLIRNPSW 120
DB 61 NPNRSOSGFRFLFOLELEADLVNPHOYSSQLLPFYESSPOVLTHTVQLTDLIRNPSW 120
QY 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
DB 121 SVHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKDGELIVELVOYCHTOMD 180
QY 181 VTDYKGETVHYAVQGDNSQVLLQILGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240
DB 181 VTDYKGETVHYAVQGDNSQVLLQILGRNAVAGLNQVNNQGLTPLHLACQLGKQEMRVLL 240

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QY 241 LCNARCNIMGPNGYPHISAMKFSQKCAEMIISMSSQIHSKDPRYGASPLHAKNAEMA 300
DB 241 LCNARCNIMGPNGYPHISAMKFSQKCAEMIISMSSQIHSKDPRYGASPLHAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHGVNMRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKGCNVNSTSSAGNTALHGVNMRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNEMIKALIVFGAEVDPNDPFGETPTFLASKIGK-LQDLMTISRARKPAFTILGSRDEK 419
DB 361 DNEMIKALIVFGAEVDPNDPFGETPTFLASKIGK-LQDLMTISRARKPAFTILGSRDEK 420
QY 420 RTDHLCLDGGGVKGLIIQLIAIEKASGVAATKDLFDWAGSTGIIALAILHLSKSM 479
DB 421 RTDHLCLDGGGVKGLIIQLIAIEKASGVAATKDLFDWAGSTGIIALAILHLSKSM 480
QY 480 AYNRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 539
DB 481 AYNRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRARSSGAFTYFRPNRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRARSSGAFTYFRPNRFLDGG 600
QY 600 LLANNPTLDMTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNP 659
DB 601 LLANNPTLDMTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNP 660
QY 660 WELAKTVFGAKELGKRVVDDCTDPDGRP 687
DB 661 WELAKTVFGAKELGKRVVDDCTDPDGRP 688

RESULT 5

US-09-519-223-23 Application US/09519223
Patent No. 6274140
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (ERO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/519,223
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/555,568
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-519-223-23

Query Match 99.6%; Score 3606.5; DB 3; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 688; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGFGRVLTFTSGVTNLFSPNPFVKEVAVADYSSDRVREEGQLIFONTNRTWCVLV 60
DB 1 MGFGRVLTFTSGVTNLFSPNPFVKEVAVADYSSDRVREEGQLIFONTNRTWCVLV 60
QY 61 NPNNSGGRFLFQLELEADLVNPHOYSSQLPFYESSPOVLTHTVLQHTDLIRNHPW 120
DB 61 NPNNSGGRFLFQLELEADLVNPHOYSSQLPFYESSPOVLTHTVLQHTDLIRNHPW 120
QY 121 SVHLAVELGIRCFHRSRIISCANCAENEGCTPLHACRKDGELVELVOYCHTQMD 180
DB 121 SVHLAVELGIRCFHRSRIISCANCAENEGCTPLHACRKDGELVELVOYCHTQMD 180
QY 181 VTDYKGETVHYAVOGDNSQVLOLLGRNAVAGLQVNNQGLTPLHLACQLGKQEMRVLL 240
DB 181 VTDYKGETVHYAVOGDNSQVLOLLGRNAVAGLQVNNQGLTPLHLACQLGKQEMRVLL 240
QY 241 LCNARCNIMGPNGYPHISAMKFSQKCAEMIISMSSQIHSKDPRYGASPLHAKNAEMA 300
DB 241 LCNARCNIMGPNGYPHISAMKFSQKCAEMIISMSSQIHSKDPRYGASPLHAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHGVNMRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKGCNVNSTSSAGNTALHGVNMRNRPDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNEMIKALIVFGAEVDPNDPFGETPTFLASKIGK-LQDLMTISRARKPAFTILGSRDEK 419
DB 361 DNEMIKALIVFGAEVDPNDPFGETPTFLASKIGK-LQDLMTISRARKPAFTILGSRDEK 420
QY 420 RTDHLCLDGGGVKGLIIQLIAIEKASGVAATKDLFDWAGSTGIIALAILHLSKSM 479
DB 421 RTDHLCLDGGGVKGLIIQLIAIEKASGVAATKDLFDWAGSTGIIALAILHLSKSM 480
QY 480 AYNRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 539
DB 481 AYNRGMVFRMKDEVFRGSRPYESGPLEEFLKREFGEHTKMTDVRKPKVMLTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRARSSGAFTYFRPNRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRFNQNVNLRPPAOPSDQLVWRARSSGAFTYFRPNRFLDGG 600
QY 600 LLANNPTLDMTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNP 659
DB 601 LLANNPTLDMTEIHEYNODLIRKQANKVKLSIVSLGTGRSPQVPTCVDFRPSNP 660
QY 660 WELAKTVFGAKELGKRVVDDCTDPDGRP 687
DB 661 WELAKTVFGAKELGKRVVDDCTDPDGRP 688

RESULT 6

US-09-927-180-23 Application US/09927180
Patent No. 6645736
GENERAL INFORMATION:
APPLICANT: Jones, Simon
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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Job time : 123.588 secs

Publication No. US2003010482A1
GENERAL INFORMATION:
APPLICANT: Immunex Corp.
APPLICANT: Bird, Timothy
APPLICANT: Virca, G.D.
TITLE OF INVENTION: DEATH ASSOCIATED KINASE CONTAINING ANKYRIN REPEATS
FILE OF INVENTION: (DAKAR)
FILE REFERENCE: 2889-US
CURRENT APPLICATION NUMBER: US/10/299,327
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US/09/509,802
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 786
TYPE: PRT
ORGANISM: Mus sp.
US-10-299-327-2

Query Match 8.3%; Score 302; DB 14; Length 786;
Best Local Similarity 31.0%; Pred. No. 5.3e-18;
Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNHPWSVAHLAVELGIRECFHRSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVOYCHTOMDVTYKGETVFHYAVO-GDNSQVQLLGRNAVAGLQVNNQGLTPLHLACQ 229
DB 491 LLARKTSVNAKDEQWTLHFAAQNGDEASTRLLEKN--ASVNEVDFEGRTPMHVAQ 548
QY 230 LGQEMVRVLLCNARCNIMPGNGY-PIHSAMKFSQKCAEMIISDSSQIHSKDPRYGA 288
DB 549 HGOENIVRTLRRGVGVGLQKDAWPLHYAAWQGHLPVKKLAKQPGVSVNAQ-TLDGR 607
QY 289 SPLHWAK---NAEMARMLKRCGNVNSTSSAGNTALHVGVMNRFPDCAIVLLTHGANADA 345
DB 608 TPLHAAQQRHYRVARILIDLCSDVNICSLQAQTPHLVAAETGHTSTARLLHHRGAGKEA 667
QY 346 RGEHGNTPHLAMSKONVEMIKALIVFGAEVDTPNDPFGETPTFLASKIGKLO----- 397
DB 668 LTSEGYTALHAAQNGHLATVKLLIEEKADVMARGPLNQTALHLLAAARGHSEVVELVSA 727
QY 398 DLMHIS 403
DB 728 DLIDLS 733

RESULT 15
US-10-128-174-31
Sequence 31, Application US/10128174
Publication No. US20030199462A1
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
TITLE OF INVENTION: Methods and Compositions for Regulating Cellular Signaling
FILE REFERENCE: UM-06967
CURRENT APPLICATION NUMBER: US/10/128,174
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31
LENGTH: 786
TYPE: PRT
ORGANISM: Mus musculus
US-10-128-174-31

Query Match 8.3%; Score 302; DB 14; Length 786;
Best Local Similarity 31.0%; Pred. No. 5.3e-18;
Matches 95; Conservative 51; Mismatches 140; Indels 20; Gaps 9;

QY 112 DLIRNHPWSVAHLAVELGIRECFHRSRIISCANCAENEEGCTPLHLAC-RKGDGEILVE 170
DB 434 DLVLD-SSASLLHLAVEAGQEECVKWLNNANPNLTNRKGSTPLHMAVERKGRG--IVE 490
QY 171 LVOYCHTOMDVTYKGETVFHYAVO-GDNSQVQLLGRNAVAGLQVNNQGLTPLHLACQ 229
DB 491 LLARKTSVNAKDEQWTLHFAAQNGDEASTRLLEKN--ASVNEVDFEGRTPMHVAQ 548
QY 230 LGQEMVRVLLCNARCNIMPGNGY-PIHSAMKFSQKCAEMIISDSSQIHSKDPRYGA 288
DB 549 HGOENIVRTLRRGVGVGLQKDAWPLHYAAWQGHLPVKKLAKQPGVSVNAQ-TLDGR 607
QY 289 SPLHWAK---NAEMARMLKRCGNVNSTSSAGNTALHVGVMNRFPDCAIVLLTHGANADA 345
DB 608 TPLHAAQQRHYRVARILIDLCSDVNICSLQAQTPHLVAAETGHTSTARLLHHRGAGKEA 667
QY 346 RGEHGNTPHLAMSKONVEMIKALIVFGAEVDTPNDPFGETPTFLASKIGKLO----- 397
DB 668 LTSEGYTALHAAQNGHLATVKLLIEEKADVMARGPLNQTALHLLAAARGHSEVVELVSA 727
QY 398 DLMHIS 403
DB 728 DLIDLS 733

Search completed: December 15, 2004, 13:34:57


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QY 149 NBEQCTPLHACKRGDGEILVELVOYCHTQMDVTDYKGTVEHYAVQGDNSQVQLQL--G 206
Db 316 QPEGLSPLMIAVQNTQIETVSMWLDH- GADINILSSEGQNVLHVAATASSGDLIKILWET 374
QY 207 RNAVAGLNQVNOGLTPLHLACQLGKQEMVRVLLLCNARCNIMGPN- 254
Db 375 KKCETMINQTSNGYTPAYVA-----LINACLSNCQTLRGFGGGIQSSDSTQMAN 424
QY 255 PTHSANKFSQ--KGCAEMIISDSSOIHKSOPRYGASPLHWAKNAMARMMLKR--GCN 309
Db 425 PIIGAKRGKGLDEVSLRKMLELKQDGLTETPTGNTVHCAINKKCLILLMEKFRDQTD 484
QY 310 VNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKAL 369
Db 485 PEARNALQOTPLHTFVKDELGLVMTLSAYGVMDAQDINGNTPLHCAVTRGNTETARM 544
QY 370 IVFGAEVDPNDGFTPTFLASKIGKQLDLMHISRAR-----KPAFI----- 411
Db 545 LCLGAKPDIKNRYKESPRHIAARLTKAKMDIVRALIICGAGACDDGFGICAFGCMHKT 604
QY 412 -----LGSM-----RDEKRT 421
Db 605 GLTSCKTQLGSSSDSQSMEDRVKDIHVSNDNAASAPYFVLPDPTQVVEEAVERNETRA 664
QY 422 HDH-----LCLDGGGVKGLIIIIQLLIAIEKASGVATKDL 456
Db 665 FPHEEALKRVKNKELVEKKKTSNVINVLGDDGGIRGLVTVQMLICLEAFDLRPLIDY 724
QY 457 FQWAGTSTGGILALAILHKSMAVYRGMVFRMKDEVRFG-SRPYESGPLEFLKREFGE 515
Db 725 FQWIGATSTGCIYMTMTGGSRLKQRYLYLMEKQDLFDSWTRPYDTKTLETFIQRAFGA 784
QY 516 HTKMTDVRKPKVMTGLSDROPALHLFRNYDAPETVREPRENVNLRPPAQPSDQLV 575
Db 785 DRLMGDIKPRFFCTTVRADTFFVQLELLNRYLPISEKE---NNDLGF---TDPNELII 838
QY 576 WRAARSSGAAPTYFRPN-GRFLDGGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSI 634
Db 839 WKATRRSSAAPTYSASEGKFIDGGMISNNPVLDMSDIGFYNTTCQKWRIPKQVMDMGC 898
QY 635 VVSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGMVVDCTDPPGR 687
Db 899 VLSVGTGITPICVD-PSVFEMNDLFGMLR---GMKNLSLVVIDQATATEGAP 947

RESULT 9
US-10-369-493-6690
; Sequence 6690, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6690
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6690

Query Match 17.58; Score 634.5; DB 14; Length 1023;
Best Local Similarity 24.28; Pred. No. 3.2e-48;
Matches 187; Conservative 148; Mismatches 287; Indels 151; Gaps 21;

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QY 37 RVREBQILFQNTNRTWDCVLPNRSQSGRLLFQLELEAD--ALNVFHQYSQQLPFF 94
Db 204 RAKEEEL--KNKELYHLAITLYNENNEKYVMSLFRSHKLAADVVALCERCPENPELPRV 260
QY 95 YESSQV--LHTEVLQHLTLIRHPSVSAHLAVELGIRECFHH---SRIISCANCAE 148
Db 261 PFKVNIIDKYLHT-----IFHELDRNMTWKSVHISKIGLLEFFENMEKHLKLYNLIV 315
QY 149 NBEQCTPLHACKRGDGEILVELVOYCHTQMDVTDYKGTVEHYAVQGDNSQVQLQL--G 206
Db 316 QPEGLSPLMIAVQNTQIETVSMWLDH- GADINILSSEGQNVLHVAATASSGDLIKILWET 374
QY 207 RNAVAGLNQVNOGLTPLHLACQLGKQEMVRVLLLCNARCNIMGPN- 254
Db 375 KKCETMINQTSNGYTPAYVA-----LINACLSNCQTLRGFGGGIQSSDSTQMAN 424
QY 255 PTHSANKFSQ--KGCAEMIISDSSOIHKSOPRYGASPLHWAKNAMARMMLKR--GCN 309
Db 425 PIIGAKRGKGLDEVSLRKMLELKQDGLTETPTGNTVHCAINKKCLILLMEKFRDQTD 484
QY 310 VNSTSSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSKDNVEMIKAL 369
Db 485 PEARNALQOTPLHTFVKDELGLVMTLSAYGVMDAQDINGNTPLHCAVTRGNTETARM 544
QY 370 IVFGAEVDPNDGFTPTFLASKIGKQLDLMHISRAR-----KPAFI----- 411
Db 545 LCLGAKPDIKNRYKESPRHIAARLTKAKMDIVRALIICGAGACDDGFGICAFGCMHKT 604
QY 412 -----LGSM-----RDEKRT 421
Db 605 GLTSCKTQLGSSSDSQSMEDRVKDIHVSNDNAASAPYFVLPDPTQVVEEAVERNETRA 664
QY 422 HDH-----LCLDGGGVKGLIIIIQLLIAIEKASGVATKDL 456
Db 665 FPHEEALKRVKNKELVEKKKTSNVINVLGDDGGIRGLVTVQMLICLEAFDLRPLIDY 724
QY 457 FQWAGTSTGGILALAILHKSMAVYRGMVFRMKDEVRFG-SRPYESGPLEFLKREFGE 515
Db 725 FQWIGATSTGCIYMTMTGGSRLKQRYLYLMEKQDLFDSWTRPYDTKTLETFIQRAFGA 784
QY 516 HTKMTDVRKPKVMTGLSDROPALHLFRNYDAPETVREPRENVNLRPPAQPSDQLV 575
Db 785 DRLMGDIKPRFFCTTVRADTFFVQLELLNRYLPISEKE---NNDLGF---TDPNELII 838
QY 576 WRAARSSGAAPTYFRPN-GRFLDGGGLLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSI 634
Db 839 WKATRRSSAAPTYSASEGKFIDGGMISNNPVLDMSDIGFYNTTCQKWRIPKQVMDMGC 898
QY 635 VVSLGTGRSPQVPVTCVDFRPSNPWELAKTVFGAKELGMVVDCTDPPGR 687
Db 899 VLSVGTGITPICVD-PSVFEMNDLFGMLR---GMKNLSLVVIDQATATEGAP 947

RESULT 10
US-10-369-493-4998
; Sequence 4998, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4998
; LENGTH: 468

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SEQUENCE CHARACTERISTICS:
LENGTH: 292 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-927-180-19

Query Match 42.3%; Score 1531; DB 9; Length 292;
Best Local Similarity 100.0%; Pred. No. 5.2e-131; Indels 0; Gaps 0;
Matches 292; Conservative 0; Mismatches 0;

QY 396 LQDLMHISRARPFAILGSRMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 455
Db 1 LQDLMHISRARPFAILGSRMRDEKTHDHLCLDGGGVKGLIIQLLIAIEKASGVATKD 60

QY 456 LFDWVAGTSTGGILALAILHLSKSMAYRMGMFRMKDEVRFGSRPYSGPLEFLKREFGE 515
Db 61 LFDWVAGTSTGGILALAILHLSKSMAYRMGMFRMKDEVRFGSRPYSGPLEFLKREFGE 120

QY 516 HTKMTDVRKPKVMLTGTLSDROPAPLHLFRNYDAPETVREPRNQNNVLRPPAQPSDQLV 575
Db 121 HTKMTDVRKPKVMLTGTLSDROPAPLHLFRNYDAPETVREPRNQNNVLRPPAQPSDQLV 180

QY 576 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKGOANKVLSIV 635
Db 181 WRAARSSGAAPTYFRPNRFLDGLLANNPTLDAMTEIHEYNDLIRKGOANKVLSIV 240

QY 636 VSLGTGRSPQVPTCVDPVFRPSPNWLAKTVFGAKELGKMMVDCCTDPPGRP 687
Db 241 VSLGTGRSPQVPTCVDPVFRPSPNWLAKTVFGAKELGKMMVDCCTDPPGRP 292

RESULT 7
US-10-369-493-6865
; Sequence 6865, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6865
; LENGTH: 1071
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6865

Query Match 17.9%; Score 647.5; DB 14; Length 1071;
Best Local Similarity 27.0%; Pred. No. 2.3e-49;
Matches 194; Conservative 126; Mismatches 260; Indels 139; Gaps 20;

QY 69 FRLFQLEADALVNFHQSOLLPEYSSPQVLHTEVL---QHLTDLIRNHPSSVAH 124
Db 315 FSLFRATDKKDLMLHLCDKESFLTSLDMSTMRADILRSKIBELVIOIRLPHYHMH 374

QY 125 LVELGIRECFHRSRI-----ISCANCAENESEGTPLHLACRGDGEILVELVOY 174
Db 375 VAATDRLOFFSDGMKTKWNETLEPESQLRCLCHTENCYPVHLATMDRQKIVERLLEL 434

QY 175 CHTQMDVTYKGTVFHYAVQGNDSQVQLLGRNAVAG---LNQVNNQGLTPLHLACQLG 231
Db 435 DPTLFCETDKAGNVVHHV---NSSFCAQIINDRCQPASQHFIDERNMDGQSPLENAVSTA 491

QY 232 KOEMVRVLLLCNARCINMGPNGYPIHSAMKFSQKCAEMIISM-----DSS 277
Db 492 KPLVATFL-----ICKGAKFTGRDRNELFVAMTSKNAQSVVWLTDXP 535

QY 278 QIHSKDPRYGASPLHWAKNAEMARMLLKR-----GCNVNSTSSAGNTALHVGVMNRPDCA 333
Db 536 EIANERDALGNSAIHVALYKESLNALLNRKVELGLDIDVKNNAGETALLFITTRKPDLL 595

QY 334 IVLLT---HCANADARGEHNTPLHLAMS-----KONVEMIKALIVFGAEVDTPNDPGET 385
Db 596 PLLVTLTYAHGANNATDPHGNTALHKSAAALVDAKISLBECVKFLISAGSNPNKINDURGES 655

QY 386 PFLASKIKGLQDLMHISR-----RKPAFLG-----SMRDE----- 418
Db 656 PHLAASL-QNQEMLAAILKAGATRCPKGYKGRSNCRHDCSSAEDEYEBETLQIRIGNE 714

QY 419 -----KRTDHLCLDGGGVKGLIIQLLIAIEKASGVA 452
Db 715 SDYEKTEFTASEKLIQDTLDGSRRGKAKAVNLISMDGGGIRGLVIIQTLLIAIEERLGD 774

QY 453 TKDLPDWVAGTSTGGILALAILHLSKSMAYRMGMFRMKDEVRFG-SRPYESGPLEFLKR 511
Db 775 IFKYFDWSAGTSGSILMAGLATGKSLREMQQTYLLDKDRVDFGIMPPYDVTVQLEKFIQD 834

QY 512 EFGHTKMTDVRKPKVMLTGTLSDROPAPLHLFRNYDAPETVREPRNQNNVLRPPAQPS 571
Db 835 QGTGT-VWEIYFPRLMISAVNSEKLPVLEWARYKPAKV-----APETPK 881

QY 572 DQLVRAARSSGAAPTYFRPN-GRFLDGLLANNPTLDAMTEIHEYNDLIRKGOANKVK 630
Db 882 EMPLMALARSTAAAPVLFKPESEDYIDGGIISNNPALDLMSEVHAYNRELQLSGRKSDAV 941

QY 631 KLSIVVSLGTGRSPQVPTCVDPFR---PSNPHELAKTVFGAKELGKMMVDCCTDPPGRP 687
Db 942 QMNVLSFGTG---QIPSTVIETLSIDSNPLQSIKTI---KNLAAMFIDQATASEGAP 994

RESULT 8
US-10-369-493-6689
; Sequence 6689, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6689
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6689

Query Match 17.5%; Score 634.5; DB 14; Length 1023;
Best Local Similarity 24.2%; Pred. No. 3.2e-48;
Matches 187; Conservative 148; Mismatches 287; Indels 151; Gaps 21;

QY 37 RVREBQGLIFQNTNRTWDCVLVNPNSQSGFRFLQLEAD--ALVNFHQSOLLPPF 94
Db 204 RAKEEEL---KNKPLYHLAITYLNENNEKYVMSLFRSHKLADVVVALCERCENPELFRV 260

QY 95 YESSQV---LHTEVLQHLTDLIRNHPSSVAHLAVELGIRECFH---SRIISCANCAE 148
Db 261 FPKNVNIKDYLT-----IFHELDRNTMTKSVHISKIGLBYFENMKHKLKYLNLIV 315

Db 102 LCNARCNIMGPNYPIYSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 161
QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 162 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 221
QY 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGK----- 395
Db 222 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGRLVTRKAILTLTLRTVGAECFPPING 281
QY 396 -----LQDLMIHSRARKPAFTILGSMRDEKRTDHL 425
Db 282 VPBQCSAAPHFPSLERQPPISUNLQDLMIHSRARKPAFTILGSMRDEKRTDHL 341
QY 426 LCLDGGGVKGLIIQLIIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 485
Db 342 LCLDGGGVKGLIIQLIIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSMAVMRGM 401
QY 486 YFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 545
Db 402 YFRMKDEVFRGSRPYESGPLEEFKREFGEHTKMTDVRKPKVMLTGTLSDRQPAELHLFR 461
QY 546 NYDAPETVREPFRNQNVLNRPAPQSDQLVWRAARSSGAAPTFRPNGRFLDGLLANNP 605
Db 462 NYDAPETVREPFRNQNVLNRPAPQSDQLVWRAARSSGAAPTFRPNGRFLDGLLANNP 521
QY 606 TLDAMTEIHEYNDLIRKQANKVKKLSIVSLGTSRSPQVPTCVDFRPNPNWELAKT 665
Db 522 TLDAMTEIHEYNDLIRKQANKVKKLSIVSLGTSRSPQVPTCVDFRPNPNWELAKT 581
QY 666 VFGAKELGRKVVDCCTDPDGR 686
Db 582 VFGAKELGRKVVDCCTDPDGR 602

RESULT 5
US-09-927-180-17
; Sequence 17, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-927-180-17
Query Match 57.6%; Score 2084; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.3e-161; Indels 0; Gaps 0;
Matches 394; Conservative 0; Mismatches 0;
QY 1 MOFFGRLVNTSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MOFFGRLVNTSGVTNLFNSNPRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLPQLLEADALVNFHQYSSQLLPFYESSQVLHTEVQLHLDLIRNHPSW 120
Db 61 NPNRSQSGFRLPQLLEADALVNFHQYSSQLLPFYESSQVLHTEVQLHLDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHRIISCANCAENEECTPLHLACRKGDEIILVELVQYCHTQMD 180
Db 121 SVAHLAVELGIRECFHHRIISCANCAENEECTPLHLACRKGDEIILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVLQLGRNAVAGLNQNNQGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGPNYPIHSAMKFSQKCAEMIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKGCNVNSTSSAGNTALHVGVMNRNFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIG 394
Db 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIG 394
RESULT 6
US-09-927-180-19
; Sequence 19, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 19:
; TYPE: amino acid

QY 600 LLANNPTLDAMTEIHEYNODLIRKGOANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNODLIRKGOANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660

QY 660 WELAKTVFGAKELGKMWVDCCTDPDGRP 687
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688

RESULT 3

US-09-927-180-2
; Sequence 2, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-927-180-2
Query Match 91.2%; Score 3302.5; DB 9; Length 752;
Best Local Similarity 90.4%; Pred. No. 2.6e-292;
Matches 62; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
QY 1 MQPFGRLVNTFSGVTLNFSNPFPRVKEVAVADYTSRDRVEEGQLILFQNTPNRTWDCVLV 60
Db 1 MQPFGRLVNTLSSVTNLFNSNPFPRVKEISVADYTSHERVREEGQLILFQNASNRTWDCILV 60
QY 61 NPNRSQSGFRLLFQLEADALVNFHQYSQSLLPFYESSQVLHTEVQLHQLTDLIRNHPSW 120
Db 61 SPRNHSIGFRLLFQLEADALVNFQFSQPLPFYESSQVLHTEVQLHQLSDDLIRSHPSW 120
QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKGDSILVELVQYCHTQMD 180
Db 121 TVTHLAVELGIRCFHHSRIISCANSTENEGCTPLHLACRKGDSILVELVQYCHTQMD 180
QY 181 VTDYKGETVPHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDNKGETAHYAVQGDNSQVLQLLGNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240

QY 241 LCNARCNIMGPNGYPITHSANKFSQKCAEMIIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNIMGPNGYPHTANKFSQKCAEMIIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRGCVNNTSAGNTALHVGVMNRNFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
Db 301 RMLLKRGCDVSTSAAGNTALHVAVMNRNFDCAIIVLLTVGANAGTPEHNTPLHLAISK 360
QY 361 DNVEIMKALIVFGAEVDTNDGETPTFLASKIGK-LQDLMHISRARKPAFILGSRDEK 419
Db 361 DNVEIMKALIVFGAEVDTNDGETPTFAFNASKISKQLQDLMPIISRARKPAFILSSMRDEK 420
QY 420 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKSM 479
Db 421 RTHDHLCLDGGVKGKLIILQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHSKSM 480
QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFKREFGHEHTKMTDVRKPKVMLTGTLSRQPA 539
Db 481 AYMRGVYFRMKDEVFRGSRPYESGPLEEFKREFGHEHTKMTDVKPKVMLTGTLSRQPA 540
QY 540 ELHLFRNYDAPETVREPRENQNVNLPAPQSDOLVWRAARSSGAAPTYFRPNRGRLDGG 599
Db 541 ELHLFRNYDAPETVREPRENQNVNLPKPTQPADQLVWRAARSSGAAPTYFRPNRGRLDGG 600
QY 600 LLANNPTLDAMTEIHEYNODLIRKGOANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNQDMIRKGGCNKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 4

US-10-108-260A-3778
; Sequence 3778, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3778
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3778

Query Match 75.2%; Score 2723; DB 15; Length 667;
Best Local Similarity 73.3%; Pred. No. 2e-239;
Matches 543; Conservative 2; Mismatches 2; Indels 194; Gaps 2;

QY 1 MQPFGRLVNTFSGVTLNFSNPFPRVKEVAVADYTSRDRVEEGQLILFQNTPNRTWDCVLV 60
Db 1 MQPFGRLVNTFSGVTLNFSNPFPRVKEVAVADYTSRDRVEEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLLFQLEADALVNFHQYSQSLLPFYESSQVLHTEVQLHQLTDLIRNHPSW 120
Db 61 YPRNSQSGFRLLFQLEADALVNFHQYS- - - - - 89
QY 121 SVAHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKGDSILVELVQYCHTQMD 180
Db 90 - - - - - 89
QY 181 VTDYKGETVPHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 90 - - - - - QLGKQEMVRVLL 101
QY 241 LCNARCNIMGPNGYPITHSANKFSQKCAEMIIISMDSQIHSKDPYRGASPLHWAKNAEMA 300

LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-927-180-21

Query Match 100.0%; Score 3620; DB 9; Length 687;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPTNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPTNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLFPYESSQVLHTEVQLHQLTDLIRNHPSW 120
DB 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLFPYESSQVLHTEVQLHQLTDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQDGNQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQDGNQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNSTSSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHISRAKPAFILGSMRDEKR 420
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHISRAKPAFILGSMRDEKR 420
QY 421 THDHLCLDGGVKGLIIQLLIAIEKASGATKDLFDWVAGTSTGGIILALAILHLSKMA 480
DB 421 THDHLCLDGGVKGLIIQLLIAIEKASGATKDLFDWVAGTSTGGIILALAILHLSKMA 480
QY 481 YMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLTGLSDRQPAE 540
DB 481 YMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLTGLSDRQPAE 540
QY 541 LHLFRNYDAPETVREPRFNQVNLRPAPQSDQLVWRAARSSGAAPTYPNPGRFLDGGI 600
DB 541 LHLFRNYDAPETVREPRFNQVNLRPAPQSDQLVWRAARSSGAAPTYPNPGRFLDGGI 600
QY 601 LANNPDLDAWTEHYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTVCTDVRFPSPNW 660
DB 601 LANNPDLDAWTEHYNQDLIRKQANKVKLSIVVSLGTGRSPQVPTVCTDVRFPSPNW 660
QY 661 ELAKTVFGAKELGMVVDCCCTDPDGRP 687
DB 661 ELAKTVFGAKELGMVVDCCCTDPDGRP 687
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RESULT 2

US-09-927-180-23
Sequence 23, Application US/09927180
Patent No. US20020106364A1
GENERAL INFORMATION:

APPLICANT: Jones, Simon

Tang, Jim

TITLE OF INVENTION: Calcium Independent Phospholipase A2/B

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genetics Institute, Inc.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-927-180-23

Query Match 99.6%; Score 3606.5; DB 9; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

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QY 1 MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPTNRTWDCVLV 60
DB 1 MOFFGRLVNTFSGVTNLFSPNPRVKEVAVADYTSDDRVREEGQLILFQNTPTNRTWDCVLV 60
QY 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLFPYESSQVLHTEVQLHQLTDLIRNHPSW 120
DB 61 NPNRSQSGFRLFQLELEADALVNFHQSOLLFPYESSQVLHTEVQLHQLTDLIRNHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDEILVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQDGNQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQDGNQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
QY 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIMGPNGYPIHSAKFSQKCAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLKRCGNVNSTSSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLKRCGNVNSTSSAGNTALHVGWVRNRFDCAIIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHISRAKPAFILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDFGETPTFLASKIGK-LQDLMIHISRAKPAFILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGLIIQLLIAIEKASGATKDLFDWVAGTSTGGIILALAILHLSKSM 479
DB 421 RTHDHLCLDGGVKGLIIQLLIAIEKASGATKDLFDWVAGTSTGGIILALAILHLSKSM 480
QY 480 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLTGLSDRQPA 539
DB 481 AYMRGMYFRMKDEVFRGSRPYESGPLEEFLKREFGHTKMTDVRKPKVMTLTGLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRFNQVNLRPAPQSDQLVWRAARSSGAAPTYPNPGRFLDGG 599
DB 541 ELHLFRNYDAPETVREPRFNQVNLRPAPQSDQLVWRAARSSGAAPTYPNPGRFLDGG 600
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OM protein - protein search, using sw model

Run on: December 15, 2004, 13:13:21 ; Search time 120.588 Seconds
(without alignments)
2034.879 Million cell updates/sec

Title: US-10-612-668-21

Perfect score: 3620

Sequence: 1 MQFFGLVNTFGSVTNLFSN.....GAKELGKVVDDCTDPDGRP 687

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:**

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|---------------------|
| 1 | 3620 | 100.0 | 687 | 9 | US-09-927-180-21 |
| 2 | 3606.5 | 99.6 | 688 | 9 | US-09-927-180-23 |
| 3 | 3302.5 | 91.2 | 752 | 9 | US-09-927-180-2 |
| 4 | 2723 | 75.2 | 667 | 15 | US-10-108-260A-3778 |
| 5 | 2084 | 57.6 | 394 | 9 | US-09-927-180-17 |
| 6 | 1531 | 42.3 | 292 | 9 | US-09-927-180-19 |
| 7 | 647.5 | 17.9 | 1071 | 14 | US-10-369-493-6865 |
| 8 | 634.5 | 17.5 | 1023 | 14 | US-10-369-493-6889 |
| 9 | 634.5 | 17.5 | 1023 | 14 | US-10-369-493-6690 |
| 10 | 324.5 | 9.0 | 468 | 14 | US-10-369-493-4998 |
| 11 | 324 | 9.0 | 1330 | 15 | US-10-108-260A-3237 |
| 12 | 302 | 8.3 | 786 | 14 | US-10-164-080-2 |
| 13 | 302 | 8.3 | 786 | 14 | US-10-299-327-2 |

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| 14 | 302 | 8.3 | 786 | 14 | US-10-128-174-13 | Sequence 13, Appl |
| 15 | 302 | 8.3 | 786 | 14 | US-10-128-174-31 | Sequence 31, Appl |
| 16 | 302 | 8.3 | 786 | 14 | US-10-128-174-32 | Sequence 32, Appl |
| 17 | 302 | 8.3 | 786 | 14 | US-10-128-174-33 | Sequence 33, Appl |
| 18 | 302 | 8.3 | 787 | 10 | US-09-866-050A-334 | Sequence 334, Appl |
| 19 | 301.5 | 8.3 | 347 | 14 | US-10-128-174-30 | Sequence 30, Appl |
| 20 | 300.5 | 8.3 | 1724 | 9 | US-09-964-899-43 | Sequence 43, Appl |
| 21 | 300 | 8.3 | 1762 | 14 | US-10-205-194-117 | Sequence 117, Appl |
| 22 | 296 | 8.2 | 3913 | 15 | US-10-334-143-45 | Sequence 45, Appl |
| 23 | 290 | 8.0 | 720 | 15 | US-10-433-794-20 | Sequence 20, Appl |
| 24 | 290 | 8.0 | 765 | 14 | US-10-128-174-3 | Sequence 3, Appl |
| 25 | 290 | 8.0 | 765 | 14 | US-10-128-174-34 | Sequence 34, Appl |
| 26 | 290 | 8.0 | 765 | 14 | US-10-128-174-35 | Sequence 35, Appl |
| 27 | 290 | 8.0 | 765 | 14 | US-10-128-174-36 | Sequence 36, Appl |
| 28 | 290 | 8.0 | 765 | 14 | US-10-128-174-37 | Sequence 37, Appl |
| 29 | 290 | 8.0 | 765 | 14 | US-10-128-174-38 | Sequence 38, Appl |
| 30 | 290 | 8.0 | 765 | 14 | US-10-128-174-39 | Sequence 39, Appl |
| 31 | 290 | 8.0 | 765 | 14 | US-10-128-174-40 | Sequence 40, Appl |
| 32 | 290 | 8.0 | 765 | 14 | US-10-128-174-41 | Sequence 41, Appl |
| 33 | 290 | 8.0 | 765 | 14 | US-10-128-174-42 | Sequence 42, Appl |
| 34 | 290 | 8.0 | 765 | 14 | US-10-128-174-43 | Sequence 43, Appl |
| 35 | 290 | 8.0 | 765 | 14 | US-10-128-174-44 | Sequence 44, Appl |
| 36 | 290 | 8.0 | 765 | 15 | US-10-182-243-56 | Sequence 56, Appl |
| 37 | 284.5 | 7.9 | 784 | 14 | US-10-164-080-7 | Sequence 7, Appl |
| 38 | 284.5 | 7.9 | 784 | 15 | US-10-258-951-70 | Sequence 70, Appl |
| 39 | 282.5 | 7.8 | 784 | 14 | US-10-354-358-38 | Sequence 38, Appl |
| 40 | 282.5 | 7.8 | 784 | 14 | US-10-128-174-2 | Sequence 12, Appl |
| 41 | 279.5 | 7.7 | 784 | 16 | US-10-658-904-2 | Sequence 2, Appl |
| 42 | 279.5 | 7.7 | 784 | 16 | US-10-648-593-153 | Sequence 153, Appl |
| 43 | 278.5 | 7.7 | 1053 | 14 | US-10-291-172-343 | Sequence 343, Appl |
| 44 | 278.5 | 7.7 | 1053 | 15 | US-10-221-278-343 | Sequence 343, Appl |
| 45 | 273.5 | 7.6 | 1704 | 14 | US-10-369-978-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1

US-09-927-180-21
; Sequence 21, Application US/09927180
; Patent No. US20020106364A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/927,180
; FILING DATE: 09-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/519,223
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:

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Db 121 SVAHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKGDSBILVELVOYCHTQMD 180
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QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
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Db 361 DNVEMIKALIVFGAEVDTNPNDFGTPTFLASKIG 394

RESULT 15

US-09-519-223-17
; Sequence 17, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/519,223
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/555,568
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-519-223-17

Query Match 57.6%; Score 2084; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.6e-217;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MQFFGRLVNTFSGVTNLFNSNPFPRKVEAVADYTSDDRVREGQLILFQNTPNRTWDCVLV 60

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Db 61 NPRNSQSGRLFOLELEADALVNFHQYSSQLLPFYESSQVLTHTVQLHQLTDLIRNHPW 120
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Db 121 SVAHLAVELGIRCFHHSRIISCANCAENEGCTPLHLACRKGDSBILVELVOYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
Db 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
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QY 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
Db 301 RMLLKRCGNVNSTSSAGNTALHVGVMNRFDCAIIVLLTHGANADARGEHGNTPHLAMSK 360
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Db 361 DNVEMIKALIVFGAEVDTNPNDFGTPTFLASKIG 394

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Job time : 37.0255 secs

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QY 660 WELAKTVFGAKELGKMVDDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMVDDCCTDPDGR 687

RESULT 13
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; Sequence 2, Application PC/TUS9508069
; GENERAL INFORMATION:
; APPLICANT: GENETICS INSTITUTE, INC.
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08069
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08069-2

Query Match 91.2%; Score 3302.5; DB 5; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MOFFGRLVNTSGVTLNLSNPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MOFFGRLVNTLSVTLNLSNPNFRVKEISVADYTSHERVREEGQLILFQNASRTWDCVLV 60
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Db 61 SPNPHSGFRLQLESEADALVNFQFSQQLPPFYESSQVLHVEVQLHLSLIRSHPSW 120
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Db 121 TVTHLAVALGIRECFHSHRIISCANSTENEECTPLHLACRGDSEILVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLLGRNAVAGLNQVNNQGLTPLHLACOLGKQEMVRVLL 240
Db 181 VTDNKGTAHFHYAVQGDNSQVLLGKNASAGLNQVNNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNTINGPYPIHSAKTSQKGCABMIIISDSSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNNVGPSPFIHTAMKFSQKGCABMIIISDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRGCNNVNTSSAGNTALHVGWNRNPFDCAVILLTHGANADARGEHNTPLHLASK 360
Db 301 RMLLRGCDDVDSAGNTALHVAVMNRNFDVCMVLLTYGANAGTPGEGHNTPLHLATSK 360
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Db 361 DNVMEMIKALIVFGAEVDTNDPFGETPTAFMASKISQLOQLMPLISRAKPAFILSSMRDEK 420
QY 420 RTHDHLCLLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKSM 479
Db 421 RIHDLCLLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGILALAILHLSKSM 480
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Db 481 AYMRGMYFRMKDEVFRGSRPYSGPLEEFLEKREFGHTKMTDVRKPKVMTLGTLSDRQA 540
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Db 541 ELHLFRNYDAPETVREPRNQNVNLRPPAQPDSQDLVWRAARSSGAAPTFRPGRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNDLIRKQKQKXKLSIVVSLGTGRSPQVPTCDVDFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNDLIRKQKQKXKLSIVVSLGTGRSPQVPTCDVDFRPSNP 660
QY 660 WELAKTVFGAKELGKMVDDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMVDDCCTDPDGR 687

RESULT 14
US-08-555-568B-17
; Sequence 17, Application US/085555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/555.568B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5951
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-17

Query Match 57.6%; Score 2084; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 2.6e-217;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOFFGRLVNTSGVTLNLSNPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
Db 1 MOFFGRLVNTSGVTLNLSNPNFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGFRLQLELEADALVNFHQYSSQLLPFYESSPQVLHTEVQLHQLTLIRNHPSW 120

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/555,568
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-519-223-2

Query Match 91.2%; Score 3302.5; DB 3; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
 QY 1 MQPFGRLVNTSGVTLNFSNPRVKEVAVADYTSDDVREEGQLILFQNTPTNRWDCVLL 60
 DB 1 MQPFGRLVNTSSVTLNFSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60
 QY 61 NPNRSQSGFRLFQLEADALVNFHQSQQLPPFYESSQVLTHTVQLHLDLIRNHPWS 120
 DB 61 SPNPHSGFRLFQLESEADALVNFQFSQQLPPFYESSQVLTHTVQLHLDLIRSHPSW 120
 QY 121 SVHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDDGILVELVQYCHTQMD 180
 DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSILVELVQYCHAQMD 180
 QY 181 VTDYKGTVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVRVLL 240
 DB 181 VTDNKGTAFHYAVQGDNSQVLLQGLGNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
 QY 241 LCNARCNMGPNYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
 DB 241 LCNARCNVMPGSPFIHTAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
 QY 301 RMLKRGCVNNTSSAGNTALHVGVRNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCDVDTSAAGNTALHVAVMNRNFDVCMVLLTYGANAGTPEHGNTPHLAISK 360
 QY 361 DNMEMIKALIVFGAEVDTNDPFGTETPLASKIGK-LQDLMIHSRARKPAFILGSRDEK 419
 DB 361 DNMEMIKALIVFGAEVDTNDPFGTETPAFWASKISKQLQDLMPISARKPAFILSSMRDEK 420
 QY 420 RTHDHLCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSWM 479
 DB 420 RTHDHLCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSWM 479
 QY 480 AYRGMVFRMKDEVRGSRYSGLPEELKRFEGEHTMTDVRKPKVMTGLTSLDRQA 539
 DB 481 AYRGMVFRMKDEVRGSRYSGLPEELKRFEGEHTMTDVRKPKVMTGLTSLDRQA 540
 QY 540 ELHLFRNYDAPETVRPRFNQVNLPPAPQPSQVLVRAARSSGAAPTFRPNGRFLDGG 599
 DB 541 ELHLFRNYDAPETVRPRFNQVNLPPAPQPSQVLVRAARSSGAAPTFRPNGRFLDGG 600
 QY 600 LLANPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTCDVDFRPSNP 659
 DB 601 LLANPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPTCDVDFRPSNP 660
 QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
 DB 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 12
 US-09-927-180-2
 ; Sequence 2, Application US/09927180

; Patent No. 6645736
 ; GENERAL INFORMATION:
 ; APPLICANT: Jones, Simon
 ; Tang, Jim
 ; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genetics Institute, Inc.
 ; STREET: 87 CambridgePark Drive
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02140
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION NUMBER: US/09/927,180
 ; FILING DATE: 09-Aug-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/519,223
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brown, Scott A.
 ; REGISTRATION NUMBER: 32,724
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 498-8224
 ; TELEFAX: (617) 876-5851
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 752 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-09-927-180-2

Query Match 91.2%; Score 3302.5; DB 4; Length 752;
 Best Local Similarity 90.4%; Pred. No. 0;
 Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
 QY 1 MQPFGRLVNTSGVTLNFSNPRVKEVAVADYTSDDVREEGQLILFQNTPTNRWDCVLL 60
 DB 1 MQPFGRLVNTSSVTLNFSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60
 QY 61 NPNRSQSGFRLFQLEADALVNFHQSQQLPPFYESSQVLTHTVQLHLDLIRNHPWS 120
 DB 61 SPNPHSGFRLFQLESEADALVNFQFSQQLPPFYESSQVLTHTVQLHLDLIRSHPSW 120
 QY 121 SVHLAVELGIRECFHHSRIISCANCAENEGCTPLHLACRKGDDGILVELVQYCHTQMD 180
 DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEGCTPLHLACRKGDSILVELVQYCHAQMD 180
 QY 181 VTDYKGTVFHYAVQGDNSQVLLQGLGRNAVAGLNQVNNQGLTPLHLACOLGQKQEMVRVLL 240
 DB 181 VTDNKGTAFHYAVQGDNSQVLLQGLGNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
 QY 241 LCNARCNMGPNYPIHSAKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
 DB 241 LCNARCNVMPGSPFIHTAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
 QY 301 RMLKRGCVNNTSSAGNTALHVGVRNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
 DB 301 RMLKRGCDVDTSAAGNTALHVAVMNRNFDVCMVLLTYGANAGTPEHGNTPHLAISK 360
 QY 361 DNMEMIKALIVFGAEVDTNDPFGTETPLASKIGK-LQDLMIHSRARKPAFILGSRDEK 419
 DB 361 DNMEMIKALIVFGAEVDTNDPFGTETPAFWASKISKQLQDLMPISARKPAFILSSMRDEK 420
 QY 420 RTHDHLCLDGGVKGGLIIQLLIAIEKASGVATKDLFDWVAGTSTGGILALAILHKSWM 479

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QY 301 RMLKRGCVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
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Db 301 RMLKRGCDVDSISAGNTALHVAVMNRFDCAI VLLTHGANAGTGEHNTPLHLAISK 360
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QY 361 DNVMEMIKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 DNVMEMIKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
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QY 420 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGTLALAILHLSKSM 479
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGTLALAILHLSKSM 480
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 480 AYMRGMVFRMKDEVPFRGSRPYESGPLEELKREFEGEHTKMTDVRKPKVMLTGTLSDRQA 539
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 AYMRGMVFRMKDEVPFRGSRPYESGPLEELKREFEGEHTKMTDVRKPKVMLTGTLSDRQA 540
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QY 540 ELHLFRNYDAPETVREPRFNQNVLRPPAQPSDQLVWRAARSSGAAPTFRPGRFLDGG 599
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Db 541 ELHLFRNYDAPETVREPRFNQNVLRPPAQPSDQLVWRAARSSGAAPTFRPGRFLDGG 600
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QY 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSI VVSLGTGRSPQVPTCDVFRPSPNP 659
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Db 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSI VVSLGTGRSPQVPTCDVFRPSPNP 660
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
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RESULT 10

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US-08-555-568B-2
; Sequence 2, Application US/08555568B
; Patent No. 5976854
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-555-568B-2
Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
QY 1 MQFFGRLVNTLSSVNLFSNPRFRVKEISVADYTSHERVREEGQLILFQNSRNTWDCILV 60
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Db 1 MQFFGRLVNTLSSVNLFSNPRFRVKEISVADYTSHERVREEGQLILFQNSRNTWDCILV 60
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QY 61 NPNRSGSGLRLQLLEADALVNFHOYSQQLLPFFYESSQVLTHTVQLHLTDLIRNHPWS 120
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Db 61 SPNPHSGSGLRLQLLEADALVNFHOYSQQLLPFFYESSQVLTHTVQLHLTDLIRNHPWS 120
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QY 121 SYAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRKGDDGSEILVELVOYCHTOMD 180
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Db 121 TYTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRKGDSSEILVELVOYCHAQMD 180
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QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNQVNNQGLTPLHLACQLGKQEMVRVLL 240
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Db 181 VTDNKGETAFAHYAVQGDNSQVLQLLGNASAGLNQVNNQGLTPLHLACQMGQEMVRVLL 240
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QY 241 LCNARCNMGPNYGIPIHSAMKFSQGCABMIISMSSQIHSKDPYRGASPLHWAKNAEMA 300
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Db 241 LCNARCNMGPSGFPPIHTAMKFSQGCABMIISMSSQIHSKDPYRGASPLHWAKNAEMA 300
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QY 301 RMLLXRGCVNSTSSAGNTALHVGVMNRFDCAI VLLTHGANADARGEHNTPLHLAMSK 360
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Db 301 RMLLXRGCDVDSISAGNTALHVAVMNRFDCAI VLLTHGANAGTGEHNTPLHLAISK 360
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QY 361 DNVMEMIKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 419
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Db 361 DNVMEMIKALIVFGAEVDTNDPGETPTFLASKIGK-LQDLMIHSRARKPAFILGSMRDEK 420
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QY 420 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGTLALAILHLSKSM 479
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Db 421 RTHDHLCLDGGVKGVLIIQLLIAIEKASGVATKDLFDWVAGTSGGTLALAILHLSKSM 480
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QY 480 AYMRGMVFRMKDEVPFRGSRPYESGPLEELKREFEGEHTKMTDVRKPKVMLTGTLSDRQA 539
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 AYMRGMVFRMKDEVPFRGSRPYESGPLEELKREFEGEHTKMTDVRKPKVMLTGTLSDRQA 540
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QY 540 ELHLFRNYDAPETVREPRFNQNVLRPPAQPSDQLVWRAARSSGAAPTFRPGRFLDGG 599
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Db 541 ELHLFRNYDAPETVREPRFNQNVLRPPAQPSDQLVWRAARSSGAAPTFRPGRFLDGG 600
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QY 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSI VVSLGTGRSPQVPTCDVFRPSPNP 659
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Db 601 LLANNPTLDAMTEIHEYNQDLIRKQANKVKLSI VVSLGTGRSPQVPTCDVFRPSPNP 660
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QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687
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RESULT 11

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US-09-519-223-2
; Sequence 2, Application US/09519223
; Patent No. 6274140
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
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Db 541 ELHLFRNYDAPEVIREPRFNQINLKPTQPADQLVWRAARSSGAAPTFRNGRFLDGG 600
QY 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNQDMIRKQGNKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 8
US-08-422-106-2
; Sequence 2, Application US/08422106
; Patent No. 5589170
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,106
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-422-106-2

Query Match 91.2%; Score 3302.5; DB 1; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGLRLVNTFSQVTLNFSNPRVKEVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
Db 1 MQFFGLRLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60

QY 61 NPNRSQSGFRLFOLELEADALVNFHQYSSQLLPFYESSQVLTHTVQLHLDLIRNHPSW 120
Db 61 SPNPHSGFRLFOLESEADALVNFQFSSQLPPFYESSQVLTHTVQLHLDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180
Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240
Db 181 VTDNGETAFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240

QY 241 LCNARCNMGPNGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNMGPSGPFPIHTAMKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300

QY 301 RMLLKGCNNVSTSSAGNTALHVGVMNRNFDCAI VLLTHCANADARGEHNTPLHLAMSK 360
Db 301 RMLLKGCDDVSTSSAGNTALHVGVMNRNFDCAI VLLTHCANADARGEHNTPLHLAMSK 360

QY 361 DNVEIMKALIVFAEVDTPNDTFTFLASKICK-LQDLMIHSRARKPAFIIGSNRDEK 419
Db 361 DNMEMIKALIVFAEVDTPNDTFTFAFMAKISKQLQDLMLPSRARKPAFIIGSNRDEK 420

QY 420 RTHDHLCLDGGVGKGLIIQLLIAIEKASGVATKOLFQWVAGTSTGGILALAILHKSMM 479

Db 421 RIHDHLLCLDGGVGKGLVIQLLIAIEKASGVATKOLFQWVAGTSTGGILALAILHKSMM 480
QY 480 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLKREFEHGTQTDVVRKPKVMLTGTLSDRQPA 539
Db 481 AYMRGMYFRMKDEVPFRGSRPYESGPLEBFLKREFEHGTQTDVVRKPKVMLTGTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRFNQINLRPPAPQSDQLVWRAARSSGAAPTFRNGRFLDGG 599
Db 541 ELHLFRNYDAPETVREPRFNQINLRPPAPQSDQLVWRAARSSGAAPTFRNGRFLDGG 600

QY 600 LLANNPTLDAMTEIHEYNQDLIRKQANKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 659
Db 601 LLANNPTLDAMTEIHEYNQDMIRKQGNKVKKLSIVVSLGTGRSPQVPVTCVDVFRPSNP 660
QY 660 WELAKTVFGAKELGKMWVDCCTDPDGR 686
Db 661 WELAKTVFGAKELGKMWVDCCTDPDGR 687

RESULT 9
US-08-735-716-2
; Sequence 2, Application US/08735716
; Patent No. 5840511
; GENERAL INFORMATION:
; APPLICANT: Jones, Simon
; APPLICANT: Tang, Jim
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/735,716
; FILING DATE: 23-OCT-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/281,193
; FILING DATE: 27-JUL-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-735-716-2

Query Match 91.2%; Score 3302.5; DB 2; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MQFFGLRLVNTFSQVTLNFSNPRVKEVADYTSDDRVREEGQLILFQNTNRTWDCVLV 60
Db 1 MQFFGLRLVNTLSSVTNLFNSNPRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60

QY 61 NPNRSQSGFRLFOLELEADALVNFHQYSSQLLPFYESSQVLTHTVQLHLDLIRNHPSW 120
Db 61 SPNPHSGFRLFOLESEADALVNFQFSSQLPPFYESSQVLTHTVQLHLDLIRNHPSW 120

QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180
Db 121 TVTHLAVELGIRECFHHSRIISCANSTENEEGCTPLHLACRKGDSILVELVOYCHTQMD 180

QY 181 VTDYKGETVFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240
Db 181 VTDNGETAFHYAVQGDNSQVQLLGRNAVAGLNQVNNQGLTPLHLACOLGQEMVRVLL 240

QY 241 LCNARCNMGPNGYPIHSAKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300
Db 241 LCNARCNMGPSGPFPIHTAMKFSQKGAEMIISMDSQIHSKDPYRGASPLHWAKNAEMA 300

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/927,180
FILING DATE: 09-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/519,223
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-927-180-23

Query Match 99.6%; Score 3606.5; DB 4; Length 688;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 686; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 MQFFGRLVNTFSGVTNLFNSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTFSGVTNLFNSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
QY 61 NPNRSQSGRLPQLELEADALVNFHOYSQQLPFFYESSQVLTHTVQLHLDLIRNHPWS 120
DB 61 NPNRSQSGRLPQLELEADALVNFHOYSQQLPFFYESSQVLTHTVQLHLDLIRNHPWS 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRGDGGELVELVQYCHTQMD 180
DB 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRGDGGELVELVQYCHTQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240
QY 241 LCNARCNIINGPYTHSANKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIINGPYTHSANKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
QY 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
DB 301 RMLLRKGCNVNSTSAGNTALHVGVMNRFDCAIVLLTHGANADARGEHNTPLHLAMSK 360
QY 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGTLALAILHKSXM 479
DB 420 RTHDHLCLDGGVKGIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGTLALAILHKSXM 480
QY 480 AYMRGMVFRMKDEVPFRGSRPYESGPLEEFLEKFEFGHTKMTDVRPKVMTLCTLSDRQPA 539
DB 480 AYMRGMVFRMKDEVPFRGSRPYESGPLEEFLEKFEFGHTKMTDVRPKVMTLCTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRENQNVNLRPPAQPDSQDLVWRAARSSGAAPTYYFRPNRFLDGG 599
DB 540 ELHLFRNYDAPETVREPRENQNVNLRPPAQPDSQDLVWRAARSSGAAPTYYFRPNRFLDGG 600
QY 600 LLANNPTLDAMTEIHYNDLIRKQANKVKKLSIVVSLGTRSGSQVPTCVDFRPSNP 659
DB 600 LLANNPTLDAMTEIHYNDLIRKQANKVKKLSIVVSLGTRSGSQVPTCVDFRPSNP 660

QY 660 WELAKTVFGAKELGKMWVDCCTDPDGRP 687
DB 661 WELAKTVFGAKELGKMWVDCCTDPDGRP 688

RESULT 7

US-08-281-193-2
Sequence 2, Application US/08281193
Patent No. 5466595
GENERAL INFORMATION:
APPLICANT: Jones, Simon
APPLICANT: Tang, Jim
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B
NUMBER OF SEQUENCES: 15
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/281,193
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-281-193-2

Query Match 91.2%; Score 3302.5; DB 1; Length 752;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 621; Conservative 31; Mismatches 34; Indels 1; Gaps 1;
QY 1 MQFFGRLVNTFSGVTNLFNSNPRFRVKEVAVADYTSDDRVREEGQLILFQNTPNRTWDCVLV 60
DB 1 MQFFGRLVNTLSSVNTLNFNSNPRFRVKEISVADYTSHERVREEGQLILFQNASRNTWDCILV 60
QY 61 NPNRSQSGRLPQLELEADALVNFHOYSQQLPFFYESSQVLTHTVQLHLDLIRNHPWS 120
DB 61 SPRNPHSGRLPQLESEADALVNFQFSQQLPFFYESSQVLTHTVQLHLDLIRSHPSW 120
QY 121 SVAHLAVELGIRECFHHSRIISCANCAENEECTPLHLACRGDGGELVELVQYCHTQMD 180
DB 121 TVTHLAVELGIRECFHHSRIISCANSTENEECTPLHLACRGDSEILVELVQYCHAQMD 180
QY 181 VTDYKGETVFHYAVQGDNSQVLQLLGRNAVAGLNVNNOGLTPLHLACQLGKQEMVRVLL 240
DB 181 VTDNKGETAFAHYAVQGDNSQVLQLLGNASAGLNQVKNQGLTPLHLACQMGKQEMVRVLL 240
QY 241 LCNARCNIINGPYTHSANKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
DB 241 LCNARCNIINGPSPFIHTAMKFSQKCAEMIIISMDSSQIHSKDPYRGASPLHWAKNAEMA 300
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DB 301 RMLLRKGCVDVSTSAAGNTALHVAVMNRFDCAIVLLTHGANADARGEHNTPLHLAISK 360
QY 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 419
DB 361 DNVEIMKALIVFGAEVDTNDPFGTPTFLASKIGK-LQDLMIHSRARKPAFTILGSMRDEK 420
QY 420 RTHDHLCLDGGVKGIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGTLALAILHKSXM 479
DB 421 RTHDHLCLDGGVKGIIIIQLLIAIEKASGVATKDLFDWVAGTSTGGTLALAILHKSXM 480
QY 480 AYMRGMVFRMKDEVPFRGSRPYESGPLEEFLEKFEFGHTKMTDVRPKVMTLCTLSDRQPA 539
DB 481 AYMRGMVFRMKDEVPFRGSRPYESGPLEEFLEKFEFGHTKMTDVRPKVMTLCTLSDRQPA 540
QY 540 ELHLFRNYDAPETVREPRENQNVNLRPPAQPDSQDLVWRAARSSGAAPTYYFRPNRFLDGG 599